(X63617) GAR1 [Saccharomyces cerevisiae] >gi_487935 (U00060) Gar1p: Small nucleolar RNA protein required for pre-rRNA splicing [Saccharomyces cerevisiae]

Seq. No.	220059
Seq. ID	LIB3149-039-Q1-K1-F12
Method	BLASTX
NCBI GI	g4432837
BLAST score	219
E value	8.0e-18
Match length	132
% identity	42
NCBI Description	(AC006283) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220060
Seq. ID	LIB3149-039-Q1-K1-F3
Method	BLASTX
NCBI GI	g4490332
BLAST score	344
E value	2.0e-32
Match length	119
% identity	59
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	220061
Seq. ID	LIB3149-039-Q1-K1-F4
Method	BLASTX
NCBI GI	g4098129
BLAST score	700
E value	4.0e-74
Match length	138
% identity	96
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	220062
Seq. ID	LIB3149-039-Q1-K1-F5
Method	BLASTN
NCBI GI	g1777727
BLAST score	51
E value	5.0e-20
Match length	160
% identity	82
NCBI Description	Gossypium hirsutum 18S ribosomal RNA gene, partial sequence

Seq. No.	220063
Seq. ID	LIB3149-039-Q1-K1-F6
Method	BLASTX
NCBI GI	g2190992
BLAST score	346
E value	1.0e-32
Match length	104
% identity	64
NCBI Description	(AF004358) glutathione S-transferase TSI-1 [Aegilops tauschii]

Seq. No.	220064
Seq. ID	LIB3149-039-Q1-K1-F7

Method	BLASTX
NCBI GI	g1771780
BLAST score	533
E value	1.0e-54
Match length	132
% identity	83
NCBI Description	(Y10024) ubiquitin extension protein [Solanum tuberosum]

Seq. No.	220065
Seq. ID	LIB3149-039-Q1-K1-G1
Method	BLASTX
NCBI GI	g1346524
BLAST score	390
E value	7.0e-38
Match length	125
% identity	67
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi_497900 (M73430) S-adenosyl methionine synthetase [Populus deltoides]

Seq. No.	220066
Seq. ID	LIB3149-039-Q1-K1-G12
Method	BLASTX
NCBI GI	g3122703
BLAST score	289
E value	5.0e-26
Match length	76
% identity	74
NCBI Description	60S RIBOSOMAL PROTEIN L23A >gi_2641201 (AF031542) ribosomal protein L23a [Fritillaria agrestis]

Seq. No.	220067
Seq. ID	LIB3149-039-Q1-K1-G5
Method	BLASTX
NCBI GI	g1173043
BLAST score	213
E value	4.0e-17
Match length	48
% identity	88
NCBI Description	60S RIBOSOMAL PROTEIN L38 >gi_479441_pir__S33899 ribosomal protein L38 - tomato (cv. Moneymaker) >gi_313027_emb_CAA49599_ (X69979) ribosomal protein L38 [Lycopersicon esculentum]

Seq. No.	220068
Seq. ID	LIB3149-039-Q1-K1-G9
Method	BLASTX
NCBI GI	g1709061
BLAST score	286
E value	3.0e-34
Match length	131
% identity	53
NCBI Description	PROBABLE METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE PRECURSOR (ACYLATING) (MMSDH) >gi_3875820_emb_CAA88946_ (Z49127) similar to methylmalonate-semialdehyde dehydrogenase; cDNA EST EMBL:Z14764 comes from this gene;

cDNA EST EMBL:Z14949 comes from this gene; cDNA EST EMBL:D26762 comes from this gene; cDNA EST EMBL:D26766 comes from thi

Seq. No.	220069
Seq. ID	LIB3149-039-Q1-K1-H2
Method	BLASTX
NCBI GI	g567893
BLAST score	155
E value	2.0e-10
Match length	77
% identity	48
NCBI Description	(L37382) beta-galactosidase-complementation protein [Cloning vector]

Seq. No.	220070
Seq. ID	LIB3149-039-Q1-K1-H4
Method	BLASTX
NCBI GI	g2829899
BLAST score	317
E value	3.0e-29
Match length	140
% identity	45
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	220071
Seq. ID	LIB3149-039-Q1-K1-H7
Method	BLASTX
NCBI GI	g1113861
BLAST score	208
E value	1.0e-16
Match length	84
% identity	55
NCBI Description	(U39930) nitrate reductase [Chlorella vulgaris] >gi_1113863 (U39931) nitrate reductase [Chlorella vulgaris]

Seq. No.	220072
Seq. ID	LIB3149-039-Q1-K1-H8
Method	BLASTX
NCBI GI	g3549669
BLAST score	173
E value	1.0e-12
Match length	49
% identity	71
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	220073
Seq. ID	LIB3149-040-Q1-K1-A12
Method	BLASTX
NCBI GI	g2911042
BLAST score	465
E value	1.0e-46
Match length	135
% identity	69
NCBI Description	(AL021961) Phosphoglycerate dehydrogenase - like protein

[Arabidopsis thaliana]

Seq. No.	220074
Seq. ID	LIB3149-040-Q1-K1-A2
Method	BLASTX
NCBI GI	g3169028
BLAST score	165
E value	2.0e-11
Match length	65
% identity	48
NCBI Description	(AL023702) putative cationic amino acid transporter [Streptomyces coelicolor]

Seq. No.	220075
Seq. ID	LIB3149-040-Q1-K1-A5
Method	BLASTX
NCBI GI	g4544432
BLAST score	472
E value	2.0e-47
Match length	135
% identity	70
NCBI Description	(AC006955) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana]

Seq. No.	220076
Seq. ID	LIB3149-040-Q1-K1-A7
Method	BLASTX
NCBI GI	g2842480
BLAST score	492
E value	8.0e-50
Match length	116
% identity	53
NCBI Description	(AL021749) ADP, ATP carrier-like protein [Arabidopsis thaliana]

Seq. No.	220077
Seq. ID	LIB3149-040-Q1-K1-A8
Method	BLASTX
NCBI GI	g2760325
BLAST score	293
E value	2.0e-26
Match length	127
% identity	48
NCBI Description	(AC002130) F1N21.10 [Arabidopsis thaliana]

Seq. No.	220078
Seq. ID	LIB3149-040-Q1-K1-A9
Method	BLASTX
NCBI GI	g1172977
BLAST score	553
E value	6.0e-57
Match length	124
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	220079

Seq. ID	LIB3149-040-Q1-K1-B1
Method	BLASTX
NCBI GI	g1076314
BLAST score	511
E value	5.0e-52
Match length	110
% identity	85
NCBI Description	cystathionine gamma-lyase (EC 4.4.1.1) 1 - Arabidopsis thaliana (fragment) >gi_499166_emb_CAA56143_ (X79707) CYS1 [Arabidopsis thaliana]

Seq. No.	220080
Seq. ID	LIB3149-040-Q1-K1-B10
Method	BLASTX
NCBI GI	g3219353
BLAST score	195
E value	3.0e-15
Match length	39
% identity	90
NCBI Description	(AF061514) manganese superoxide dismutase [Gossypium hirsutum]

Seq. No.	220081
Seq. ID	LIB3149-040-Q1-K1-B3
Method	BLASTX
NCBI GI	g3915847
BLAST score	649
E value	3.0e-68
Match length	134
% identity	91
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	220082
Seq. ID	LIB3149-040-Q1-K1-B5
Method	BLASTX
NCBI GI	g994736
BLAST score	142
E value	5.0e-09
Match length	53
% identity	55
NCBI Description	(M18327) LacOPZ-alpha peptide from pUC9; putative [cloning vectors] >gi_994738 (M18328) LacOPZ-alpha peptide from pUC9; putative [cloning vectors] >gi_994740 (M18329) LacOPZ-alpha peptide from pUC9; putative [cloning vectors]

Seq. No.	220083
Seq. ID	LIB3149-040-Q1-K1-B6
Method	BLASTX
NCBI GI	g4163997
BLAST score	264
E value	4.0e-23
Match length	108
% identity	50
NCBI Description	(AF087483) alpha-xylosidase precursor [Arabidopsis thaliana]

Seq. No.	220084
Seq. ID	LIB3149-040-Q1-K1-C1
Method	BLASTX
NCBI GI	g3738329
BLAST score	181
E value	2.0e-13
Match length	46
% identity	83
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	220085
Seq. ID	LIB3149-040-Q1-K1-C12
Method	BLASTX
NCBI GI	g2911042
BLAST score	175
E value	1.0e-12
Match length	58
% identity	59
NCBI Description	(AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	220086
Seq. ID	LIB3149-040-Q1-K1-C3
Method	BLASTX
NCBI GI	g129248
BLAST score	164
E value	2.0e-11
Match length	100
% identity	21
NCBI Description	ORGAN SPECIFIC PROTEIN S2 >gi_72318_pir__KNPMS2 protein S2 - garden pea >gi_295831_emb_CAA35944_ (X51595) S2 protein [Pisum sativum]

Seq. No.	220087
Seq. ID	LIB3149-040-Q1-K1-C8
Method	BLASTX
NCBI GI	g133829
BLAST score	195
E value	6.0e-15
Match length	72
% identity	57
NCBI Description	30S RIBOSOMAL PROTEIN S17, CHLOROPLAST PRECURSOR (CS17) >gi_81948_pir__B35542 ribosomal protein S17 - garden pea (fragment) >gi_169068 (M31025) ribosomal protein S17 [Pisum sativum]

Seq. No.	220088
Seq. ID	LIB3149-040-Q1-K1-D11
Method	BLASTX
NCBI GI	g3176687
BLAST score	354
E value	1.0e-33
Match length	95
% identity	68
NCBI Description	(AC003671) Strong similarity to trehalose-6-phosphate synthase homolog from A. thaliana chromosome 4 contig gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and

gb_R64855 come from this gene. [Arabidopsis thaliana]

Seq. No.	220089
Seq. ID	LIB3149-040-Q1-K1-D3
Method	BLASTX
NCBI GI	g3550661
BLAST score	210
E value	9.0e-17
Match length	54
% identity	74
NCBI Description	(AJ001310) 39 kDa EF-Hand containing protein [Solanum tuberosum]

Seq. No.	220090
Seq. ID	LIB3149-040-Q1-K1-D4
Method	BLASTX
NCBI GI	g4103154
BLAST score	357
E value	5.0e-34
Match length	130
% identity	55
NCBI Description	(AF020717) histidyl-tRNA synthetase [Triticum aestivum]

Seq. No.	220091
Seq. ID	LIB3149-040-Q1-K1-D6
Method	BLASTX
NCBI GI	g124226
BLAST score	383
E value	5.0e-37
Match length	79
% identity	94
NCBI Description	INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D) >gi_100278_pir__S21059 translation initiation factor eIF-5A.2 - curled-leaved tobacco >gi_19702_emb_CAA45104_ (X63542) eukaryotic initiation factor 5A (2) [Nicotiana plumbaginifolia]

Seq. No.	220092
Seq. ID	LIB3149-040-Q1-K1-D7
Method	BLASTX
NCBI GI	g124226
BLAST score	337
E value	1.0e-31
Match length	79
% identity	84
NCBI Description	INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D) >gi_100278_pir__S21059 translation initiation factor eIF-5A.2 - curled-leaved tobacco >gi_19702_emb_CAA45104_ (X63542) eukaryotic initiation factor 5A (2) [Nicotiana plumbaginifolia]

Seq. No.	220093
Seq. ID	LIB3149-040-Q1-K1-D8
Method	BLASTX
NCBI GI	g464734
BLAST score	229
E value	3.0e-19

Match length	53
% identity	85
NCBI Description	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi_481237_pir__S38379 adenosylhomocysteinase (EC 3.3.1.1) - Madagascar periwinkle >gi_407412_emb_CAA81527_ (Z26881) S-adenosyl-L-homocysteine hydrolase [Catharanthus roseus]
Seq. No.	220094
Seq. ID	LIB3149-040-Q1-K1-D9
Method	BLASTX
NCBI GI	g549056
BLAST score	398
E value	8.0e-39
Match length	129
% identity	64
NCBI Description	T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA) >gi_631651_pir__S43059 CCT (chaperonin containing TCP-1) beta chain - mouse >gi_468546_emb_CAA83428_ (Z31553) CCT (chaperonin containing TCP-1) beta subunit [Mus musculus]
Seq. No.	220095
Seq. ID	LIB3149-040-Q1-K1-E12
Method	BLASTX
NCBI GI	g3860277
BLAST score	299
E value	4.0e-27
Match length	62
% identity	92
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]
Seq. No.	220096
Seq. ID	LIB3149-040-Q1-K1-E2
Method	BLASTX
NCBI GI	g1136298
BLAST score	480
E value	2.0e-48
Match length	102
% identity	87
NCBI Description	(D61377) WIPK [Nicotiana tabacum]
Seq. No.	220097
Seq. ID	LIB3149-040-Q1-K1-E6
Method	BLASTN
NCBI GI	g2924257
BLAST score	36
E value	3.0e-11
Match length	80
% identity	86
NCBI Description	Tobacco chloroplast genome DNA
Seq. No.	220098
Seq. ID	LIB3149-040-Q1-K1-E7
Method	BLASTX
NCBI GI	g2760325

BLAST score 320
E value 1.0e-29
Match length 131
% identity 51
NCBI Description (AC002130) F1N21.10 [Arabidopsis thaliana]

Seq. No. 220099
Seq. ID LIB3149-040-Q1-K1-E9
Method BLASTN
NCBI GI g2264305
BLAST score 44
E value 2.0e-15
Match length 81
% identity 96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK23, complete sequence [Arabidopsis thaliana]

Seq. No. 220100
Seq. ID LIB3149-040-Q1-K1-F1
Method BLASTX
NCBI GI g4490332
BLAST score 174
E value 2.0e-12
Match length 80
% identity 51
NCBI Description (AL035656) putative protein [Arabidopsis thaliana]

Seq. No. 220101
Seq. ID LIB3149-040-Q1-K1-F2
Method BLASTX
NCBI GI g4455194
BLAST score 260
E value 1.0e-22
Match length 65
% identity 75
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 220102
Seq. ID LIB3149-040-Q1-K1-F3
Method BLASTX
NCBI GI g2980795
BLAST score 567
E value 1.0e-58
Match length 119
% identity 91
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 220103
Seq. ID LIB3149-040-Q1-K1-F5
Method BLASTX
NCBI GI g729618
BLAST score 519
E value 5.0e-53
Match length 134
% identity 78
NCBI Description 78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 2 (GRP 78-2) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG 2) (BIP

2) >gi_82172_pir__PQ0262 luminal binding protein BLP-2 - common tobacco (fragment) >gi_100338_pir__S21878 heat shock protein BiP homolog blp2 - common tobacco (fragment) >gi_19807_emb_CAA42661_ (X60059) luminal binding protein (BiP) [Nicotiana tabacum]

Seq. No.	220104
Seq. ID	LIB3149-040-Q1-K1-F6
Method	BLASTX
NCBI GI	g3986119
BLAST score	305
E value	4.0e-32
Match length	131
% identity	60
NCBI Description	(AB013101) 1-aminocyclopropane-1-carboxylate oxidase [Lycopersicon esculentum]

Seq. No.	220105
Seq. ID	LIB3149-040-Q1-K1-F7
Method	BLASTX
NCBI GI	g1439609
BLAST score	552
E value	7.0e-57
Match length	110
% identity	53
NCBI Description	(U62778) delta-tonoplast intrinsic protein [Gossypium hirsutum]

Seq. No.	220106
Seq. ID	LIB3149-040-Q1-K1-F9
Method	BLASTX
NCBI GI	g3582436
BLAST score	474
E value	1.0e-47
Match length	131
% identity	70
NCBI Description	(AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]

Seq. No.	220107
Seq. ID	LIB3149-040-Q1-K1-G1
Method	BLASTX
NCBI GI	g3413170
BLAST score	628
E value	9.0e-66
Match length	128
% identity	95
NCBI Description	(AJ010227) 40S ribosomal protein S6 [Cicer arietinum]

Seq. No.	220108
Seq. ID	LIB3149-040-Q1-K1-G10
Method	BLASTX
NCBI GI	g508304
BLAST score	149
E value	7.0e-10
Match length	63
% identity	49
NCBI Description	(L22305) corC [Medicago sativa]

Seq. No.	220109
Seq. ID	LIB3149-040-Q1-K1-G12
Method	BLASTX
NCBI GI	g2275213
BLAST score	407
E value	8.0e-40
Match length	125
% identity	61
NCBI Description	(AC002337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220110
Seq. ID	LIB3149-040-Q1-K1-G5
Method	BLASTX
NCBI GI	g3318611
BLAST score	261
E value	2.0e-23
Match length	57
% identity	97
NCBI Description	(AB016063) mitochondrial phosphate transporter [Glycine max]

Seq. No.	220111
Seq. ID	LIB3149-040-Q1-K1-G6
Method	BLASTX
NCBI GI	g4539422
BLAST score	629
E value	7.0e-66
Match length	135
% identity	81
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]

Seq. No.	220112
Seq. ID	LIB3149-040-Q1-K1-G7
Method	BLASTX
NCBI GI	g2935529
BLAST score	412
E value	2.0e-40
Match length	105
% identity	69
NCBI Description	(AF049069) No definition line found [Pinus radiata]

Seq. No.	220113
Seq. ID	LIB3149-040-Q1-K1-H1
Method	BLASTX
NCBI GI	g3123264
BLAST score	417
E value	4.0e-41
Match length	85
% identity	91
NCBI Description	60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279_ (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220114
Seq. ID	LIB3149-040-Q1-K1-H11
Method	BLASTX
NCBI GI	g4539543

BLAST score	484
E value	6.0e-49
Match length	116
% identity	83
NCBI Description	(AJ133422) glyceraldehyde-3-phosphate dehydrogenase [Nicotiana tabacum]

Seq. No.	220115
Seq. ID	LIB3149-040-Q1-K1-H3
Method	BLASTX
NCBI GI	g1469930
BLAST score	211
E value	4.0e-17
Match length	69
% identity	70
NCBI Description	(U48777) fiber-specific acyl carrier protein [Gossypium hirsutum]

Seq. No.	220116
Seq. ID	LIB3149-040-Q1-K1-H6
Method	BLASTX
NCBI GI	g3452497
BLAST score	597
E value	4.0e-62
Match length	133
% identity	87
NCBI Description	(Y17796) ketol-acid reductoisomerase [Pisum sativum]

Seq. No.	220117
Seq. ID	LIB3149-040-Q1-K1-H8
Method	BLASTX
NCBI GI	g4090533
BLAST score	558
E value	2.0e-57
Match length	136
% identity	79
NCBI Description	(U68215) ACC oxidase [Carica papaya]

Seq. No.	220118
Seq. ID	LIB3149-040-Q1-K1-H9
Method	BLASTX
NCBI GI	g2829862
BLAST score	146
E value	2.0e-09
Match length	99
% identity	40
NCBI Description	(AC002396) Similar to glucosyltransferases [Arabidopsis thaliana]

Seq. No.	220119
Seq. ID	LIB3149-042-Q1-K1-A1
Method	BLASTX
NCBI GI	g1495768
BLAST score	401
E value	3.0e-39
Match length	110
% identity	69

NCBI Description	(Z68506) chloroplast inner envelope protein, 110 kD (IEP110) [Pisum sativum]
Seq. No.	220120
Seq. ID	LIB3149-042-Q1-K1-A11
Method	BLASTX
NCBI GI	g508304
BLAST score	286
E value	3.0e-26
Match length	70
% identity	76
NCBI Description	(L22305) corC [Medicago sativa]
Seq. No.	220121
Seq. ID	LIB3149-042-Q1-K1-A4
Method	BLASTX
NCBI GI	g4567202
BLAST score	559
E value	1.0e-57
Match length	116
% identity	94
NCBI Description	(AC007168) putative myo-inositol 1-phosphate synthase [Arabidopsis thaliana]
Seq. No.	220122
Seq. ID	LIB3149-042-Q1-K1-A5
Method	BLASTX
NCBI GI	g1076511
BLAST score	380
E value	9.0e-37
Match length	116
% identity	68
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - kidney bean >gi_758250_emb_CAA59799_ (X85804) H(+)-transporting ATPase [Phaseolus vulgaris]
Seq. No.	220123
Seq. ID	LIB3149-042-Q1-K1-A9
Method	BLASTX
NCBI GI	g141614
BLAST score	172
E value	1.0e-12
Match length	63
% identity	65
NCBI Description	ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1) >gi_82662_pir__B22831 22K zein precursor (clone M1) - maize >gi_22527_emb_CAA24722_ (V01475) reading frame zein [Zea mays] >gi_224510_prf__1107201D zein M1 [Zea mays]
Seq. No.	220124
Seq. ID	LIB3149-042-Q1-K1-B1
Method	BLASTX
NCBI GI	g464621
BLAST score	355
E value	1.0e-33
Match length	120
% identity	60

NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]
Seq. No.	220125
Seq. ID	LIB3149-042-Q1-K1-B11
Method	BLASTX
NCBI GI	g4056506
BLAST score	236
E value	3.0e-20
Match length	62
% identity	74
NCBI Description	(AC005896) nodulin-like protein [Arabidopsis thaliana]
Seq. No.	220126
Seq. ID	LIB3149-042-Q1-K1-B3
Method	BLASTX
NCBI GI	g1397319
BLAST score	149
E value	1.0e-09
Match length	112
% identity	31
NCBI Description	(U61953) No definition line found [Caenorhabditis elegans]
Seq. No.	220127
Seq. ID	LIB3149-042-Q1-K1-B4
Method	BLASTX
NCBI GI	g3860315
BLAST score	454
E value	3.0e-45
Match length	99
% identity	85
NCBI Description	(AJ012684) 40S ribosomal protein S19 [Cicer arietinum]
Seq. No.	220128
Seq. ID	LIB3149-042-Q1-K1-B5
Method	BLASTX
NCBI GI	g3860315
BLAST score	433
E value	6.0e-43
Match length	104
% identity	79
NCBI Description	(AJ012684) 40S ribosomal protein S19 [Cicer arietinum]
Seq. No.	220129
Seq. ID	LIB3149-042-Q1-K1-B7
Method	BLASTX
NCBI GI	g4417280
BLAST score	381
E value	9.0e-37
Match length	95
% identity	80
NCBI Description	(AC007019) putative ATP synthase [Arabidopsis thaliana]
Seq. No.	220130
Seq. ID	LIB3149-042-Q1-K1-B9

Method	BLASTX
NCBI GI	g2497752
BLAST score	173
E value	9.0e-13
Match length	51
% identity	63
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1321911_emb_CAA65475_ (X96714) lipid transfer protein [Prunus dulcis]

Seq. No.	220131
Seq. ID	LIB3149-042-Q1-K1-C10
Method	BLASTX
NCBI GI	g2507281
BLAST score	352
E value	1.0e-33
Match length	65
% identity	100
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_ (X97380) atran2 [Arabidopsis thaliana]

Seq. No.	220132
Seq. ID	LIB3149-042-Q1-K1-C4
Method	BLASTX
NCBI GI	g1172995
BLAST score	206
E value	3.0e-16
Match length	79
% identity	56
NCBI Description	60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal protein L22 - rat >gi_710295_emb_CAA55204_ (X78444) ribosomal protein L22 [Rattus norvegicus] >gi_1093952_prf__2105193A ribosomal protein L22 [Rattus norvegicus]

Seq. No.	220133
Seq. ID	LIB3149-042-Q1-K1-C6
Method	BLASTX
NCBI GI	g3024126
BLAST score	687
E value	1.0e-72
Match length	132
% identity	97
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine synthetase 1 [Catharanthus roseus]

Seq. No.	220134
Seq. ID	LIB3149-042-Q1-K1-C7
Method	BLASTX
NCBI GI	g133867
BLAST score	242
E value	1.0e-20
Match length	56
% identity	84
NCBI Description	40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal

	protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays]
Seq. No.	220135
Seq. ID	LIB3149-042-Q1-K1-C8
Method	BLASTX
NCBI GI	g3046705
BLAST score	201
E value	9.0e-16
Match length	59
% identity	71
NCBI Description	(AL022198) ribosomal protein S11 - like (partial) [Arabidopsis thaliana]
Seq. No.	220136
Seq. ID	LIB3149-042-Q1-K1-C9
Method	BLASTX
NCBI GI	g1922251
BLAST score	284
E value	9.0e-26
Match length	58
% identity	95
NCBI Description	(Y12072) farnesyl pyrophosphate synthase [Gossypium arboreum]
Seq. No.	220137
Seq. ID	LIB3149-042-Q1-K1-D11
Method	BLASTX
NCBI GI	g3128228
BLAST score	441
E value	3.0e-44
Match length	86
% identity	94
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]
Seq. No.	220138
Seq. ID	LIB3149-042-Q1-K1-D12
Method	BLASTX
NCBI GI	g399414
BLAST score	441
E value	3.0e-44
Match length	87
% identity	98
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_322865_pir__JC1454 translation elongation factor eEF-1 alpha chain - wheat >gi_170776 (M90077) translation elongation factor 1 alpha-subunit [Triticum aestivum] >gi_949878_emb_CAA90651_ (Z50789) elongation factor 1-alpha [Hordeum vulgare]
Seq. No.	220139
Seq. ID	LIB3149-042-Q1-K1-D7
Method	BLASTX
NCBI GI	g3421123
BLAST score	379

E value	1.0e-36
Match length	84
% identity	83
NCBI Description	(AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis thaliana]

Seq. No.	220140
Seq. ID	LIB3149-042-Q1-K1-D8
Method	BLASTX
NCBI GI	g131770
BLAST score	349
E value	5.0e-33
Match length	97
% identity	65
NCBI Description	40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024) (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3DO24 ribosomal protein S9.e - slime mold (Dictyostelium discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein [Dictyostelium discoideum]

Seq. No.	220141
Seq. ID	LIB3149-042-Q1-K1-E1
Method	BLASTX
NCBI GI	g464707
BLAST score	155
E value	3.0e-13
Match length	58
% identity	71
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	220142
Seq. ID	LIB3149-042-Q1-K1-E11
Method	BLASTX
NCBI GI	g2558962
BLAST score	156
E value	1.0e-10
Match length	62
% identity	53
NCBI Description	(AF025667) histone H2B1 [Gossypium hirsutum]

Seq. No.	220143
Seq. ID	LIB3149-042-Q1-K1-E4
Method	BLASTX

NCBI GI	g586076
BLAST score	733
E value	5.0e-78
Match length	144
% identity	96
NCBI Description	TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta tubulin 1 [Lupinus albus]

Seq. No.	220144
Seq. ID	LIB3149-042-Q1-K1-E6
Method	BLASTX
NCBI GI	g3451473
BLAST score	179
E value	5.0e-13
Match length	112
% identity	39
NCBI Description	(AL031349) 4-nitrophenylphosphatase [Schizosaccharomyces pombe]

Seq. No.	220145
Seq. ID	LIB3149-042-Q1-K1-E7
Method	BLASTX
NCBI GI	g3894172
BLAST score	313
E value	6.0e-29
Match length	117
% identity	47
NCBI Description	(AC005312) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No.	220146
Seq. ID	LIB3149-042-Q1-K1-E8
Method	BLASTX
NCBI GI	g2244929
BLAST score	150
E value	1.0e-09
Match length	75
% identity	43
NCBI Description	(Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No.	220147
Seq. ID	LIB3149-042-Q1-K1-F1
Method	BLASTX
NCBI GI	g729882
BLAST score	143
E value	6.0e-09
Match length	25
% identity	92
NCBI Description	CASEIN KINASE II BETA' CHAIN (CK II) >gi_1076300_pir__S47968 casein kinase II (EC 2.7.1.-) beta chain CKB2 - Arabidopsis thaliana >gi_467975 (U03984) casein kinase II beta subunit CKB2 [Arabidopsis thaliana] >gi_2245122_emb_CAB10544_ (Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No.	220148

Seq. ID	LIB3149-042-Q1-K1-F10
Method	BLASTX
NCBI GI	g4101589
BLAST score	247
E value	2.0e-21
Match length	76
% identity	61
NCBI Description	(AF005050) aspartyl aminopeptidase [Homo sapiens]

Seq. No.	220149
Seq. ID	LIB3149-042-Q1-K1-F12
Method	BLASTX
NCBI GI	g4127456
BLAST score	210
E value	5.0e-17
Match length	70
% identity	66
NCBI Description	(AJ010818) Cpn21 protein [Arabidopsis thaliana]

Seq. No.	220150
Seq. ID	LIB3149-042-Q1-K1-F4
Method	BLASTX
NCBI GI	g2065531
BLAST score	396
E value	2.0e-45
Match length	117
% identity	75
NCBI Description	(U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No.	220151
Seq. ID	LIB3149-042-Q1-K1-F5
Method	BLASTX
NCBI GI	g2632254
BLAST score	503
E value	3.0e-51
Match length	105
% identity	87
NCBI Description	(Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No.	220152
Seq. ID	LIB3149-042-Q1-K1-F7
Method	BLASTX
NCBI GI	g1841870
BLAST score	294
E value	1.0e-26
Match length	78
% identity	73
NCBI Description	(U87222) elongation factor 1-beta [Pimpinella brachycarpa]

Seq. No.	220153
Seq. ID	LIB3149-042-Q1-K1-F8
Method	BLASTX
NCBI GI	g1841870
BLAST score	318
E value	2.0e-29
Match length	95
% identity	69

NCBI Description (U87222) elongation factor 1-beta [Pimpinella brachycarpa]

Seq. No. 220154
Seq. ID LIB3149-042-Q1-K1-F9
Method BLASTN
NCBI GI g1418705
BLAST score 76
E value 8.0e-35
Match length 178
% identity 96
NCBI Description G.hirsutum metallothionein-like gene

Seq. No. 220155
Seq. ID LIB3149-042-Q1-K1-G10
Method BLASTX
NCBI GI g2581785
BLAST score 358
E value 2.0e-34
Match length 86
% identity 77
NCBI Description (U94999) class 2 non-symbiotic hemoglobin [Arabidopsis thaliana]

Seq. No. 220156
Seq. ID LIB3149-042-Q1-K1-G2
Method BLASTX
NCBI GI g322750
BLAST score 640
E value 4.0e-67
Match length 128
% identity 95
NCBI Description ubiquitin / ribosomal protein CEP52 - wood tobacco >gi_170217 (M74100) ubiquitin fusion protein [Nicotiana sylvestris]

Seq. No. 220157
Seq. ID LIB3149-042-Q1-K1-G4
Method BLASTX
NCBI GI g1703380
BLAST score 448
E value 1.0e-44
Match length 87
% identity 98
NCBI Description ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607_ (D17760) ADP-ribosylation factor [Oryza sativa]

Seq. No. 220158
Seq. ID LIB3149-042-Q1-K1-G5
Method BLASTX
NCBI GI g2431769
BLAST score 208
E value 1.0e-16
Match length 55
% identity 76
NCBI Description (U62752) acidic ribosomal protein P1a [Zea mays]

Seq. No. 220159

Seq. ID	LIB3149-042-Q1-K1-G6
Method	BLASTX
NCBI GI	g3894387
BLAST score	208
E value	2.0e-16
Match length	135
% identity	5
NCBI Description	(AF053995) Hcr2-0B [Lycopersicon esculentum]

Seq. No.	220160
Seq. ID	LIB3149-042-Q1-K1-G7
Method	BLASTX
NCBI GI	g3413167
BLAST score	354
E value	1.0e-33
Match length	71
% identity	96
NCBI Description	(AJ010225) elongation factor 1-alpha [Cicer arietinum]

Seq. No.	220161
Seq. ID	LIB3149-042-Q1-K1-G8
Method	BLASTX
NCBI GI	g3319882
BLAST score	265
E value	3.0e-23
Match length	62
% identity	82
NCBI Description	(AJ004960) elongation factor 1-alpha (EF1-a) [Cicer arietinum]

Seq. No.	220162
Seq. ID	LIB3149-042-Q1-K1-H11
Method	BLASTX
NCBI GI	g3128228
BLAST score	334
E value	1.0e-31
Match length	70
% identity	90
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	220163
Seq. ID	LIB3149-042-Q1-K1-H3
Method	BLASTX
NCBI GI	g1754522
BLAST score	170
E value	4.0e-21
Match length	106
% identity	52
NCBI Description	(D89984) ornithine decarboxylase [Nicotiana tabacum]

Seq. No.	220164
Seq. ID	LIB3149-042-Q1-K1-H5
Method	BLASTX
NCBI GI	g464707
BLAST score	432

E value	6.0e-43
Match length	107
% identity	83
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]
Seq. No.	220165
Seq. ID	LIB3149-042-Q1-K1-H6
Method	BLASTX
NCBI GI	g464707
BLAST score	239
E value	4.0e-20
Match length	78
% identity	62
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]
Seq. No.	220166
Seq. ID	LIB3149-042-Q1-K1-H8
Method	BLASTX
NCBI GI	g3024020
BLAST score	602
E value	1.0e-62
Match length	130
% identity	87
NCBI Description	INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D) >gi_2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation factor 5A3 [Solanum tuberosum]
Seq. No.	220167
Seq. ID	LIB3149-043-Q1-K1-A1

Method	BLASTN
NCBI GI	g642263
BLAST score	187
E value	1.0e-101
Match length	347
% identity	88
NCBI Description	R.enysii ITS2 and 28S rRNA gene (partial)

Seq. No.	220168
Seq. ID	LIB3149-043-Q1-K1-A2
Method	BLASTX
NCBI GI	g1350707
BLAST score	121
E value	1.0e-12
Match length	52
% identity	70
NCBI Description	60S RIBOSOMAL PROTEIN L29 >gi_539923_pir__JC2012 ribosomal protein 17K - mouse >gi_404766 (L08651) ribosomal protein [Mus musculus]

Seq. No.	220169
Seq. ID	LIB3149-043-Q1-K1-A3
Method	BLASTX
NCBI GI	g124224
BLAST score	610
E value	1.0e-63
Match length	122
% identity	93
NCBI Description	INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) >gi_100345_pir__S21060 translation initiation factor eIF-5A - common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No.	220170
Seq. ID	LIB3149-043-Q1-K1-A6
Method	BLASTX
NCBI GI	g126959
BLAST score	297
E value	4.0e-27
Match length	83
% identity	75
NCBI Description	TONOPLAST INTRINSIC PROTEIN, ROOT-SPECIFIC RB7-5A (RT-TIP) >gi_82192_pir__JQ1011 TobRB7-5A protein - common tobacco >gi_100371_pir__S13719 probable membrane channel protein - common tobacco >gi_20011_emb_CAA38634_ (X54855) possible membrane channel protein [Nicotiana tabacum]

Seq. No.	220171
Seq. ID	LIB3149-043-Q1-K1-A8
Method	BLASTX
NCBI GI	g3873845
BLAST score	150
E value	1.0e-09
Match length	54
% identity	48
NCBI Description	(Z82256) similar to 60S ribosomal protein L29; cDNA EST yk493f9.3 comes from this gene [Caenorhabditis elegans]

Seq. No.	220172
Seq. ID	LIB3149-043-Q1-K1-B2
Method	BLASTN
NCBI GI	g2687434
BLAST score	237
E value	1.0e-131
Match length	277
% identity	96
NCBI Description	Eucryphia lucida large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	220173
Seq. ID	LIB3149-043-Q1-K1-B4
Method	BLASTX
NCBI GI	g4432840
BLAST score	321
E value	8.0e-30
Match length	106
% identity	61
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	220174
Seq. ID	LIB3149-043-Q1-K1-B7
Method	BLASTX
NCBI GI	g2829871
BLAST score	259
E value	5.0e-39
Match length	103
% identity	72
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	220175
Seq. ID	LIB3149-043-Q1-K1-C1
Method	BLASTX
NCBI GI	g3694872
BLAST score	474
E value	9.0e-48
Match length	116
% identity	76
NCBI Description	(AF092547) profilin [Ricinus communis]

Seq. No.	220176
Seq. ID	LIB3149-043-Q1-K1-C10
Method	BLASTX
NCBI GI	g730526
BLAST score	475
E value	6.0e-48
Match length	97
% identity	88
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No.	220177
Seq. ID	LIB3149-043-Q1-K1-C11

Method	BLASTX
NCBI GI	g1917019
BLAST score	508
E value	1.0e-51
Match length	128
% identity	77
NCBI Description	(U92045) ribosomal protein S6 RPS6-1 [Zea mays]

Seq. No.	220178
Seq. ID	LIB3149-043-Q1-K1-C12
Method	BLASTX
NCBI GI	g2529665
BLAST score	628
E value	9.0e-66
Match length	129
% identity	92
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	220179
Seq. ID	LIB3149-043-Q1-K1-C2
Method	BLASTX
NCBI GI	g3128177
BLAST score	335
E value	1.0e-31
Match length	82
% identity	80
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	220180
Seq. ID	LIB3149-043-Q1-K1-C3
Method	BLASTX
NCBI GI	g2827552
BLAST score	482
E value	1.0e-48
Match length	108
% identity	41
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	220181
Seq. ID	LIB3149-043-Q1-K1-C4
Method	BLASTX
NCBI GI	g2894603
BLAST score	188
E value	3.0e-14
Match length	74
% identity	16
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	220182
Seq. ID	LIB3149-043-Q1-K1-C5
Method	BLASTX
NCBI GI	g2119353
BLAST score	287
E value	8.0e-26
Match length	115
% identity	50

NCBI Description	calmodulin - moss (Physcomitrella patens)
Seq. No.	220183
Seq. ID	LIB3149-043-Q1-K1-C6
Method	BLASTX
NCBI GI	g514322
BLAST score	416
E value	6.0e-41
Match length	122
% identity	63
NCBI Description	(L34772) RNA polymerase subunit [Arabidopsis thaliana] >gi_1586549_prf__2204246A RNA polymerase [Arabidopsis thaliana]
Seq. No.	220184
Seq. ID	LIB3149-043-Q1-K1-C9
Method	BLASTX
NCBI GI	g1352821
BLAST score	626
E value	2.0e-65
Match length	119
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	220185
Seq. ID	LIB3149-043-Q1-K1-D1
Method	BLASTX
NCBI GI	g3834309
BLAST score	283
E value	2.0e-25
Match length	89
% identity	54
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb_L16983 Daucus carota and a member of S locus glycoprotein family PF_00954. ESTs gb_F13813, gb_T21052, gb_R30218 and gb_W43262 come from this gene. [Arabidopsis thaliana]
Seq. No.	220186
Seq. ID	LIB3149-043-Q1-K1-D4
Method	BLASTX
NCBI GI	g4039014
BLAST score	478
E value	3.0e-48
Match length	127
% identity	66
NCBI Description	(AF037338) cleft lip and palate transmembrane protein 1 [Homo sapiens] >gi_4063033 (AF037339) cleft lip and palate transmembrane protein 1 [Homo sapiens] >gi_4502897_ref_NP_001285.1_pCLPTM1_ cleft lip and palate associated transmembrane protein
Seq. No.	220187
Seq. ID	LIB3149-043-Q1-K1-D6

Method	BLASTX
NCBI GI	g2494620
BLAST score	277
E value	1.0e-24
Match length	71
% identity	68
NCBI Description	SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN >gi_975319 (U31902) succinate dehydrogenase iron-sulfur protein subunit [Paracoccus denitrificans]

Seq. No.	220188
Seq. ID	LIB3149-043-Q1-K1-D7
Method	BLASTX
NCBI GI	g2996166
BLAST score	339
E value	7.0e-32
Match length	66
% identity	91
NCBI Description	(AF051757) putative 60S ribosomal protein L15 [Picea mariana] >gi_2996168 (AF051758) putative 60S ribosomal protein L15 [Picea mariana] >gi_2996170 (AF051759) putative 60S ribosomal protein L15 [Picea mariana]

Seq. No.	220189
Seq. ID	LIB3149-043-Q1-K1-D9
Method	BLASTN
NCBI GI	g1335861
BLAST score	55
E value	4.0e-22
Match length	212
% identity	84
NCBI Description	Glycine max clathrin heavy chain mRNA, complete cds

Seq. No.	220190
Seq. ID	LIB3149-043-Q1-K1-E12
Method	BLASTX
NCBI GI	g1296816
BLAST score	566
E value	1.0e-58
Match length	111
% identity	99
NCBI Description	(X94995) naringenin-chalcone synthase [Juglans sp.]

Seq. No.	220191
Seq. ID	LIB3149-043-Q1-K1-E8
Method	BLASTX
NCBI GI	g133812
BLAST score	323
E value	5.0e-30
Match length	74
% identity	86
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S16 >gi_71000_pir__R3IS16 ribosomal protein S16 - white mustard chloroplast >gi_12217_emb_CAA31944_ (X13609) 16S ribosomal protein [Sinapis alba]

Seq. No. 220192

Seq. ID	LIB3149-043-Q1-K1-F12
Method	BLASTX
NCBI GI	g1174621
BLAST score	191
E value	2.0e-14
Match length	86
% identity	49
NCBI Description	T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA) (CCT-THETA) >gi_1083259_pir__JC4073 TCP-1 containing cytosolic chaperonin (CCT) theta chain - mouse >gi_695625_emb_CAA85521_ (Z37164) CCTtheta, theta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus]

Seq. No.	220193
Seq. ID	LIB3149-043-Q1-K1-F3
Method	BLASTX
NCBI GI	g2118220
BLAST score	412
E value	2.0e-40
Match length	117
% identity	75
NCBI Description	H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P1) - Arabidopsis thaliana >gi_926929 (L44581) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi_926933 (L44583) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi_3096941_emb_CAA18851.1_ (AL023094) vacuolar H+-transporting ATPase 16K chain [Arabidopsis thaliana] >gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting ATPase 16K chain P2, vacuolar [Arabidopsis thaliana]

Seq. No.	220194
Seq. ID	LIB3149-043-Q1-K1-F4
Method	BLASTX
NCBI GI	g3122060
BLAST score	300
E value	3.0e-27
Match length	60
% identity	97
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_2598657_emb_CAA10847_ (AJ222579) elongation factor 1-alpha (EF1-a) [Vicia faba]

Seq. No.	220195
Seq. ID	LIB3149-043-Q1-K1-F5
Method	BLASTX
NCBI GI	g4567251
BLAST score	155
E value	3.0e-10
Match length	32
% identity	78
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.	220196
Seq. ID	LIB3149-043-Q1-K1-F6
Method	BLASTX
NCBI GI	g2911058

BLAST score	206
E value	3.0e-16
Match length	88
% identity	45
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	220197
Seq. ID	LIB3149-043-Q1-K1-F9
Method	BLASTX
NCBI GI	g113029
BLAST score	384
E value	3.0e-37
Match length	73
% identity	100
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68209_pir__WZCNIU isocitrate lyase (EC 4.1.3.1) - upland cotton >gi_18486_emb_CAA36381_ (X52136) isocitrate lyase (AA 1-576) [Gossypium hirsutum]

Seq. No.	220198
Seq. ID	LIB3149-043-Q1-K1-G12
Method	BLASTX
NCBI GI	g557472
BLAST score	211
E value	7.0e-17
Match length	126
% identity	37
NCBI Description	(U15178) arabinosidase [Bacteroides ovatus]

Seq. No.	220199
Seq. ID	LIB3149-043-Q1-K1-G2
Method	BLASTX
NCBI GI	g3450889
BLAST score	340
E value	5.0e-32
Match length	97
% identity	73
NCBI Description	(AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No.	220200
Seq. ID	LIB3149-043-Q1-K1-G3
Method	BLASTX
NCBI GI	g3450889
BLAST score	149
E value	9.0e-10
Match length	72
% identity	53
NCBI Description	(AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No.	220201
Seq. ID	LIB3149-043-Q1-K1-G5
Method	BLASTX
NCBI GI	g2662341
BLAST score	654
E value	8.0e-69
Match length	129
% identity	98

NCBI Description	(D63580) EF-1 alpha [Oryza sativa] >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza sativa] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha [Oryza sativa]

Seq. No.	220202
Seq. ID	LIB3149-043-Q1-K1-G8
Method	BLASTN
NCBI GI	g1654275
BLAST score	156
E value	8.0e-83
Match length	156
% identity	100
NCBI Description	Cienfuegosia tripartita 5.8S ribosomal RNA gene and internal transcribed spacer 1 and

Seq. No.	220203
Seq. ID	LIB3149-043-Q1-K1-H11
Method	BLASTX
NCBI GI	g464707
BLAST score	514
E value	2.0e-52
Match length	117
% identity	85
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	220204
Seq. ID	LIB3149-043-Q1-K1-H12
Method	BLASTX
NCBI GI	g1076414
BLAST score	277
E value	1.0e-24
Match length	118
% identity	51
NCBI Description	subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis thaliana (fragment) >gi_757534_emb_CAA59963_ (X85974) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	220205
Seq. ID	LIB3149-043-Q1-K1-H4
Method	BLASTX
NCBI GI	g3157933
BLAST score	514

E value	2.0e-52
Match length	120
% identity	79
NCBI Description	(AC002131) Contains similarity to box helicases gb_U29097 from C. elegans and to the ENBP1 gene product gb_X95995 from Vicia sativa. [Arabidopsis thaliana]

Seq. No.	220206
Seq. ID	LIB3149-043-Q1-K1-H5
Method	BLASTX
NCBI GI	g3687243
BLAST score	241
E value	2.0e-20
Match length	61
% identity	77
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	220207
Seq. ID	LIB3149-043-Q1-K1-H8
Method	BLASTX
NCBI GI	g3860277
BLAST score	486
E value	4.0e-49
Match length	128
% identity	75
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	220208
Seq. ID	LIB3149-043-Q1-K1-H9
Method	BLASTX
NCBI GI	g2827082
BLAST score	521
E value	3.0e-53
Match length	120
% identity	79
NCBI Description	(AF020272) malate dehydrogenase [Medicago sativa]

Seq. No.	220209
Seq. ID	LIB3149-044-Q1-K1-A1
Method	BLASTX
NCBI GI	g3212116
BLAST score	267
E value	2.0e-23
Match length	107
% identity	49
NCBI Description	(Y17393) prefoldin subunit 2 [Mus musculus]

Seq. No.	220210
Seq. ID	LIB3149-044-Q1-K1-A10
Method	BLASTX
NCBI GI	g4371282
BLAST score	497
E value	2.0e-50
Match length	110

% identity	86
NCBI Description	(AC006260) putative 60S ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	220211
Seq. ID	LIB3149-044-Q1-K1-A11
Method	BLASTX
NCBI GI	g2648032
BLAST score	628
E value	1.0e-65
Match length	141
% identity	79
NCBI Description	(AJ001374) alpha-glucosidase [Solanum tuberosum]

Seq. No.	220212
Seq. ID	LIB3149-044-Q1-K1-A12
Method	BLASTX
NCBI GI	g2500195
BLAST score	319
E value	2.0e-29
Match length	65
% identity	95
NCBI Description	RAC-LIKE GTP BINDING PROTEIN RHO1 >gi_974780_emb_CAA89050_ (Z49191) small G protein [Beta vulgaris]

Seq. No.	220213
Seq. ID	LIB3149-044-Q1-K1-A2
Method	BLASTX
NCBI GI	g547886
BLAST score	300
E value	2.0e-27
Match length	118
% identity	58
NCBI Description	MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME) (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME) >gi_542102_pir__S42939 malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) precursor - Flaveria pringlei >gi_1084444_pir__S52016 malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) - Flaveria pringlei >gi_459441_emb_CAA54986_ (X78069) malate dehydrogenase (oxaloacetate decarboxylating) (NADP+) [Flaveria pringlei]

Seq. No.	220214
Seq. ID	LIB3149-044-Q1-K1-A3
Method	BLASTX
NCBI GI	g4454033
BLAST score	186
E value	5.0e-14
Match length	54
% identity	59
NCBI Description	(AL035394) putative potassium transport protein [Arabidopsis thaliana]

Seq. No.	220215
Seq. ID	LIB3149-044-Q1-K1-A4
Method	BLASTX

NCBI GI g3893081
BLAST score 523
E value 2.0e-53
Match length 138
% identity 70
NCBI Description (AJ012747) MLH1 protein [Arabidopsis thaliana]

Seq. No. 220216
Seq. ID LIB3149-044-Q1-K1-A5
Method BLASTX
NCBI GI g4508079
BLAST score 156
E value 7.0e-11
Match length 74
% identity 45
NCBI Description (AC005882) 66284 [Arabidopsis thaliana]

Seq. No. 220217
Seq. ID LIB3149-044-Q1-K1-A6
Method BLASTX
NCBI GI g1518540
BLAST score 590
E value 3.0e-61
Match length 127
% identity 91
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No. 220218
Seq. ID LIB3149-044-Q1-K1-A7
Method BLASTX
NCBI GI g547886
BLAST score 505
E value 3.0e-51
Match length 137
% identity 74
NCBI Description MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME) (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME) >gi_542102_pir__S42939 malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) precursor - Flaveria pringlei >gi_1084444_pir__S52016 malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) - Flaveria pringlei >gi_459441_emb_CAA54986_ (X78069) malate dehydrogenase (oxaloacetate decarboxylating) (NADP+) [Flaveria pringlei]

Seq. No. 220219
Seq. ID LIB3149-044-Q1-K1-B10
Method BLASTX
NCBI GI g2119937
BLAST score 701
E value 3.0e-74
Match length 140
% identity 98
NCBI Description translation initiation factor eIF-4A.13 - common tobacco (fragment)

Seq. No. 220220

Seq. ID	LIB3149-044-Q1-K1-B12
Method	BLASTX
NCBI GI	g3924597
BLAST score	212
E value	6.0e-17
Match length	133
% identity	37
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	220221
Seq. ID	LIB3149-044-Q1-K1-B3
Method	BLASTX
NCBI GI	g3915847
BLAST score	396
E value	2.0e-38
Match length	84
% identity	88
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	220222
Seq. ID	LIB3149-044-Q1-K1-C11
Method	BLASTX
NCBI GI	g4206210
BLAST score	462
E value	3.0e-46
Match length	141
% identity	64
NCBI Description	(AF071527) putative calcium channel [Arabidopsis thaliana] >gi_4263043_gb_AAD15312_ (AC005142) putative calcium channel [Arabidopsis thaliana]

Seq. No.	220223
Seq. ID	LIB3149-044-Q1-K1-C12
Method	BLASTX
NCBI GI	g169989
BLAST score	506
E value	2.0e-51
Match length	111
% identity	88
NCBI Description	(L12157) NADPH-specific isocitrate dehydrogenase [Glycine max]

Seq. No.	220224
Seq. ID	LIB3149-044-Q1-K1-C2
Method	BLASTX
NCBI GI	g2829899
BLAST score	299
E value	3.0e-27
Match length	124
% identity	47
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	220225
Seq. ID	LIB3149-044-Q1-K1-C7

Method	BLASTN
NCBI GI	g3241927
BLAST score	52
E value	3.0e-20
Match length	112
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	220226
Seq. ID	LIB3149-044-Q1-K1-C9
Method	BLASTX
NCBI GI	g1362078
BLAST score	231
E value	2.0e-19
Match length	62
% identity	63
NCBI Description	endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1) - common nasturtium >gi_311835_emb_CAA48324_ (X68254) cellulase [Tropaeolum majus]

Seq. No.	220227
Seq. ID	LIB3149-044-Q1-K1-D2
Method	BLASTN
NCBI GI	g974781
BLAST score	33
E value	5.0e-09
Match length	120
% identity	86
NCBI Description	C.blumei kinetoplast met gene for cobalamine-independent methionine synthase

Seq. No.	220228
Seq. ID	LIB3149-044-Q1-K1-D3
Method	BLASTX
NCBI GI	g730645
BLAST score	440
E value	1.0e-43
Match length	114
% identity	79
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]

Seq. No.	220229
Seq. ID	LIB3149-044-Q1-K1-D7
Method	BLASTX
NCBI GI	g464621
BLAST score	375
E value	4.0e-36
Match length	83
% identity	88

NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]
Seq. No.	220230
Seq. ID	LIB3149-044-Q1-K1-D8
Method	BLASTX
NCBI GI	g218288
BLAST score	281
E value	5.0e-25
Match length	136
% identity	29
NCBI Description	(D11111) chloroplast 33 kd ribonucleoprotein (cp33) [Nicotiana sylvestris] >gi_311952_emb_CAA41253_ (X58356) 33 kd chloroplast ribonucleoprotein [Nicotiana sylvestris]
Seq. No.	220231
Seq. ID	LIB3149-044-Q1-K1-E11
Method	BLASTX
NCBI GI	g1905910
BLAST score	422
E value	1.0e-41
Match length	144
% identity	54
NCBI Description	(AD000092) putative human phenylalanine tRNA synthetase [Homo sapiens]
Seq. No.	220232
Seq. ID	LIB3149-044-Q1-K1-E2
Method	BLASTX
NCBI GI	g1351983
BLAST score	207
E value	1.0e-16
Match length	88
% identity	50
NCBI Description	ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING) 1 (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE 1) >gi_2147131_pir__S57931 asparagine synthase (glutamine-hydrolysing) (EC 6.3.5.4) - Lotus japonicus >gi_2147133_pir__S69182 asparagine synthase (glutamine-hydrolysing) (EC 6.3.5.4) 1 - Lotus japonicus >gi_897771_emb_CAA61589_ (X89409) asparagine synthase (glutamine-hydrolysing) [Lotus japonicus]
Seq. No.	220233
Seq. ID	LIB3149-044-Q1-K1-E3
Method	BLASTX
NCBI GI	g1170373
BLAST score	290
E value	2.0e-47
Match length	103
% identity	96
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	220234
Seq. ID	LIB3149-044-Q1-K1-E6
Method	BLASTN
NCBI GI	g2264314
BLAST score	34
E value	2.0e-09
Match length	134
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	220235
Seq. ID	LIB3149-044-Q1-K1-E7
Method	BLASTX
NCBI GI	g2970051
BLAST score	446
E value	2.0e-44
Match length	95
% identity	89
NCBI Description	(AB012110) ARG10 [Vigna radiata]

Seq. No.	220236
Seq. ID	LIB3149-044-Q1-K1-E8
Method	BLASTX
NCBI GI	g3882183
BLAST score	192
E value	1.0e-14
Match length	58
% identity	31
NCBI Description	(AB018274) KIAA0731 protein [Homo sapiens]

Seq. No.	220237
Seq. ID	LIB3149-044-Q1-K1-F12
Method	BLASTX
NCBI GI	g4572674
BLAST score	279
E value	9.0e-25
Match length	73
% identity	73
NCBI Description	(AC006954) unknown protein [Arabidopsis thaliana]

Seq. No.	220238
Seq. ID	LIB3149-044-Q1-K1-F3
Method	BLASTX
NCBI GI	g1362086
BLAST score	540
E value	1.0e-55
Match length	108
% identity	94
NCBI Description	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir__S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]

Seq. No.	220239
Seq. ID	LIB3149-044-Q1-K1-F6
Method	BLASTX
NCBI GI	g1076746
BLAST score	313
E value	9.0e-29
Match length	80
% identity	80
NCBI Description	heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]

Seq. No.	220240
Seq. ID	LIB3149-044-Q1-K1-F7
Method	BLASTX
NCBI GI	g542179
BLAST score	695
E value	1.0e-73
Match length	139
% identity	97
NCBI Description	alpha tubulin - maize >gi_629837_pir__S39998 tubulin alpha chain - maize (fragment) >gi_393401_emb_CAA52158_ (X73980) alpha tubulin [Zea mays]

Seq. No.	220241
Seq. ID	LIB3149-044-Q1-K1-F8
Method	BLASTX
NCBI GI	g3893081
BLAST score	493
E value	6.0e-50
Match length	134
% identity	69
NCBI Description	(AJ012747) MLH1 protein [Arabidopsis thaliana]

Seq. No.	220242
Seq. ID	LIB3149-044-Q1-K1-G10
Method	BLASTX
NCBI GI	g3821280
BLAST score	455
E value	2.0e-45
Match length	117
% identity	77
NCBI Description	(AJ009952) asparagine synthetase type II [Phaseolus vulgaris]

Seq. No.	220243
Seq. ID	LIB3149-044-Q1-K1-G3
Method	BLASTX
NCBI GI	g477280
BLAST score	552
E value	7.0e-57
Match length	128
% identity	81
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) 55K protein precursor - potato >gi_410633_bbs_136740 cytochrome c reductase-processing peptidase subunit I, MPP subunit I,

P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 534 aa]

Seq. No.	220244
Seq. ID	LIB3149-044-Q1-K1-G6
Method	BLASTX
NCBI GI	g2842689
BLAST score	233
E value	2.0e-19
Match length	141
% identity	38
NCBI Description	HYPOTHETICAL 50.4 KD PROTEIN C1F8.04C IN CHROMOSOME I >gi_1638851_emb_CAB03598_ (Z81312) unknown [Schizosaccharomyces pombe]

Seq. No.	220245
Seq. ID	LIB3149-044-Q1-K1-H2
Method	BLASTX
NCBI GI	g2244910
BLAST score	143
E value	6.0e-09
Match length	141
% identity	35
NCBI Description	(Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No.	220246
Seq. ID	LIB3149-044-Q1-K1-H7
Method	BLASTX
NCBI GI	g2961358
BLAST score	614
E value	4.0e-64
Match length	137
% identity	86
NCBI Description	(AL022140) serine/threonine protein kinase like protein [Arabidopsis thaliana]

Seq. No.	220247
Seq. ID	LIB3149-044-Q1-K1-H9
Method	BLASTX
NCBI GI	g1709970
BLAST score	473
E value	1.0e-47
Match length	126
% identity	75
NCBI Description	60S RIBOSOMAL PROTEIN L10A

Seq. No.	220248
Seq. ID	LIB3149-046-Q1-K1-A1
Method	BLASTX
NCBI GI	g3608485
BLAST score	531
E value	2.0e-54
Match length	113
% identity	88
NCBI Description	(AF088915) proteasome beta subunit [Petunia x hybrida]

Seq. No. 220249

Seq. ID	LIB3149-046-Q1-K1-A10
Method	BLASTX
NCBI GI	g444791
BLAST score	249
E value	2.0e-21
Match length	112
% identity	14
NCBI Description	ubiquitin [Bos taurus]

Seq. No.	220250
Seq. ID	LIB3149-046-Q1-K1-A11
Method	BLASTN
NCBI GI	g438110
BLAST score	35
E value	2.0e-10
Match length	55
% identity	91
NCBI Description	L.albus ubiquitin extension protein

Seq. No.	220251
Seq. ID	LIB3149-046-Q1-K1-A12
Method	BLASTX
NCBI GI	g541546
BLAST score	334
E value	2.0e-31
Match length	67
% identity	20
NCBI Description	ubiquitin precursor - Volvox carteri >gi_395295_emb_CAA52290_ (X74214) polyubiquitin [Volvox carteri]

Seq. No.	220252
Seq. ID	LIB3149-046-Q1-K1-A8
Method	BLASTX
NCBI GI	g2827002
BLAST score	221
E value	4.0e-18
Match length	82
% identity	51
NCBI Description	(AF005993) HSP70 [Triticum aestivum]

Seq. No.	220253
Seq. ID	LIB3149-046-Q1-K1-A9
Method	BLASTX
NCBI GI	g2119045
BLAST score	537
E value	4.0e-55
Match length	130
% identity	78
NCBI Description	small nuclear ribonucleoprotein U1A - potato >gi_1050840_emb_CAA90282_ (Z49990) U1snRNP-specific protein, U1A [Solanum tuberosum]

Seq. No.	220254
Seq. ID	LIB3149-046-Q1-K1-B11
Method	BLASTX
NCBI GI	g3123264

BLAST score	468
E value	5.0e-47
Match length	118
% identity	76
NCBI Description	60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279_ (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220255
Seq. ID	LIB3149-046-Q1-K1-B12
Method	BLASTX
NCBI GI	g730547
BLAST score	249
E value	3.0e-28
Match length	85
% identity	75
NCBI Description	60S RIBOSOMAL PROTEIN L27

Seq. No.	220256
Seq. ID	LIB3149-046-Q1-K1-B3
Method	BLASTX
NCBI GI	g4097547
BLAST score	282
E value	2.0e-25
Match length	67
% identity	45
NCBI Description	(U64906) ATFP3 [Arabidopsis thaliana]

Seq. No.	220257
Seq. ID	LIB3149-046-Q1-K1-B5
Method	BLASTX
NCBI GI	g2262100
BLAST score	534
E value	1.0e-54
Match length	122
% identity	80
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	220258
Seq. ID	LIB3149-046-Q1-K1-B7
Method	BLASTX
NCBI GI	g4097547
BLAST score	214
E value	2.0e-17
Match length	89
% identity	31
NCBI Description	(U64906) ATFP3 [Arabidopsis thaliana]

Seq. No.	220259
Seq. ID	LIB3149-046-Q1-K1-C4
Method	BLASTX
NCBI GI	g4490705
BLAST score	466
E value	8.0e-47
Match length	111
% identity	84
NCBI Description	(AL035680) ribosomal protein L14-like protein [Arabidopsis thaliana]

Seq. No.	220260
Seq. ID	LIB3149-046-Q1-K1-C6
Method	BLASTX
NCBI GI	g4530585
BLAST score	357
E value	5.0e-34
Match length	85
% identity	74
NCBI Description	(AF130978) B12D protein [Ipomoea batatas]

Seq. No.	220261
Seq. ID	LIB3149-046-Q1-K1-C7
Method	BLASTX
NCBI GI	g1084415
BLAST score	320
E value	1.0e-29
Match length	95
% identity	62
NCBI Description	RNA-binding protein - Wood tobacco >gi_624925_dbj_BAA05170_ (D26182) RNA-binding glycine rich protein (RGP-2) [Nicotiana sylvestris]

Seq. No.	220262
Seq. ID	LIB3149-046-Q1-K1-C9
Method	BLASTX
NCBI GI	g1222552
BLAST score	153
E value	3.0e-10
Match length	50
% identity	64
NCBI Description	(U49330) pectin methylesterase [Lycopersicon esculentum]

Seq. No.	220263
Seq. ID	LIB3149-046-Q1-K1-D1
Method	BLASTX
NCBI GI	g3643606
BLAST score	253
E value	1.0e-21
Match length	119
% identity	41
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220264
Seq. ID	LIB3149-046-Q1-K1-D10
Method	BLASTX
NCBI GI	g3914430
BLAST score	550
E value	1.0e-56
Match length	123
% identity	86
NCBI Description	PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi_2285800_dbj_BAA21650_ (D78172) 26S proteasome beta subunit [Spinacia oleracea]

Seq. No.	220265

Seq. ID	LIB3149-046-Q1-K1-D11
Method	BLASTX
NCBI GI	g1052973
BLAST score	174
E value	1.0e-12
Match length	46
% identity	76
NCBI Description	(U37838) fructokinase [Beta vulgaris]

Seq. No.	220266
Seq. ID	LIB3149-046-Q1-K1-D12
Method	BLASTX
NCBI GI	g4314361
BLAST score	216
E value	2.0e-17
Match length	44
% identity	95
NCBI Description	(AC006340) unknown protein [Arabidopsis thaliana]

Seq. No.	220267
Seq. ID	LIB3149-046-Q1-K1-D2
Method	BLASTX
NCBI GI	g322854
BLAST score	180
E value	3.0e-13
Match length	78
% identity	44
NCBI Description	pollen-specific protein - rice >gi_20310_emb_CAA78897_ (Z16402) pollen specific gene [Oryza sativa]

Seq. No.	220268
Seq. ID	LIB3149-046-Q1-K1-D3
Method	BLASTX
NCBI GI	g3128192
BLAST score	442
E value	6.0e-44
Match length	109
% identity	72
NCBI Description	(AC004521) axi 1-like protein [Arabidopsis thaliana]

Seq. No.	220269
Seq. ID	LIB3149-046-Q1-K1-D4
Method	BLASTX
NCBI GI	g2407800
BLAST score	532
E value	2.0e-54
Match length	133
% identity	83
NCBI Description	(Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No.	220270
Seq. ID	LIB3149-046-Q1-K1-D5
Method	BLASTX
NCBI GI	g1169840
BLAST score	356
E value	7.0e-34
Match length	71

% identity	79
NCBI Description	GIBBERELLIN-REGULATED PROTEIN 4 PRECURSOR >gi_2129591_pir__S71442 GAST1 protein homolog (clone GASA4) - Arabidopsis thaliana >gi_950099 (U15683) gibberellin-regulated [Arabidopsis thaliana]

Seq. No.	220271
Seq. ID	LIB3149-046-Q1-K1-D7
Method	BLASTX
NCBI GI	g585973
BLAST score	550
E value	1.0e-56
Match length	130
% identity	85
NCBI Description	FRUCTOKINASE >gi_626018_pir__S39997 fructokinase (EC 2.7.1.4) - potato >gi_297015_emb_CAA78283_ (Z12823) fructokinase [Solanum tuberosum] >gi_1095321_prf__2108342A fructokinase [Solanum tuberosum]

Seq. No.	220272
Seq. ID	LIB3149-046-Q1-K1-D8
Method	BLASTX
NCBI GI	g2997591
BLAST score	502
E value	6.0e-51
Match length	136
% identity	76
NCBI Description	(AF020814) glucose-6-phosphate/phosphate-translocator precursor [Pisum sativum]

Seq. No.	220273
Seq. ID	LIB3149-046-Q1-K1-E11
Method	BLASTX
NCBI GI	g1931655
BLAST score	602
E value	1.0e-62
Match length	129
% identity	86
NCBI Description	(U95973) receptor-kinase isolog [Arabidopsis thaliana]

Seq. No.	220274
Seq. ID	LIB3149-046-Q1-K1-E12
Method	BLASTX
NCBI GI	g2911073
BLAST score	418
E value	4.0e-41
Match length	128
% identity	67
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]

Seq. No.	220275
Seq. ID	LIB3149-046-Q1-K1-E4
Method	BLASTX
NCBI GI	g218157
BLAST score	358
E value	4.0e-34
Match length	78

% identity	88
NCBI Description	(D13512) cytoplasmic aldolase [Oryza sativa]

Seq. No.	220276
Seq. ID	LIB3149-046-Q1-K1-E5
Method	BLASTX
NCBI GI	g730583
BLAST score	188
E value	3.0e-14
Match length	111
% identity	41
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P2 >gi_551267_emb_CAA55047_ (X78213) 60s acidic ribosomal protein P2 [Parthenium argentatum]

Seq. No.	220277
Seq. ID	LIB3149-046-Q1-K1-E6
Method	BLASTX
NCBI GI	g4263791
BLAST score	276
E value	2.0e-24
Match length	59
% identity	90
NCBI Description	(AC006068) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	220278
Seq. ID	LIB3149-046-Q1-K1-E7
Method	BLASTX
NCBI GI	g2980770
BLAST score	394
E value	3.0e-38
Match length	129
% identity	63
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	220279
Seq. ID	LIB3149-046-Q1-K1-F1
Method	BLASTX
NCBI GI	g2780194
BLAST score	676
E value	2.0e-71
Match length	140
% identity	63
NCBI Description	(AJ003197) adenine nucleotide translocator [Lupinus albus]

Seq. No.	220280
Seq. ID	LIB3149-046-Q1-K1-F10
Method	BLASTX
NCBI GI	g4539545
BLAST score	632
E value	3.0e-66
Match length	129
% identity	94
NCBI Description	(Y16644) PRCI [Nicotiana tabacum]

Seq. No.	220281

Seq. ID	LIB3149-046-Q1-K1-F11
Method	BLASTX
NCBI GI	g3142300
BLAST score	494
E value	4.0e-50
Match length	121
% identity	69
NCBI Description	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this gene. [Arabidopsis thaliana]

Seq. No.	220282
Seq. ID	LIB3149-046-Q1-K1-F12
Method	BLASTX
NCBI GI	g3832512
BLAST score	156
E value	3.0e-11
Match length	94
% identity	44
NCBI Description	(AF097922) granule-bound glycogen (starch) synthase [Astragalus membranaceus]

Seq. No.	220283
Seq. ID	LIB3149-046-Q1-K1-F3
Method	BLASTX
NCBI GI	g399013
BLAST score	189
E value	2.0e-14
Match length	120
% identity	41
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	220284
Seq. ID	LIB3149-046-Q1-K1-F4
Method	BLASTX
NCBI GI	g121083
BLAST score	701
E value	3.0e-74
Match length	139
% identity	92
NCBI Description	GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) >gi_282926_pir__A42109 glycine dehydrogenase (decarboxylating) (EC 1.4.4.2) component P precursor - garden pea >gi_20741_emb_CAA42443_ (X59773) component of aminomethyltransferase [Pisum sativum]

Seq. No.	220285
Seq. ID	LIB3149-046-Q1-K1-F5
Method	BLASTX

NCBI GI	g2213595
BLAST score	290
E value	4.0e-26
Match length	126
% identity	48
NCBI Description	(AC000348) T7N9.15 [Arabidopsis thaliana]

Seq. No.	220286
Seq. ID	LIB3149-046-Q1-K1-F6
Method	BLASTX
NCBI GI	g2493129
BLAST score	667
E value	3.0e-70
Match length	136
% identity	99
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B SUBUNIT) >gi_459198 (U07052) vacuolar H+-ATPase subunit B [Gossypium hirsutum]

Seq. No.	220287
Seq. ID	LIB3149-046-Q1-K1-F7
Method	BLASTX
NCBI GI	g4519264
BLAST score	252
E value	1.0e-21
Match length	118
% identity	52
NCBI Description	(AB024277) vacuolar H+-ATPase B subunit [Citrus unshiu]

Seq. No.	220288
Seq. ID	LIB3149-046-Q1-K1-G1
Method	BLASTX
NCBI GI	g134672
BLAST score	554
E value	5.0e-57
Match length	132
% identity	78
NCBI Description	SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi_82145_pir__S03639 superoxide dismutase (EC 1.15.1.1) (Mn) precursor - curled-leaved tobacco >gi_19693_emb_CAA32643_ (X14482) manganese superoxide dismutase preprotein (AA -24 to 204) [Nicotiana plumbaginifolia]

Seq. No.	220289
Seq. ID	LIB3149-046-Q1-K1-G10
Method	BLASTX
NCBI GI	g2832623
BLAST score	388
E value	1.0e-37
Match length	111
% identity	65
NCBI Description	(AL021711) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	220290
Seq. ID	LIB3149-046-Q1-K1-G2
Method	BLASTX

NCBI GI	g134672
BLAST score	559
E value	1.0e-57
Match length	132
% identity	79
NCBI Description	SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi_82145_pir__S03639 superoxide dismutase (EC 1.15.1.1) (Mn) precursor - curled-leaved tobacco >gi_19693_emb_CAA32643_ (X14482) manganese superoxide dismutase preprotein (AA -24 to 204) [Nicotiana plumbaginifolia]

Seq. No.	220291
Seq. ID	LIB3149-046-Q1-K1-G3
Method	BLASTX
NCBI GI	g3643608
BLAST score	171
E value	4.0e-12
Match length	89
% identity	53
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220292
Seq. ID	LIB3149-046-Q1-K1-G4
Method	BLASTX
NCBI GI	g1076746
BLAST score	325
E value	3.0e-30
Match length	88
% identity	73
NCBI Description	heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]

Seq. No.	220293
Seq. ID	LIB3149-046-Q1-K1-G7
Method	BLASTX
NCBI GI	g114682
BLAST score	251
E value	1.0e-21
Match length	60
% identity	80
NCBI Description	ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP) >gi_100471_pir__A35227 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, mitochondrial - sweet potato >gi_168270 (J05397) F-1-ATPase delta subunit precursor (EC 3.6.1.3) [Ipomoea batatas]

Seq. No.	220294
Seq. ID	LIB3149-046-Q1-K1-H10
Method	BLASTN
NCBI GI	g1732358
BLAST score	44
E value	2.0e-15
Match length	80
% identity	89
NCBI Description	Malus domestica elongation factor 1 alpha (EF-1alpha) mRNA,

partial cds

Seq. No.	220295
Seq. ID	LIB3149-046-Q1-K1-H7
Method	BLASTX
NCBI GI	g124226
BLAST score	262
E value	7.0e-23
Match length	58
% identity	90
NCBI Description	INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D) >gi_100278_pir__S21059 translation initiation factor eIF-5A.2 - curled-leaved tobacco >gi_19702_emb_CAA45104_ (X63542) eukaryotic initiation factor 5A (2) [Nicotiana plumbaginifolia]

Seq. No.	220296
Seq. ID	LIB3149-047-Q1-K1-A2
Method	BLASTX
NCBI GI	g4210451
BLAST score	363
E value	1.0e-34
Match length	88
% identity	76
NCBI Description	(AB016472) ARR2 protein [Arabidopsis thaliana]

Seq. No.	220297
Seq. ID	LIB3149-047-Q1-K1-A3
Method	BLASTX
NCBI GI	g1350736
BLAST score	173
E value	2.0e-12
Match length	35
% identity	91
NCBI Description	60S RIBOSOMAL PROTEIN L37 >gi_629673_pir__S44313 ribosomal protein L37 - tomato >gi_483586_emb_CAA55674_ (X79074) ribosomal protein L37 [Lycopersicon esculentum]

Seq. No.	220298
Seq. ID	LIB3149-047-Q1-K1-A4
Method	BLASTX
NCBI GI	g3281868
BLAST score	238
E value	5.0e-20
Match length	53
% identity	91
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	220299
Seq. ID	LIB3149-047-Q1-K1-A5
Method	BLASTN
NCBI GI	g4006940
BLAST score	34
E value	2.0e-09
Match length	70
% identity	87
NCBI Description	Arabidopsis thaliana mRNA for voltage-dependent

anion-selective channel protein

Seq. No.	220300
Seq. ID	LIB3149-047-Q1-K1-A6
Method	BLASTX
NCBI GI	g3024629
BLAST score	154
E value	4.0e-10
Match length	118
% identity	31
NCBI Description	GAMMA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-GAMMA) >gi_423252_pir__S32369 gamma-SNAP protein - bovine >gi_298669_bbs_127528 gamma soluble NSF attachment protein, gamma SNAP=N-ethyl-maleimide-sensitive fusion protein attachment protein [cattle, brain, Peptide, 328 aa] >gi_445846_prf__1910317C NSF attachment protein (SNAP):ISOTYPE=gamma [Bos taurus]

Seq. No.	220301
Seq. ID	LIB3149-047-Q1-K1-B1
Method	BLASTX
NCBI GI	g730449
BLAST score	501
E value	7.0e-51
Match length	118
% identity	78
NCBI Description	60S RIBOSOMAL PROTEIN L13-1 (COLD INDUCED PROTEIN C24A) >gi_480647_pir__S37132 ribosomal protein L13.A - rape >gi_398918_emb_CAA80341_ (Z22618) cold induced protein (BnC24A) [Brassica napus]

Seq. No.	220302
Seq. ID	LIB3149-047-Q1-K1-B10
Method	BLASTX
NCBI GI	g2213620
BLAST score	410
E value	2.0e-40
Match length	93
% identity	88
NCBI Description	(AC000103) F21J9.13 [Arabidopsis thaliana]

Seq. No.	220303
Seq. ID	LIB3149-047-Q1-K1-B2
Method	BLASTX
NCBI GI	g1778145
BLAST score	294
E value	1.0e-26
Match length	66
% identity	80
NCBI Description	(U66402) phosphate/phosphoenolpyruvate translocator precursor [Nicotiana tabacum]

Seq. No.	220304
Seq. ID	LIB3149-047-Q1-K1-B3
Method	BLASTX
NCBI GI	g1710551
BLAST score	275

E value	2.0e-24
Match length	51
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L39 >gi_1177369_emb_CAA64728_ (X95458) ribosomal protein L39 [Zea mays]

Seq. No.	220305
Seq. ID	LIB3149-047-Q1-K1-B5
Method	BLASTX
NCBI GI	g3877252
BLAST score	175
E value	1.0e-12
Match length	74
% identity	50
NCBI Description	(Z93382) F45G2.10 [Caenorhabditis elegans]

Seq. No.	220306
Seq. ID	LIB3149-047-Q1-K1-B7
Method	BLASTX
NCBI GI	g3860255
BLAST score	305
E value	7.0e-28
Match length	140
% identity	48
NCBI Description	(AC005824) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220307
Seq. ID	LIB3149-047-Q1-K1-C11
Method	BLASTX
NCBI GI	g2832641
BLAST score	260
E value	7.0e-23
Match length	78
% identity	65
NCBI Description	(AL021710) glycolate oxidase - like protein [Arabidopsis thaliana]

Seq. No.	220308
Seq. ID	LIB3149-047-Q1-K1-C2
Method	BLASTX
NCBI GI	g3924597
BLAST score	248
E value	4.0e-21
Match length	106
% identity	49
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	220309
Seq. ID	LIB3149-047-Q1-K1-C3
Method	BLASTX
NCBI GI	g4099914
BLAST score	279
E value	8.0e-25
Match length	79
% identity	71
NCBI Description	(U91857) ethylene-responsive element binding protein homolog [Stylosanthes hamata]

09604704 - 960604

Seq. No.	220310
Seq. ID	LIB3149-047-Q1-K1-C5
Method	BLASTX
NCBI GI	g1710587
BLAST score	469
E value	3.0e-47
Match length	110
% identity	86
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P0 >gi_1196897 (L46848) acidic ribosomal protein P0 [Glycine max]

Seq. No.	220311
Seq. ID	LIB3149-047-Q1-K1-D1
Method	BLASTX
NCBI GI	g4510421
BLAST score	263
E value	6.0e-23
Match length	104
% identity	52
NCBI Description	(AC006929) unknown protein [Arabidopsis thaliana]

Seq. No.	220312
Seq. ID	LIB3149-047-Q1-K1-D3
Method	BLASTX
NCBI GI	g2764941
BLAST score	415
E value	9.0e-41
Match length	101
% identity	70
NCBI Description	(X98255) transcriptionally stimulated by gibberellins; expressed in meristematic region, and style [Arabidopsis thaliana]

Seq. No.	220313
Seq. ID	LIB3149-047-Q1-K1-D6
Method	BLASTX
NCBI GI	g3135269
BLAST score	342
E value	3.0e-32
Match length	122
% identity	65
NCBI Description	(AC003058) unknown protein [Arabidopsis thaliana]

Seq. No.	220314
Seq. ID	LIB3149-047-Q1-K1-D9
Method	BLASTX
NCBI GI	g3482918
BLAST score	390
E value	4.0e-38
Match length	90
% identity	84
NCBI Description	(AC003970) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	220315
Seq. ID	LIB3149-047-Q1-K1-E1

Method	BLASTX
NCBI GI	g3341685
BLAST score	321
E value	4.0e-35
Match length	117
% identity	72
NCBI Description	(AC003672) unknown protein [Arabidopsis thaliana]

Seq. No.	220316
Seq. ID	LIB3149-047-Q1-K1-E10
Method	BLASTX
NCBI GI	g1173209
BLAST score	363
E value	6.0e-35
Match length	92
% identity	82
NCBI Description	40S RIBOSOMAL PROTEIN S16 >gi_541835_pir__S41193 ribosomal protein S16 protein - upland cotton >gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit [Gossypium hirsutum]

Seq. No.	220317
Seq. ID	LIB3149-047-Q1-K1-E4
Method	BLASTX
NCBI GI	g4512664
BLAST score	511
E value	5.0e-52
Match length	136
% identity	68
NCBI Description	(AC006931) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana] >gi_4544471_gb_AAD22378.1_AC006580_10 (AC006580) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana]

Seq. No.	220318
Seq. ID	LIB3149-047-Q1-K1-E7
Method	BLASTX
NCBI GI	g1449179
BLAST score	261
E value	9.0e-23
Match length	112
% identity	49
NCBI Description	(D86506) N-ethylmaleimide sensitive fusion protein [Nicotiana tabacum]

Seq. No.	220319
Seq. ID	LIB3149-047-Q1-K1-E8
Method	BLASTX
NCBI GI	g1449179
BLAST score	448
E value	1.0e-44
Match length	137
% identity	67
NCBI Description	(D86506) N-ethylmaleimide sensitive fusion protein [Nicotiana tabacum]

Seq. No.	220320

Seq. ID	LIB3149-047-Q1-K1-F1
Method	BLASTX
NCBI GI	g4455364
BLAST score	368
E value	3.0e-35
Match length	127
% identity	52
NCBI Description	(AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No.	220321
Seq. ID	LIB3149-047-Q1-K1-F10
Method	BLASTX
NCBI GI	g3044218
BLAST score	143
E value	4.0e-09
Match length	43
% identity	67
NCBI Description	(AF057144) signal peptidase [Arabidopsis thaliana]

Seq. No.	220322
Seq. ID	LIB3149-047-Q1-K1-F11
Method	BLASTX
NCBI GI	g1173073
BLAST score	198
E value	1.0e-15
Match length	75
% identity	59
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P2 >gi_1076787_pir__S54179 acidic ribosomal protein 60S - maize >gi_2130117_pir__S65781 acidic ribosomal protein P2 - maize >gi_790508_emb_CAA60251_ (X86553) 60S acidic ribosomal protein [Zea mays]

Seq. No.	220323
Seq. ID	LIB3149-047-Q1-K1-F2
Method	BLASTX
NCBI GI	g1483218
BLAST score	153
E value	2.0e-17
Match length	78
% identity	63
NCBI Description	(X99793) induced upon wounding stress [Arabidopsis thaliana]

Seq. No.	220324
Seq. ID	LIB3149-047-Q1-K1-F4
Method	BLASTX
NCBI GI	g3024020
BLAST score	653
E value	1.0e-68
Match length	129
% identity	94
NCBI Description	INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D) >gi_2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation factor 5A3 [Solanum tuberosum]

Seq. No.	220325
Seq. ID	LIB3149-047-Q1-K1-F5
Method	BLASTX
NCBI GI	g3421109
BLAST score	612
E value	7.0e-64
Match length	130
% identity	90
NCBI Description	(AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis thaliana]

Seq. No.	220326
Seq. ID	LIB3149-047-Q1-K1-F7
Method	BLASTX
NCBI GI	g3021355
BLAST score	360
E value	3.0e-34
Match length	79
% identity	65
NCBI Description	(AJ005081) UDP-galactose 4-epimerase [Cyamopsis tetragonoloba]

Seq. No.	220327
Seq. ID	LIB3149-047-Q1-K1-F9
Method	BLASTX
NCBI GI	g2425066
BLAST score	376
E value	2.0e-36
Match length	92
% identity	75
NCBI Description	(AF019147) cysteine proteinase Mir3 [Zea mays]

Seq. No.	220328
Seq. ID	LIB3149-047-Q1-K1-G1
Method	BLASTX
NCBI GI	g1619300
BLAST score	528
E value	5.0e-54
Match length	112
% identity	90
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	220329
Seq. ID	LIB3149-047-Q1-K1-G10
Method	BLASTX
NCBI GI	g158146
BLAST score	153
E value	2.0e-10
Match length	62
% identity	50
NCBI Description	(M37610) polytene protein [Drosophila melanogaster]

Seq. No.	220330
Seq. ID	LIB3149-047-Q1-K1-G11
Method	BLASTX
NCBI GI	g1350680
BLAST score	390

E value	4.0e-38
Match length	94
% identity	78
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	220331
Seq. ID	LIB3149-047-Q1-K1-G2
Method	BLASTX
NCBI GI	g322750
BLAST score	658
E value	3.0e-69
Match length	128
% identity	99
NCBI Description	ubiquitin / ribosomal protein CEP52 - wood tobacco >gi_170217 (M74100) ubiquitin fusion protein [Nicotiana sylvestris]

Seq. No.	220332
Seq. ID	LIB3149-047-Q1-K1-G8
Method	BLASTX
NCBI GI	g2961300
BLAST score	556
E value	3.0e-57
Match length	126
% identity	86
NCBI Description	(AJ225027) ribosomal protein L24 [Cicer arietinum]

Seq. No.	220333
Seq. ID	LIB3149-047-Q1-K1-H6
Method	BLASTX
NCBI GI	g3193303
BLAST score	202
E value	9.0e-16
Match length	100
% identity	40
NCBI Description	(AF069298) similar to several proteins containing a tandem repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis thaliana]

Seq. No.	220334
Seq. ID	LIB3149-047-Q1-K1-H9
Method	BLASTX
NCBI GI	g2228773
BLAST score	195
E value	3.0e-15
Match length	56
% identity	71
NCBI Description	(AF001454) Dc3 promoter-binding factor-2 [Helianthus annuus]

Seq. No.	220335
Seq. ID	LIB3149-048-Q1-K1-A2
Method	BLASTX
NCBI GI	g113232
BLAST score	126
E value	6.0e-12

Match length	45
% identity	87
NCBI Description	ACTIN 2 >gi_100150_pir__S07003 actin 2 - carrot

Seq. No.	220336
Seq. ID	LIB3149-048-Q1-K1-A5
Method	BLASTX
NCBI GI	g4240207
BLAST score	170
E value	4.0e-12
Match length	118
% identity	33
NCBI Description	(AB020666) KIAA0859 protein [Homo sapiens]

Seq. No.	220337
Seq. ID	LIB3149-048-Q1-K1-A6
Method	BLASTX
NCBI GI	g1053047
BLAST score	582
E value	2.0e-60
Match length	116
% identity	100
NCBI Description	(U38425) histone H3 [Glycine max] >gi_1053049 (U38426) histone H3 [Glycine max] >gi_1053051 (U38427) histone H3 [Glycine max]

Seq. No.	220338
Seq. ID	LIB3149-048-Q1-K1-A7
Method	BLASTX
NCBI GI	g2765366
BLAST score	158
E value	1.0e-10
Match length	72
% identity	46
NCBI Description	(Y14038) putative Ole e 1 protein [Betula pendula]

Seq. No.	220339
Seq. ID	LIB3149-048-Q1-K1-A9
Method	BLASTX
NCBI GI	g2894612
BLAST score	361
E value	2.0e-34
Match length	106
% identity	68
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	220340
Seq. ID	LIB3149-048-Q1-K1-B10
Method	BLASTX
NCBI GI	g1841870
BLAST score	360
E value	3.0e-34
Match length	116
% identity	65
NCBI Description	(U87222) elongation factor 1-beta [Pimpinella brachycarpa]

Seq. No.	220341

Seq. ID	LIB3149-048-Q1-K1-B2
Method	BLASTX
NCBI GI	g2114046
BLAST score	547
E value	3.0e-56
Match length	120
% identity	88
NCBI Description	(AB002147) water channel protein [Nicotiana excelsior]

Seq. No.	220342
Seq. ID	LIB3149-048-Q1-K1-B3
Method	BLASTX
NCBI GI	g2454182
BLAST score	495
E value	2.0e-50
Match length	108
% identity	88
NCBI Description	(U80185) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	220343
Seq. ID	LIB3149-048-Q1-K1-B5
Method	BLASTX
NCBI GI	g586004
BLAST score	519
E value	5.0e-53
Match length	107
% identity	89
NCBI Description	SUPEROXIDE DISMUTASE [CU-ZN] >gi_421962_pir__S34267 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato >gi_542090_pir__S40404 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato >gi_311971_emb_CAA51654_ (X73139) superoxide dismutase [Ipomoea batatas]

Seq. No.	220344
Seq. ID	LIB3149-048-Q1-K1-B6
Method	BLASTX
NCBI GI	g2789660
BLAST score	342
E value	3.0e-32
Match length	127
% identity	51
NCBI Description	(AF040102) p105 [Arabidopsis thaliana]

Seq. No.	220345
Seq. ID	LIB3149-048-Q1-K1-B9
Method	BLASTX
NCBI GI	g1531672
BLAST score	136
E value	4.0e-12
Match length	93
% identity	51
NCBI Description	(U68461) actin [Striga asiatica]

Seq. No.	220346
Seq. ID	LIB3149-048-Q1-K1-C1
Method	BLASTX

NCBI GI	g1653142
BLAST score	175
E value	1.0e-12
Match length	85
% identity	46
NCBI Description	(D90911) hypothetical protein [Synechocystis sp.]

Seq. No.	220347
Seq. ID	LIB3149-048-Q1-K1-C11
Method	BLASTX
NCBI GI	g974782
BLAST score	636
E value	1.0e-66
Match length	126
% identity	96
NCBI Description	(Z49150) cobalamine-independent methionine synthase [Solenostemon scutellarioides]

Seq. No.	220348
Seq. ID	LIB3149-048-Q1-K1-C12
Method	BLASTX
NCBI GI	g974782
BLAST score	302
E value	1.0e-27
Match length	101
% identity	64
NCBI Description	(Z49150) cobalamine-independent methionine synthase [Solenostemon scutellarioides]

Seq. No.	220349
Seq. ID	LIB3149-048-Q1-K1-C2
Method	BLASTX
NCBI GI	g2828296
BLAST score	546
E value	3.0e-56
Match length	112
% identity	60
NCBI Description	(AL021687) RNase L inhibitor [Arabidopsis thaliana]

Seq. No.	220350
Seq. ID	LIB3149-048-Q1-K1-C3
Method	BLASTX
NCBI GI	g2765366
BLAST score	158
E value	1.0e-10
Match length	72
% identity	46
NCBI Description	(Y14038) putative Ole e 1 protein [Betula pendula]

Seq. No.	220351
Seq. ID	LIB3149-048-Q1-K1-C6
Method	BLASTX
NCBI GI	g71638
BLAST score	244
E value	8.0e-21
Match length	45
% identity	100

NCBI Description	actin - soybean >gi_18532_emb_CAA23728_ (V00450) actin [Glycine max] >gi_223413_prf__0804316A actin [Glycine max]
Seq. No.	220352
Seq. ID	LIB3149-048-Q1-K1-D1
Method	BLASTX
NCBI GI	g1703375
BLAST score	660
E value	2.0e-69
Match length	130
% identity	99
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]
Seq. No.	220353
Seq. ID	LIB3149-048-Q1-K1-D12
Method	BLASTX
NCBI GI	g228316
BLAST score	385
E value	3.0e-37
Match length	123
% identity	57
NCBI Description	albumin [Theobroma cacao]
Seq. No.	220354
Seq. ID	LIB3149-048-Q1-K1-D2
Method	BLASTX
NCBI GI	g4567283
BLAST score	259
E value	2.0e-22
Match length	66
% identity	79
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]
Seq. No.	220355
Seq. ID	LIB3149-048-Q1-K1-D9
Method	BLASTX
NCBI GI	g2653446
BLAST score	164
E value	2.0e-11
Match length	36
% identity	94
NCBI Description	(AB009077) proton pyrophosphatase [Vigna radiata]
Seq. No.	220356
Seq. ID	LIB3149-048-Q1-K1-E11
Method	BLASTX
NCBI GI	g4006827
BLAST score	620
E value	9.0e-65
Match length	143
% identity	81
NCBI Description	(AC005970) subtilisin-like protease [Arabidopsis thaliana]
Seq. No.	220357
Seq. ID	LIB3149-048-Q1-K1-E2
Method	BLASTX

NCBI GI	g1495251
BLAST score	167
E value	7.0e-12
Match length	98
% identity	44
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	220358
Seq. ID	LIB3149-048-Q1-K1-E5
Method	BLASTX
NCBI GI	g595957
BLAST score	420
E value	2.0e-51
Match length	122
% identity	78
NCBI Description	(U17098) Br FatA1 [Brassica rapa]

Seq. No.	220359
Seq. ID	LIB3149-048-Q1-K1-E9
Method	BLASTX
NCBI GI	g3212869
BLAST score	689
E value	7.0e-73
Match length	143
% identity	90
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	220360
Seq. ID	LIB3149-048-Q1-K1-F1
Method	BLASTX
NCBI GI	g4454464
BLAST score	438
E value	1.0e-43
Match length	114
% identity	69
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	220361
Seq. ID	LIB3149-048-Q1-K1-F10
Method	BLASTX
NCBI GI	g4091080
BLAST score	380
E value	1.0e-36
Match length	139
% identity	58
NCBI Description	(AF045571) nucleic acid binding protein [Oryza sativa]

Seq. No.	220362
Seq. ID	LIB3149-048-Q1-K1-F12
Method	BLASTX
NCBI GI	g1708995
BLAST score	148
E value	1.0e-09
Match length	49
% identity	63
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_726030

(U17240) S-adenosylmethionine synthetase [Actinidia chinensis]

Seq. No.	220363
Seq. ID	LIB3149-048-Q1-K1-F2
Method	BLASTX
NCBI GI	g4490937
BLAST score	153
E value	4.0e-10
Match length	111
% identity	40
NCBI Description	(AJ132261) hypothetical helicase K12H4.8-like protein [Homo sapiens]

Seq. No.	220364
Seq. ID	LIB3149-048-Q1-K1-F4
Method	BLASTX
NCBI GI	g416662
BLAST score	427
E value	2.0e-42
Match length	99
% identity	78
NCBI Description	21 KD SEED PROTEIN PRECURSOR >gi_99954_pir__S16252 trypsin inhibitor homolog - soybean >gi_21909_emb_CAA39860_ (X56509) 21 kDa seed protein [Theobroma cacao]

Seq. No.	220365
Seq. ID	LIB3149-048-Q1-K1-F6
Method	BLASTX
NCBI GI	g2662343
BLAST score	174
E value	8.0e-13
Match length	55
% identity	65
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	220366
Seq. ID	LIB3149-048-Q1-K1-F7
Method	BLASTX
NCBI GI	g4512705
BLAST score	349
E value	3.0e-33
Match length	98
% identity	72
NCBI Description	(AC006569) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	220367
Seq. ID	LIB3149-048-Q1-K1-F9
Method	BLASTX
NCBI GI	g1408471
BLAST score	523
E value	2.0e-53
Match length	116
% identity	81
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing

factor 1 [Arabidopsis thaliana]

Seq. No.	220368
Seq. ID	LIB3149-048-Q1-K1-G1
Method	BLASTX
NCBI GI	g1350720
BLAST score	223
E value	1.0e-18
Match length	45
% identity	91
NCBI Description	60S RIBOSOMAL PROTEIN L32

Seq. No.	220369
Seq. ID	LIB3149-048-Q1-K1-G10
Method	BLASTX
NCBI GI	g3834309
BLAST score	377
E value	3.0e-36
Match length	115
% identity	56
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb_L16983 Daucus carota and a member of S locus glycoprotein family PF_00954. ESTs gb_F13813, gb_T21052, gb_R30218 and gb_W43262 come from this gene. [Arabidopsis thaliana]

Seq. No.	220370
Seq. ID	LIB3149-048-Q1-K1-G2
Method	BLASTX
NCBI GI	g464707
BLAST score	264
E value	4.0e-23
Match length	64
% identity	80
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	220371
Seq. ID	LIB3149-048-Q1-K1-G8
Method	BLASTX
NCBI GI	g2414622
BLAST score	298
E value	4.0e-27
Match length	107
% identity	52

NCBI Description (Z99259) conserved protein [Schizosaccharomyces pombe]

Seq. No. 220372
Seq. ID LIB3149-048-Q1-K1-H1
Method BLASTX
NCBI GI g3402693
BLAST score 465
E value 1.0e-46
Match length 128
% identity 73
NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]

Seq. No. 220373
Seq. ID LIB3149-048-Q1-K1-H12
Method BLASTX
NCBI GI g1621268
BLAST score 557
E value 2.0e-57
Match length 140
% identity 69
NCBI Description (Z81012) unknown [Ricinus communis]

Seq. No. 220374
Seq. ID LIB3149-048-Q1-K1-H6
Method BLASTX
NCBI GI g3122673
BLAST score 465
E value 1.0e-46
Match length 122
% identity 75
NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_
(Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No. 220375
Seq. ID LIB3149-048-Q1-K1-H7
Method BLASTX
NCBI GI g1946355
BLAST score 431
E value 1.0e-42
Match length 124
% identity 66
NCBI Description (U93215) maize transposon MuDR mudrA protein isolog
[Arabidopsis thaliana] >gi_2880040 (AC002340) maize
transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No. 220376
Seq. ID LIB3149-049-Q1-K1-A1
Method BLASTX
NCBI GI g2982303
BLAST score 194
E value 4.0e-15
Match length 48
% identity 75
NCBI Description (AF051236) hypothetical protein [Picea mariana]

Seq. No. 220377
Seq. ID LIB3149-049-Q1-K1-A12

Method	BLASTX
NCBI GI	g902584
BLAST score	504
E value	2.0e-51
Match length	102
% identity	15
NCBI Description	(U29159) polyubiquitin containing 7 ubiquitin monomers [Zea mays]

Seq. No.	220378
Seq. ID	LIB3149-049-Q1-K1-A5
Method	BLASTX
NCBI GI	g1522681
BLAST score	157
E value	1.0e-10
Match length	114
% identity	29
NCBI Description	(U49240) symplekin [Homo sapiens] >gi_2143262_emb_CAA71861_ (Y10931) symplekin [Homo sapiens]

Seq. No.	220379
Seq. ID	LIB3149-049-Q1-K1-A6
Method	BLASTX
NCBI GI	g2832681
BLAST score	153
E value	5.0e-10
Match length	32
% identity	88
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	220380
Seq. ID	LIB3149-049-Q1-K1-A7
Method	BLASTX
NCBI GI	g81452
BLAST score	142
E value	8.0e-09
Match length	29
% identity	97
NCBI Description	tubulin beta chain - red goosefoot (fragment) >gi_82057_pir__S06045 tubulin beta chain - carrot (fragment) >gi_829259_emb_CAA34673_ (X16700) tubulin like protein fragment (AA 1-77) [Chenopodium rubrum] >gi_829261_emb_CAA34609_ (X16608) tubulin like protein fragment (AA 1-77) [Daucus carota]

Seq. No.	220381
Seq. ID	LIB3149-049-Q1-K1-A8
Method	BLASTX
NCBI GI	g3355470
BLAST score	431
E value	1.0e-42
Match length	124
% identity	68
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	220382

Seq. ID	LIB3149-049-Q1-K1-B1
Method	BLASTX
NCBI GI	g4539543
BLAST score	612
E value	6.0e-64
Match length	124
% identity	97
NCBI Description	(AJ133422) glyceraldehyde-3-phosphate dehydrogenase [Nicotiana tabacum]

Seq. No.	220383
Seq. ID	LIB3149-049-Q1-K1-B10
Method	BLASTX
NCBI GI	g1708313
BLAST score	147
E value	2.0e-09
Match length	60
% identity	57
NCBI Description	HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi_999396_bbs_163637 (S77849) heat-shock Protein=HSP81-3 [Arabidopsis thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis thaliana]

Seq. No.	220384
Seq. ID	LIB3149-049-Q1-K1-B2
Method	BLASTX
NCBI GI	g2583128
BLAST score	511
E value	5.0e-52
Match length	128
% identity	76
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220385
Seq. ID	LIB3149-049-Q1-K1-B4
Method	BLASTX
NCBI GI	g3249096
BLAST score	624
E value	3.0e-65
Match length	134
% identity	88
NCBI Description	(AC003114) Match to mRNA for importin alpha-like protein 4 (impa4) gb_Y14616 from A. thaliana. ESTs gb_N96440, gb_N37503, gb_N37498 and gb_T42198 come from this gene. [Arabidopsis thaliana]

Seq. No.	220386
Seq. ID	LIB3149-049-Q1-K1-B5
Method	BLASTX
NCBI GI	g1173218
BLAST score	617
E value	2.0e-64
Match length	122
% identity	98
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	220387
Seq. ID	LIB3149-049-Q1-K1-B7
Method	BLASTX
NCBI GI	g2795805
BLAST score	384
E value	4.0e-37
Match length	110
% identity	66
NCBI Description	(AC003674) putative protein kinase [Arabidopsis thaliana] >gi_3355493 (AC004218) putative protein kinase [Arabidopsis thaliana]

Seq. No.	220388
Seq. ID	LIB3149-049-Q1-K1-B8
Method	BLASTX
NCBI GI	g3036802
BLAST score	237
E value	6.0e-20
Match length	128
% identity	40
NCBI Description	(AL022373) putative protein [Arabidopsis thaliana] >gi_3805864_emb_CAA21484_ (AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	220389
Seq. ID	LIB3149-049-Q1-K1-B9
Method	BLASTX
NCBI GI	g1708313
BLAST score	145
E value	3.0e-09
Match length	48
% identity	71
NCBI Description	HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi_999396_bbs_163637 (S77849) heat-shock Protein=HSP81-3 [Arabidopsis thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis thaliana]

Seq. No.	220390
Seq. ID	LIB3149-049-Q1-K1-C1
Method	BLASTX
NCBI GI	g2244750
BLAST score	680
E value	7.0e-72
Match length	132
% identity	99
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	220391
Seq. ID	LIB3149-049-Q1-K1-C10
Method	BLASTX
NCBI GI	g4210330
BLAST score	570
E value	5.0e-59
Match length	127

% identity	83
NCBI Description	(AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]

Seq. No.	220392
Seq. ID	LIB3149-049-Q1-K1-C11
Method	BLASTX
NCBI GI	g4210330
BLAST score	214
E value	3.0e-17
Match length	113
% identity	47
NCBI Description	(AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]

Seq. No.	220393
Seq. ID	LIB3149-049-Q1-K1-C12
Method	BLASTX
NCBI GI	g1222552
BLAST score	222
E value	2.0e-18
Match length	50
% identity	82
NCBI Description	(U49330) pectin methylesterase [Lycopersicon esculentum]

Seq. No.	220394
Seq. ID	LIB3149-049-Q1-K1-C4
Method	BLASTX
NCBI GI	g2829899
BLAST score	300
E value	3.0e-27
Match length	122
% identity	48
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	220395
Seq. ID	LIB3149-049-Q1-K1-C6
Method	BLASTX
NCBI GI	g543905
BLAST score	715
E value	6.0e-76
Match length	132
% identity	96
NCBI Description	BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162) brassinosteroid-regulated protein [Glycine max]

Seq. No.	220396
Seq. ID	LIB3149-049-Q1-K1-C8
Method	BLASTX
NCBI GI	g1843527
BLAST score	453
E value	3.0e-45
Match length	118
% identity	77
NCBI Description	(U73747) annexin [Gossypium hirsutum]

Seq. No.	220397
Seq. ID	LIB3149-049-Q1-K1-C9
Method	BLASTX
NCBI GI	g4210330
BLAST score	614
E value	4.0e-64
Match length	130
% identity	88
NCBI Description	(AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]

Seq. No.	220398
Seq. ID	LIB3149-049-Q1-K1-D11
Method	BLASTX
NCBI GI	g2224731
BLAST score	242
E value	1.0e-20
Match length	95
% identity	57
NCBI Description	(AB004932) Aux22d [Vigna radiata]

Seq. No.	220399
Seq. ID	LIB3149-049-Q1-K1-D7
Method	BLASTX
NCBI GI	g1834353
BLAST score	165
E value	2.0e-18
Match length	107
% identity	48
NCBI Description	(Y10986) hypothetical protein 194 [Arabidopsis thaliana]

Seq. No.	220400
Seq. ID	LIB3149-049-Q1-K1-D8
Method	BLASTX
NCBI GI	g3892052
BLAST score	352
E value	2.0e-33
Match length	86
% identity	79
NCBI Description	(AC002330) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	220401
Seq. ID	LIB3149-049-Q1-K1-D9
Method	BLASTX
NCBI GI	g3947719
BLAST score	240
E value	2.0e-20
Match length	51
% identity	92
NCBI Description	(AJ012653) ribosomal protein S28 [Prunus persica] >gi_3947721_emb_CAA10102_ (AJ012654) ribosomal protein S28 [Prunus persica] >gi_3947723_emb_CAA10103_ (AJ012655) ribosomal protein S28 [Prunus persica]

Seq. No.	220402

Seq. ID	LIB3149-049-Q1-K1-E1
Method	BLASTX
NCBI GI	g3096949
BLAST score	541
E value	1.0e-55
Match length	124
% identity	81
NCBI Description	(Y16328) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic nucleotide-gated cation channel [Arabidopsis thaliana]

Seq. No.	220403
Seq. ID	LIB3149-049-Q1-K1-E10
Method	BLASTX
NCBI GI	g2505940
BLAST score	574
E value	2.0e-59
Match length	124
% identity	87
NCBI Description	(Y13071) 26S proteasome, non-ATPase subunit [Mus musculus]

Seq. No.	220404
Seq. ID	LIB3149-049-Q1-K1-E4
Method	BLASTX
NCBI GI	g3033544
BLAST score	147
E value	2.0e-09
Match length	78
% identity	38
NCBI Description	(AF055873) hypothetical protein [Synechococcus PCC7942]

Seq. No.	220405
Seq. ID	LIB3149-049-Q1-K1-E5
Method	BLASTX
NCBI GI	g115486
BLAST score	530
E value	3.0e-54
Match length	104
% identity	57
NCBI Description	CALMODULIN-2/3/5 >gi_99671_pir__S22503 calmodulin - Arabidopsis thaliana >gi_1076437_pir__S53006 calmodulin - leaf mustard >gi_2146726_pir__S71513 calmodulin - Arabidopsis thaliana >gi_166651 (M38380) calmodulin-2 [Arabidopsis thaliana] >gi_166653 (M73711) calmodulin-3 [Arabidopsis thaliana] >gi_474183_emb_CAA47690_ (X67273) calmodulin [Arabidopsis thaliana] >gi_497992 (U10150) calmodulin [Brassica napus] >gi_899058 (M88307) calmodulin [Brassica juncea] >gi_1183005_dbj_BAA08283_ (D45848) calmodulin [Arabidopsis thaliana] >gi_3402706 (AC004261) unknown protein [Arabidopsis thaliana] >gi_3885333 (AC005623) calmodulin [Arabidopsis thaliana] >gi_228407_prf__1803520A calmodulin 2 [Arabidopsis thaliana]

Seq. No.	220406
Seq. ID	LIB3149-049-Q1-K1-E8
Method	BLASTX

NCBI GI g1001631
BLAST score 238
E value 5.0e-20
Match length 129
% identity 40
NCBI Description (D64002) integral membrane protein [Synechocystis sp.]

Seq. No. 220407
Seq. ID LIB3149-049-Q1-K1-E9
Method BLASTX
NCBI GI g2505940
BLAST score 569
E value 7.0e-59
Match length 122
% identity 88
NCBI Description (Y13071) 26S proteasome, non-ATPase subunit [Mus musculus]

Seq. No. 220408
Seq. ID LIB3149-049-Q1-K1-F4
Method BLASTX
NCBI GI g1220196
BLAST score 671
E value 8.0e-71
Match length 134
% identity 98
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No. 220409
Seq. ID LIB3149-049-Q1-K1-F7
Method BLASTX
NCBI GI g1363482
BLAST score 159
E value 9.0e-11
Match length 84
% identity 48
NCBI Description IAA11 protein - Arabidopsis thaliana >gi_972925 (U18413) IAA11 [Arabidopsis thaliana]

Seq. No. 220410
Seq. ID LIB3149-049-Q1-K1-G1
Method BLASTX
NCBI GI g1363482
BLAST score 286
E value 1.0e-25
Match length 125
% identity 55
NCBI Description IAA11 protein - Arabidopsis thaliana >gi_972925 (U18413) IAA11 [Arabidopsis thaliana]

Seq. No. 220411
Seq. ID LIB3149-049-Q1-K1-G10
Method BLASTX
NCBI GI g2833388
BLAST score 393
E value 1.0e-46
Match length 130
% identity 74

NCBI Description	GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi_629660_pir__S43341 ADPglucose--starch glucosyltransferase (EC 2.4.1.21) precursor - cassava >gi_437042_emb_CAA52273_ (X74160) starch (bacterial glycogen) synthase [Manihot esculenta]
Seq. No.	220412
Seq. ID	LIB3149-049-Q1-K1-G5
Method	BLASTN
NCBI GI	g2760168
BLAST score	34
E value	1.0e-09
Match length	88
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]
Seq. No.	220413
Seq. ID	LIB3149-049-Q1-K1-G6
Method	BLASTX
NCBI GI	g3482967
BLAST score	605
E value	5.0e-63
Match length	137
% identity	80
NCBI Description	(AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana]
Seq. No.	220414
Seq. ID	LIB3149-049-Q1-K1-G7
Method	BLASTN
NCBI GI	g2529657
BLAST score	38
E value	5.0e-12
Match length	70
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	220415
Seq. ID	LIB3149-049-Q1-K1-H10
Method	BLASTX
NCBI GI	g1174448
BLAST score	198
E value	2.0e-15
Match length	61
% identity	61
NCBI Description	TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) >gi_547391 (L32016) alpha-subunit; putative [Arabidopsis thaliana]
Seq. No.	220416
Seq. ID	LIB3149-050-Q1-K1-A11
Method	BLASTX
NCBI GI	g1351987

BLAST score	307
E value	3.0e-29
Match length	90
% identity	72
NCBI Description	ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) >gi_507946 (L29083) glutamine-dependent asparagine synthetase [Arabidopsis thaliana]

Seq. No.	220417
Seq. ID	LIB3149-050-Q1-K1-A12
Method	BLASTX
NCBI GI	g4314400
BLAST score	229
E value	3.0e-19
Match length	73
% identity	60
NCBI Description	(AC006232) putative selenium-binding protein [Arabidopsis thaliana]

Seq. No.	220418
Seq. ID	LIB3149-050-Q1-K1-A3
Method	BLASTX
NCBI GI	g1477428
BLAST score	710
E value	2.0e-75
Match length	134
% identity	96
NCBI Description	(X99623) alpha-tubulin 1 [Hordeum vulgare]

Seq. No.	220419
Seq. ID	LIB3149-050-Q1-K1-A4
Method	BLASTX
NCBI GI	g1477428
BLAST score	405
E value	3.0e-46
Match length	110
% identity	85
NCBI Description	(X99623) alpha-tubulin 1 [Hordeum vulgare]

Seq. No.	220420
Seq. ID	LIB3149-050-Q1-K1-B11
Method	BLASTX
NCBI GI	g3128228
BLAST score	416
E value	4.0e-41
Match length	88
% identity	89
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	220421
Seq. ID	LIB3149-050-Q1-K1-B12
Method	BLASTX
NCBI GI	g1053047
BLAST score	354

E value	7.0e-34
Match length	85
% identity	85
NCBI Description	(U38425) histone H3 [Glycine max] >gi_1053049 (U38426) histone H3 [Glycine max] >gi_1053051 (U38427) histone H3 [Glycine max]

Seq. No.	220422
Seq. ID	LIB3149-050-Q1-K1-B7
Method	BLASTX
NCBI GI	g2943792
BLAST score	625
E value	2.0e-65
Match length	128
% identity	88
NCBI Description	(AB006809) PV72 [Cucurbita sp.]

Seq. No.	220423
Seq. ID	LIB3149-050-Q1-K1-B8
Method	BLASTN
NCBI GI	g2264305
BLAST score	34
E value	1.0e-09
Match length	117
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK23, complete sequence [Arabidopsis thaliana]

Seq. No.	220424
Seq. ID	LIB3149-050-Q1-K1-C12
Method	BLASTX
NCBI GI	g3850573
BLAST score	353
E value	9.0e-34
Match length	94
% identity	69
NCBI Description	(AC005278) Similar to gi_1652733 glycogen operon protein GlgX from Synechocystis sp. genome gb_D90908. ESTs gb_H36690, gb_AA712462, gb_AA651230 and gb_N95932 come from this gene. [Arabidopsis thaliana]

Seq. No.	220425
Seq. ID	LIB3149-050-Q1-K1-C2
Method	BLASTX
NCBI GI	g133785
BLAST score	297
E value	3.0e-27
Match length	77
% identity	82
NCBI Description	40S RIBOSOMAL PROTEIN S14 >gi_70945_pir__R3RT14 ribosomal protein S14 - rat >gi_57129_emb_CAA33143_ (X15040) ribosomal protein S14 (AA 1-152) [Rattus norvegicus]

Seq. No.	220426
Seq. ID	LIB3149-050-Q1-K1-C3
Method	BLASTN
NCBI GI	g4325218

BLAST score	35
E value	4.0e-10
Match length	63
% identity	89
NCBI Description	Arabidopsis thaliana hydrophobic protein (RCI2B) mRNA, complete cds

Seq. No.	220427
Seq. ID	LIB3149-050-Q1-K1-C4
Method	BLASTX
NCBI GI	g3928543
BLAST score	174
E value	2.0e-12
Match length	109
% identity	39
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	220428
Seq. ID	LIB3149-050-Q1-K1-C6
Method	BLASTX
NCBI GI	g531389
BLAST score	180
E value	3.0e-13
Match length	87
% identity	41
NCBI Description	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]

Seq. No.	220429
Seq. ID	LIB3149-050-Q1-K1-C7
Method	BLASTX
NCBI GI	g3183247
BLAST score	311
E value	1.0e-28
Match length	128
% identity	51
NCBI Description	PUTATIVE GTP-BINDING PROTEIN W08E3.3 >gi_3880615_emb_CAB07131_ (Z92773) predicted using Genefinder; Similarity to Yeast hypothetical 44.2 KD protein, putative GTP-binding protein (SW:P38219); cDNA EST EMBL:D64516 comes from this gene; cDNA EST EMBL:D65777 comes from this gene; cDNA EST EMB

Seq. No.	220430
Seq. ID	LIB3149-050-Q1-K1-C8
Method	BLASTX
NCBI GI	g485742
BLAST score	614
E value	4.0e-64
Match length	131
% identity	90
NCBI Description	(L32791) pyrophosphatase [Beta vulgaris]

Seq. No.	220431
Seq. ID	LIB3149-050-Q1-K1-C9
Method	BLASTX

NCBI GI	g1402878
BLAST score	270
E value	5.0e-24
Match length	91
% identity	59
NCBI Description	(X98130) unknown [Arabidopsis thaliana]

Seq. No.	220432
Seq. ID	LIB3149-050-Q1-K1-D4
Method	BLASTX
NCBI GI	g4115377
BLAST score	316
E value	4.0e-47
Match length	116
% identity	82
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	220433
Seq. ID	LIB3149-050-Q1-K1-E7
Method	BLASTN
NCBI GI	g18342
BLAST score	35
E value	4.0e-10
Match length	64
% identity	16
NCBI Description	Carrot gene for extensin

Seq. No.	220434
Seq. ID	LIB3149-050-Q1-K1-E9
Method	BLASTX
NCBI GI	g3913919
BLAST score	326
E value	1.0e-30
Match length	77
% identity	82
NCBI Description	ACID BETA-FRUCTOFURANOSIDASE PRECURSOR (ACID SUCROSE-6-PHOSPHATE HYDROLASE) (ACID INVERTASE) (AI) (VACUOLAR INVERTASE) >gi_2351827 (U92438) soluble acid invertase [Phaseolus vulgaris]

Seq. No.	220435
Seq. ID	LIB3149-050-Q1-K1-F3
Method	BLASTX
NCBI GI	g2621768
BLAST score	149
E value	1.0e-09
Match length	97
% identity	35
NCBI Description	(AE000848) ribonuclease PH [Methanobacterium thermoautotrophicum]

Seq. No.	220436
Seq. ID	LIB3149-050-Q1-K1-F7
Method	BLASTX
NCBI GI	g2642450
BLAST score	576
E value	1.0e-59

Match length	131
% identity	85
NCBI Description	(AC002391) putative metal ion transporter (Nramp) [Arabidopsis thaliana] >gi_3169188 (AC004401) putative metal ion transporter (Nramp) [Arabidopsis thaliana]

Seq. No.	220437
Seq. ID	LIB3149-050-Q1-K1-G10
Method	BLASTX
NCBI GI	g3337356
BLAST score	330
E value	4.0e-31
Match length	86
% identity	76
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	220438
Seq. ID	LIB3149-050-Q1-K1-G12
Method	BLASTN
NCBI GI	g4519188
BLAST score	37
E value	2.0e-11
Match length	89
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No.	220439
Seq. ID	LIB3149-050-Q1-K1-G3
Method	BLASTX
NCBI GI	g2982299
BLAST score	238
E value	4.0e-20
Match length	83
% identity	60
NCBI Description	(AF051234) transcription factor BTF3 homolog [Picea mariana]

Seq. No.	220440
Seq. ID	LIB3149-050-Q1-K1-G5
Method	BLASTX
NCBI GI	g2414622
BLAST score	246
E value	5.0e-21
Match length	102
% identity	50
NCBI Description	(Z99259) conserved protein [Schizosaccharomyces pombe]

Seq. No.	220441
Seq. ID	LIB3149-050-Q1-K1-G7
Method	BLASTX
NCBI GI	g1350680
BLAST score	162
E value	1.0e-11
Match length	65
% identity	49

NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 220442
Seq. ID LIB3149-050-Q1-K1-H10
Method BLASTX
NCBI GI g1222552
BLAST score 424
E value 4.0e-42
Match length 95
% identity 81
NCBI Description (U49330) pectin methylesterase [Lycopersicon esculentum]

Seq. No. 220443
Seq. ID LIB3149-050-Q1-K1-H9
Method BLASTN
NCBI GI g4263774
BLAST score 36
E value 6.0e-11
Match length 64
% identity 45
NCBI Description Arabidopsis thaliana chromosome II BAC T20F21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 220444
Seq. ID LIB3149-051-Q1-K1-A5
Method BLASTX
NCBI GI g4455198
BLAST score 225
E value 1.0e-18
Match length 98
% identity 53
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 220445
Seq. ID LIB3149-051-Q1-K1-A6
Method BLASTX
NCBI GI g3319882
BLAST score 460
E value 3.0e-46
Match length 99
% identity 89
NCBI Description (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer arietinum]

Seq. No. 220446
Seq. ID LIB3149-051-Q1-K1-A7
Method BLASTX
NCBI GI g3850568
BLAST score 216
E value 1.0e-17
Match length 67
% identity 66
NCBI Description (AC005278) Similar to hypothetical protein SPAC2F7.14c gi_1052797 from Schizosaccharomyces pombe cosmid gb_Z50142. [Arabidopsis thaliana]

Seq. No. 220447

Seq. ID	LIB3149-051-Q1-K1-B12
Method	BLASTX
NCBI GI	g4263713
BLAST score	285
E value	1.0e-25
Match length	69
% identity	71
NCBI Description	(AC006223) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220448
Seq. ID	LIB3149-051-Q1-K1-B4
Method	BLASTX
NCBI GI	g2760322
BLAST score	137
E value	9.0e-09
Match length	55
% identity	53
NCBI Description	(AC002130) F1N21.7 [Arabidopsis thaliana]

Seq. No.	220449
Seq. ID	LIB3149-051-Q1-K1-B5
Method	BLASTX
NCBI GI	g1222552
BLAST score	477
E value	3.0e-48
Match length	103
% identity	83
NCBI Description	(U49330) pectin methylesterase [Lycopersicon esculentum]

Seq. No.	220450
Seq. ID	LIB3149-051-Q1-K1-B7
Method	BLASTX
NCBI GI	g3882203
BLAST score	209
E value	1.0e-19
Match length	80
% identity	62
NCBI Description	(AB018284) KIAA0741 protein [Homo sapiens]

Seq. No.	220451
Seq. ID	LIB3149-051-Q1-K1-B8
Method	BLASTX
NCBI GI	g2738248
BLAST score	387
E value	1.0e-37
Match length	87
% identity	84
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	220452
Seq. ID	LIB3149-051-Q1-K1-C10
Method	BLASTN
NCBI GI	g2687435
BLAST score	275
E value	1.0e-153
Match length	303

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% identity	98
NCBI Description	Hamamelis virginiana large subunit 26S ribosomal RNA gene, partial sequence
Seq. No.	220453
Seq. ID	LIB3149-051-Q1-K1-C11
Method	BLASTN
NCBI GI	g1360093
BLAST score	35
E value	3.0e-10
Match length	47
% identity	94
NCBI Description	N.tabacum mRNA for a putative serine/threonine receptor kinase
Seq. No.	220454
Seq. ID	LIB3149-051-Q1-K1-C2
Method	BLASTX
NCBI GI	g629597
BLAST score	277
E value	1.0e-24
Match length	62
% identity	79
NCBI Description	proline-rich protein - rape >gi_545029_bbs_142669 (S68113) proline-rich SAC51 [Brassica napus=oilseed rape, pods, Peptide, 147 aa] [Brassica napus]
Seq. No.	220455
Seq. ID	LIB3149-051-Q1-K1-C3
Method	BLASTX
NCBI GI	g531829
BLAST score	154
E value	2.0e-10
Match length	74
% identity	42
NCBI Description	(U12390) beta-galactosidase alpha peptide [cloning vector pSport1]
Seq. No.	220456
Seq. ID	LIB3149-051-Q1-K1-C7
Method	BLASTN
NCBI GI	g2558961
BLAST score	222
E value	1.0e-122
Match length	234
% identity	99
NCBI Description	Gossypium hirsutum histone H2B1 mRNA, complete cds
Seq. No.	220457
Seq. ID	LIB3149-051-Q1-K1-D10
Method	BLASTX
NCBI GI	g1710546
BLAST score	365
E value	4.0e-35
Match length	81
% identity	88
NCBI Description	60S RIBOSOMAL PROTEIN L36 >gi_1276967 (U47095) putative

ribosomal protein [Daucus carota]

Seq. No.	220458
Seq. ID	LIB3149-051-Q1-K1-D3
Method	BLASTN
NCBI GI	g4098126
BLAST score	108
E value	6.0e-54
Match length	197
% identity	97
NCBI Description	Gossypium hirsutum sucrose synthase mRNA, partial cds

Seq. No.	220459
Seq. ID	LIB3149-051-Q1-K1-D4
Method	BLASTN
NCBI GI	g4098126
BLAST score	35
E value	1.0e-10
Match length	85
% identity	93
NCBI Description	Gossypium hirsutum sucrose synthase mRNA, partial cds

Seq. No.	220460
Seq. ID	LIB3149-051-Q1-K1-D7
Method	BLASTX
NCBI GI	g730526
BLAST score	194
E value	4.0e-15
Match length	91
% identity	48
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No.	220461
Seq. ID	LIB3149-051-Q1-K1-D8
Method	BLASTX
NCBI GI	g1350944
BLAST score	391
E value	4.0e-38
Match length	80
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN S17

Seq. No.	220462
Seq. ID	LIB3149-051-Q1-K1-E11
Method	BLASTX
NCBI GI	g3925703
BLAST score	425
E value	4.0e-42
Match length	98
% identity	88
NCBI Description	(X95905) 14-3-3 protein [Lycopersicon esculentum]

Seq. No.	220463
Seq. ID	LIB3149-051-Q1-K1-E12

Method	BLASTX
NCBI GI	g1354849
BLAST score	197
E value	2.0e-15
Match length	102
% identity	60
NCBI Description	(U57350) epoxide hydrolase [Nicotiana tabacum]

Seq. No.	220464
Seq. ID	LIB3149-051-Q1-K1-E4
Method	BLASTX
NCBI GI	g1351987
BLAST score	352
E value	1.0e-33
Match length	94
% identity	73
NCBI Description	ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) >gi_507946 (L29083) glutamine-dependent asparagine synthetase [Arabidopsis thaliana]

Seq. No.	220465
Seq. ID	LIB3149-051-Q1-K1-F10
Method	BLASTX
NCBI GI	g4158232
BLAST score	532
E value	1.0e-54
Match length	105
% identity	90
NCBI Description	(Y18626) reversibly glycosylated polypeptide [Triticum aestivum]

Seq. No.	220466
Seq. ID	LIB3149-051-Q1-K1-F4
Method	BLASTX
NCBI GI	g3269284
BLAST score	240
E value	2.0e-20
Match length	87
% identity	59
NCBI Description	(AL030978) histone H2A- like protein [Arabidopsis thaliana]

Seq. No.	220467
Seq. ID	LIB3149-051-Q1-K1-F6
Method	BLASTX
NCBI GI	g4522012
BLAST score	296
E value	6.0e-27
Match length	79
% identity	65
NCBI Description	(AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220468
Seq. ID	LIB3149-051-Q1-K1-F7
Method	BLASTX
NCBI GI	g4371285
BLAST score	439

E value 9.0e-44
Match length 98
% identity 85
NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 220469
Seq. ID LIB3149-051-Q1-K1-F8
Method BLASTX
NCBI GI g1877397
BLAST score 336
E value 1.0e-31
Match length 73
% identity 85
NCBI Description (Y11591) shaggy-like kinase [Ricinus communis]

Seq. No. 220470
Seq. ID LIB3149-051-Q1-K1-F9
Method BLASTX
NCBI GI g3451411
BLAST score 330
E value 5.0e-31
Match length 102
% identity 62
NCBI Description (Z98761) seryl-tRNA synthetase [Helianthus annuus]

Seq. No. 220471
Seq. ID LIB3149-051-Q1-K1-G1
Method BLASTX
NCBI GI g1352821
BLAST score 284
E value 1.0e-25
Match length 56
% identity 93
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 220472
Seq. ID LIB3149-051-Q1-K1-G11
Method BLASTX
NCBI GI g2499945
BLAST score 394
E value 2.0e-38
Match length 102
% identity 75
NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_1076363_pir__S46440 orotate phosphoribosyltransferase (EC 2.4.2.10) / orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842) pyrE-F [Arabidopsis thaliana]

Seq. No. 220473
Seq. ID LIB3149-051-Q1-K1-G2

Method	BLASTX
NCBI GI	g1617272
BLAST score	419
E value	2.0e-41
Match length	101
% identity	73
NCBI Description	(Z72151) AMP-binding protein [Brassica napus]

Seq. No.	220474
Seq. ID	LIB3149-051-Q1-K1-G4
Method	BLASTX
NCBI GI	g3037045
BLAST score	148
E value	1.0e-09
Match length	74
% identity	43
NCBI Description	(AF052621) hypothetical protein COX4AL [Mus musculus]

Seq. No.	220475
Seq. ID	LIB3149-051-Q1-K1-G9
Method	BLASTX
NCBI GI	g4580519
BLAST score	377
E value	2.0e-36
Match length	101
% identity	71
NCBI Description	(AF036303) scarecrow-like 6 [Arabidopsis thaliana]

Seq. No.	220476
Seq. ID	LIB3149-051-Q1-K1-H10
Method	BLASTX
NCBI GI	g4115377
BLAST score	432
E value	6.0e-43
Match length	111
% identity	73
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	220477
Seq. ID	LIB3149-051-Q1-K1-H4
Method	BLASTX
NCBI GI	g2281090
BLAST score	217
E value	8.0e-18
Match length	112
% identity	46
NCBI Description	(AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220478
Seq. ID	LIB3149-051-Q1-K1-H7
Method	BLASTX
NCBI GI	g4263822
BLAST score	153
E value	3.0e-10
Match length	98
% identity	36
NCBI Description	(AC006067) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No.	220479
Seq. ID	LIB3149-051-Q1-K1-H9
Method	BLASTX
NCBI GI	g2267567
BLAST score	402
E value	2.0e-39
Match length	89
% identity	87
NCBI Description	(AF009003) glycine-rich RNA binding protein 1 [Pelargonium x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding protein 2 [Pelargonium x hortorum]

Seq. No.	220480
Seq. ID	LIB3149-052-Q1-K1-A1
Method	BLASTX
NCBI GI	g4193382
BLAST score	262
E value	4.0e-23
Match length	50
% identity	90
NCBI Description	(AF083336) ribosomal protein S27 [Arabidopsis thaliana] >gi_4193384 (AF083337) ribosomal protein S27 [Arabidopsis thaliana]

Seq. No.	220481
Seq. ID	LIB3149-053-Q1-K1-A1
Method	BLASTN
NCBI GI	g2275090
BLAST score	173
E value	1.0e-92
Match length	193
% identity	97
NCBI Description	Swietenia humilis DNA for simple tandem repeat (341bp)

Seq. No.	220482
Seq. ID	LIB3149-053-Q1-K1-A11
Method	BLASTX
NCBI GI	g3914535
BLAST score	159
E value	5.0e-11
Match length	39
% identity	85
NCBI Description	60S RIBOSOMAL PROTEIN L13A >gi_2791948_emb_CAA11283_ (AJ223363) ribosomal protein L13a [Lupinus luteus]

Seq. No.	220483
Seq. ID	LIB3149-053-Q1-K1-A2
Method	BLASTX
NCBI GI	g1587206
BLAST score	361
E value	2.0e-34
Match length	116
% identity	69
NCBI Description	T complex protein [Cucumis sativus]

Seq. No.	220484
Seq. ID	LIB3149-053-Q1-K1-A3
Method	BLASTX
NCBI GI	g1587206
BLAST score	623
E value	3.0e-65
Match length	130
% identity	94
NCBI Description	T complex protein [Cucumis sativus]

Seq. No.	220485
Seq. ID	LIB3149-053-Q1-K1-A4
Method	BLASTX
NCBI GI	g1587206
BLAST score	519
E value	6.0e-53
Match length	132
% identity	79
NCBI Description	T complex protein [Cucumis sativus]

Seq. No.	220486
Seq. ID	LIB3149-053-Q1-K1-A8
Method	BLASTX
NCBI GI	g1703375
BLAST score	210
E value	8.0e-28
Match length	93
% identity	80
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]

Seq. No.	220487
Seq. ID	LIB3149-053-Q1-K1-A9
Method	BLASTX
NCBI GI	g2500026
BLAST score	556
E value	3.0e-57
Match length	126
% identity	83
NCBI Description	ADENYLOSUCCINATE SYNTHETASE PRECURSOR (IMP--ASPARTATE LIGASE) >gi_1616657 (U49389) adenylosuccinate synthetase [Arabidopsis thaliana]

Seq. No.	220488
Seq. ID	LIB3149-053-Q1-K1-B12
Method	BLASTX
NCBI GI	g643469
BLAST score	139
E value	9.0e-09
Match length	40
% identity	65
NCBI Description	(U19886) unknown [Lycopersicon esculentum]

Seq. No.	220489
Seq. ID	LIB3149-053-Q1-K1-B2
Method	BLASTX
NCBI GI	g2213425

BLAST score	314
E value	4.0e-29
Match length	70
% identity	47
NCBI Description	(Z97064) hypothetical protein [Citrus x paradisi]

Seq. No.	220490
Seq. ID	LIB3149-053-Q1-K1-B3
Method	BLASTX
NCBI GI	g399940
BLAST score	628
E value	8.0e-66
Match length	131
% identity	96
NCBI Description	MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR >gi_100004_pir__S25005 heat shock protein, 70K - kidney bean >gi_22636_emb_CAA47345_ (X66874) 70 kDa heat shock protein [Phaseolus vulgaris]

Seq. No.	220491
Seq. ID	LIB3149-053-Q1-K1-B5
Method	BLASTX
NCBI GI	g133424
BLAST score	166
E value	1.0e-11
Match length	46
% identity	72
NCBI Description	DNA-DIRECTED RNA POLYMERASE BETA CHAIN >gi_66969_pir__RNNTB DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - common tobacco chloroplast >gi_11781_emb_CAA31238_ (X12745) ORF 1070 (AA 1-1070); put. RNA polymerase beta-subunit [Nicotiana tabacum] >gi_11822_emb_CAA77346_ (Z00044) RNA polymerase beta subunit [Nicotiana tabacum]

Seq. No.	220492
Seq. ID	LIB3149-053-Q1-K1-B7
Method	BLASTN
NCBI GI	g3869069
BLAST score	36
E value	8.0e-11
Match length	226
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	220493
Seq. ID	LIB3149-053-Q1-K1-C12
Method	BLASTX
NCBI GI	g2500355
BLAST score	212
E value	3.0e-17
Match length	56
% identity	79
NCBI Description	60S RIBOSOMAL PROTEIN L10 (QM PROTEIN HOMOLOG) >gi_629704_pir__S44144 ribosomal protein L10.e, cytosolic - common tobacco (fragment) >gi_473104_emb_CAA78461_ (Z14083) HOMOLOGIE with Human WILM's tumor-related protein HUMQM

[Nicotiana tabacum]

Seq. No.	220494
Seq. ID	LIB3149-053-Q1-K1-C3
Method	BLASTX
NCBI GI	g417148
BLAST score	363
E value	1.0e-34
Match length	129
% identity	55
NCBI Description	PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A) (G2-4) >gi_99912_pir__A33654 heat shock protein 26A - soybean >gi_169981 (M20363) Gmhsp26-A [Glycine max]

Seq. No.	220495
Seq. ID	LIB3149-053-Q1-K1-C4
Method	BLASTX
NCBI GI	g1420938
BLAST score	277
E value	1.0e-24
Match length	80
% identity	69
NCBI Description	(U61379) Vigna unguiculata ascorbate peroxidase mRNA, complete cds [Vigna unguiculata]

Seq. No.	220496
Seq. ID	LIB3149-053-Q1-K1-C5
Method	BLASTX
NCBI GI	g2827544
BLAST score	211
E value	7.0e-17
Match length	44
% identity	93
NCBI Description	(AL021635) HSP associated protein like [Arabidopsis thaliana]

Seq. No.	220497
Seq. ID	LIB3149-053-Q1-K1-C7
Method	BLASTX
NCBI GI	g2894599
BLAST score	210
E value	9.0e-17
Match length	119
% identity	46
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	220498
Seq. ID	LIB3149-053-Q1-K1-D1
Method	BLASTX
NCBI GI	g4559346
BLAST score	421
E value	2.0e-41
Match length	128
% identity	64
NCBI Description	(AC006585) early nodulin 16 [Arabidopsis thaliana]

Seq. No.	220499

Seq. ID	LIB3149-053-Q1-K1-D11
Method	BLASTX
NCBI GI	g136712
BLAST score	585
E value	1.0e-60
Match length	133
% identity	80
NCBI Description	CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_81457_pir__S00454 plastoquinol--plastocyanin reductase (EC 1.10.99.1) iron-sulfur protein precursor - spinach >gi_21311_emb_CAA29590_ (X06244) Rieske FeS-precursor [Spinacia oleracea] >gi_226151_prf__1412276A rieske FeS precursor protein [Spinacia oleracea]

Seq. No.	220500
Seq. ID	LIB3149-053-Q1-K1-D12
Method	BLASTX
NCBI GI	g136707
BLAST score	242
E value	2.0e-20
Match length	52
% identity	90
NCBI Description	CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_280397_pir__S26199 plastoquinol--plastocyanin reductase (EC 1.10.99.1) iron-sulfur protein precursor - garden pea >gi_20832_emb_CAA45151_ (X63605) chloroplast Rieske FeS protein [Pisum sativum]

Seq. No.	220501
Seq. ID	LIB3149-053-Q1-K1-D3
Method	BLASTX
NCBI GI	g2499488
BLAST score	628
E value	9.0e-66
Match length	130
% identity	95
NCBI Description	PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849) pyrophosphate-dependent phosphofructokinase alpha subunit [Ricinus communis]

Seq. No.	220502
Seq. ID	LIB3149-053-Q1-K1-D5
Method	BLASTX
NCBI GI	g3335359
BLAST score	235
E value	1.0e-19
Match length	128
% identity	45
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	220503
Seq. ID	LIB3149-053-Q1-K1-D6

Method	BLASTX
NCBI GI	g3335359
BLAST score	159
E value	8.0e-11
Match length	128
% identity	36
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	220504
Seq. ID	LIB3149-053-Q1-K1-D7
Method	BLASTX
NCBI GI	g3913633
BLAST score	158
E value	4.0e-13
Match length	88
% identity	60
NCBI Description	HYPOTHETICAL PROTEIN F8A5.25 >gi_2462742 (AC002292) Unknown protein [Arabidopsis thaliana]

Seq. No.	220505
Seq. ID	LIB3149-053-Q1-K1-D8
Method	BLASTN
NCBI GI	g1419087
BLAST score	38
E value	5.0e-12
Match length	78
% identity	87
NCBI Description	N.plumbaginifolia mRNA for calreticulin

Seq. No.	220506
Seq. ID	LIB3149-053-Q1-K1-E1
Method	BLASTN
NCBI GI	g683501
BLAST score	40
E value	3.0e-13
Match length	56
% identity	93
NCBI Description	A.thaliana mRNA for 65 kDa regulatory subunit of protein phosphatase 2A

Seq. No.	220507
Seq. ID	LIB3149-053-Q1-K1-E10
Method	BLASTX
NCBI GI	g3687235
BLAST score	140
E value	1.0e-08
Match length	88
% identity	45
NCBI Description	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq. No.	220508
Seq. ID	LIB3149-053-Q1-K1-E3
Method	BLASTX
NCBI GI	g3914535
BLAST score	170
E value	3.0e-12

Match length	39
% identity	87
NCBI Description	60S RIBOSOMAL PROTEIN L13A >gi_2791948_emb_CAA11283_ (AJ223363) ribosomal protein L13a [Lupinus luteus]

Seq. No.	220509
Seq. ID	LIB3149-053-Q1-K1-E5
Method	BLASTX
NCBI GI	g3776005
BLAST score	442
E value	6.0e-44
Match length	93
% identity	94
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	220510
Seq. ID	LIB3149-053-Q1-K1-E6
Method	BLASTX
NCBI GI	g1922242
BLAST score	194
E value	7.0e-15
Match length	69
% identity	61
NCBI Description	(Y10084) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220511
Seq. ID	LIB3149-053-Q1-K1-E7
Method	BLASTX
NCBI GI	g3885515
BLAST score	447
E value	1.0e-44
Match length	103
% identity	81
NCBI Description	(AF084202) similar to ribosomal protein S26 [Medicago sativa]

Seq. No.	220512
Seq. ID	LIB3149-053-Q1-K1-F4
Method	BLASTX
NCBI GI	g531829
BLAST score	146
E value	1.0e-09
Match length	72
% identity	50
NCBI Description	(U12390) beta-galactosidase alpha peptide [cloning vector pSport1]

Seq. No.	220513
Seq. ID	LIB3149-053-Q1-K1-F5
Method	BLASTX
NCBI GI	g2894612
BLAST score	372
E value	8.0e-36
Match length	118
% identity	65
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	220514
Seq. ID	LIB3149-053-Q1-K1-F8
Method	BLASTX
NCBI GI	g4539350
BLAST score	357
E value	5.0e-34
Match length	79
% identity	78
NCBI Description	(AL035539) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	220515
Seq. ID	LIB3149-053-Q1-K1-G1
Method	BLASTX
NCBI GI	g399785
BLAST score	609
E value	2.0e-63
Match length	132
% identity	87
NCBI Description	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT) >gi_100331_pir__S21454 glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) - common tobacco >gi_19873_emb_CAA46786_ (X65973) glutamate-1-semialdehyde 2,1-aminomutase [Nicotiana tabacum]

Seq. No.	220516
Seq. ID	LIB3149-053-Q1-K1-G12
Method	BLASTX
NCBI GI	g3702343
BLAST score	323
E value	4.0e-30
Match length	114
% identity	57
NCBI Description	(AC005397) putative homeotic gene regulator [Arabidopsis thaliana]

Seq. No.	220517
Seq. ID	LIB3149-053-Q1-K1-G2
Method	BLASTX
NCBI GI	g399785
BLAST score	591
E value	2.0e-61
Match length	132
% identity	86
NCBI Description	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT) >gi_100331_pir__S21454 glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) - common tobacco >gi_19873_emb_CAA46786_ (X65973) glutamate-1-semialdehyde 2,1-aminomutase [Nicotiana tabacum]

Seq. No.	220518
Seq. ID	LIB3149-053-Q1-K1-G3
Method	BLASTX
NCBI GI	g1666173
BLAST score	477
E value	5.0e-48

Match length	114
% identity	83
NCBI Description	(Y09106) transcription factor [Nicotiana plumbaginifolia]

Seq. No.	220519
Seq. ID	LIB3149-053-Q1-K1-H12
Method	BLASTX
NCBI GI	g4176531
BLAST score	171
E value	4.0e-12
Match length	118
% identity	39
NCBI Description	(AL035263) weak similarity to chick phosphatidylcholine-sterol acetyltransferase [Schizosaccharomyces pombe]

Seq. No.	220520
Seq. ID	LIB3149-053-Q1-K1-H5
Method	BLASTX
NCBI GI	g4567304
BLAST score	140
E value	1.0e-11
Match length	120
% identity	40
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No.	220521
Seq. ID	LIB3149-054-Q1-K1-A11
Method	BLASTX
NCBI GI	g1708401
BLAST score	412
E value	2.0e-40
Match length	90
% identity	90
NCBI Description	ISOCITRATE DEHYDROGENASE (NADP) (OXALOSUCCINATE DECARBOXYLASE) (IDH) (NADP+-SPECIFIC ICDH) (IDP)

Seq. No.	220522
Seq. ID	LIB3149-054-Q1-K1-A12
Method	BLASTX
NCBI GI	g1707074
BLAST score	201
E value	9.0e-16
Match length	117
% identity	38
NCBI Description	(U80450) M01E11.2 [Caenorhabditis elegans]

Seq. No.	220523
Seq. ID	LIB3149-054-Q1-K1-A2
Method	BLASTX
NCBI GI	g2597826
BLAST score	372
E value	9.0e-36
Match length	95
% identity	73
NCBI Description	(Y14590) class IV chitinase [Arabidopsis thaliana]

Seq. No.	220524

Seq. ID LIB3149-054-Q1-K1-A3
Method BLASTX
NCBI GI g1350680
BLAST score 221
E value 5.0e-30
Match length 104
% identity 65
NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 220525
Seq. ID LIB3149-054-Q1-K1-A8
Method BLASTX
NCBI GI g4406777
BLAST score 156
E value 2.0e-10
Match length 79
% identity 43
NCBI Description (AC006532) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No. 220526
Seq. ID LIB3149-054-Q1-K1-B12
Method BLASTX
NCBI GI g3702321
BLAST score 491
E value 1.0e-49
Match length 127
% identity 38
NCBI Description (AC005397) putative TGF-beta receptor interacting protein [Arabidopsis thaliana]

Seq. No. 220527
Seq. ID LIB3149-054-Q1-K1-B3
Method BLASTX
NCBI GI g266989
BLAST score 499
E value 1.0e-50
Match length 118
% identity 83
NCBI Description GTP-BINDING PROTEIN SAR1B >gi_322517_pir__S28603 GTP-binding protein - Arabidopsis thaliana >gi_166734 (M95795) GTP-binding protein [Arabidopsis thaliana]

Seq. No. 220528
Seq. ID LIB3149-054-Q1-K1-B4
Method BLASTX
NCBI GI g3334322
BLAST score 295
E value 8.0e-27
Match length 97
% identity 62
NCBI Description GTP-BINDING PROTEIN SAR1B >gi_2108347 (U55036) small GTP-binding protein Bsar1b [Brassica rapa]

Seq. No. 220529
Seq. ID LIB3149-054-Q1-K1-C11
Method BLASTX

NCBI GI g1255951
BLAST score 290
E value 3.0e-26
Match length 59
% identity 86
NCBI Description (X96932) PS60 [Nicotiana tabacum]

Seq. No. 220530
Seq. ID LIB3149-054-Q1-K1-C12
Method BLASTX
NCBI GI g1255951
BLAST score 150
E value 4.0e-10
Match length 56
% identity 55
NCBI Description (X96932) PS60 [Nicotiana tabacum]

Seq. No. 220531
Seq. ID LIB3149-054-Q1-K1-C5
Method BLASTX
NCBI GI g3925703
BLAST score 408
E value 6.0e-40
Match length 90
% identity 91
NCBI Description (X95905) 14-3-3 protein [Lycopersicon esculentum]

Seq. No. 220532
Seq. ID LIB3149-054-Q1-K1-C6
Method BLASTX
NCBI GI g132908
BLAST score 155
E value 3.0e-10
Match length 42
% identity 69
NCBI Description 50S RIBOSOMAL PROTEIN L34 >gi_79021_pir__JQ0732 ribosomal protein L34 - Proteus mirabilis >gi_150877 (M58352) ribosomal protein L34 [Proteus mirabilis]

Seq. No. 220533
Seq. ID LIB3149-054-Q1-K1-C8
Method BLASTX
NCBI GI g1171978
BLAST score 388
E value 1.0e-37
Match length 129
% identity 25
NCBI Description POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) >gi_304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961) poly(A)-binding protein [Arabidopsis thaliana]

Seq. No. 220534
Seq. ID LIB3149-054-Q1-K1-D12
Method BLASTX
NCBI GI g2501850
BLAST score 253

E value	3.0e-32
Match length	84
% identity	87
NCBI Description	(AF012823) GDP dissociation inhibitor [Nicotiana tabacum]

Seq. No.	220535
Seq. ID	LIB3149-054-Q1-K1-D2
Method	BLASTX
NCBI GI	g4098129
BLAST score	537
E value	3.0e-55
Match length	107
% identity	92
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	220536
Seq. ID	LIB3149-054-Q1-K1-D4
Method	BLASTX
NCBI GI	g1362086
BLAST score	588
E value	4.0e-61
Match length	122
% identity	90
NCBI Description	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir__S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]

Seq. No.	220537
Seq. ID	LIB3149-054-Q1-K1-D5
Method	BLASTX
NCBI GI	g2739379
BLAST score	245
E value	6.0e-21
Match length	86
% identity	53
NCBI Description	(AC002505) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220538
Seq. ID	LIB3149-054-Q1-K1-D6
Method	BLASTX
NCBI GI	g266945
BLAST score	145
E value	3.0e-21
Match length	91
% identity	61
NCBI Description	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi_100065_pir__S19978 ribosomal protein L9 - garden pea >gi_20727_emb_CAA46273_ (X65155) GA [Pisum sativum] >gi_1279645_emb_CAA65987_ (X97322) ribosomal protein L9 [Pisum sativum]

Seq. No.	220539
Seq. ID	LIB3149-054-Q1-K1-D9

Method	BLASTX
NCBI GI	g136707
BLAST score	395
E value	2.0e-38
Match length	103
% identity	72
NCBI Description	CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_280397_pir__S26199 plastoquinol--plastocyanin reductase (EC 1.10.99.1) iron-sulfur protein precursor - garden pea >gi_20832_emb_CAA45151_ (X63605) chloroplast Rieske FeS protein [Pisum sativum]

Seq. No.	220540
Seq. ID	LIB3149-054-Q1-K1-E11
Method	BLASTX
NCBI GI	g2500380
BLAST score	564
E value	3.0e-58
Match length	104
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L44 >gi_2119128_pir__JC4923 ribosomal protein RL44 - upland cotton >gi_1553129 (U64677) ribosomal protein L44 isoform a [Gossypium hirsutum] >gi_1553131 (U64678) ribosomal protein L44 isoform b [Gossypium hirsutum]

Seq. No.	220541
Seq. ID	LIB3149-054-Q1-K1-E12
Method	BLASTX
NCBI GI	g3122753
BLAST score	185
E value	2.0e-14
Match length	48
% identity	73
NCBI Description	60S RIBOSOMAL PROTEIN L44 >gi_2244789_emb_CAB10211.1_ (Z97336) ribosomal protein [Arabidopsis thaliana]

Seq. No.	220542
Seq. ID	LIB3149-054-Q1-K1-E2
Method	BLASTX
NCBI GI	g4432841
BLAST score	306
E value	5.0e-28
Match length	82
% identity	74
NCBI Description	(AC006283) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220543
Seq. ID	LIB3149-054-Q1-K1-E3
Method	BLASTX
NCBI GI	g170354
BLAST score	431
E value	1.0e-42
Match length	87
% identity	21
NCBI Description	(M74156) pentameric polyubiquitin [Nicotiana sylvestris]

Seq. No.	220544
Seq. ID	LIB3149-054-Q1-K1-E5
Method	BLASTX
NCBI GI	g3947448
BLAST score	298
E value	4.0e-27
Match length	127
% identity	44
NCBI Description	(AL033535) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5 comes from this gene [Caenorhabdi... >gi_3947543_emb_CAA88952_ (Z49127) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5 comes from this gene [Caenorhabditi

Seq. No.	220545
Seq. ID	LIB3149-054-Q1-K1-E8
Method	BLASTX
NCBI GI	g1173223
BLAST score	340
E value	3.0e-37
Match length	87
% identity	94
NCBI Description	40S RIBOSOMAL PROTEIN S11 >gi_454848 (L28831) ribosomal protein S11 [Glycine max]

Seq. No.	220546
Seq. ID	LIB3149-054-Q1-K1-F11
Method	BLASTX
NCBI GI	g1350956
BLAST score	527
E value	7.0e-54
Match length	112
% identity	93
NCBI Description	40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No.	220547
Seq. ID	LIB3149-054-Q1-K1-F6
Method	BLASTX
NCBI GI	g1399380
BLAST score	594
E value	9.0e-62
Match length	134
% identity	82
NCBI Description	(U43683) S-adenosyl-L-methionine:delta24-sterol-C-methyltransferase [Glycine max]

Seq. No.	220548
Seq. ID	LIB3149-054-Q1-K1-F7
Method	BLASTX
NCBI GI	g2780194
BLAST score	538
E value	3.0e-55

Match length	111
% identity	60
NCBI Description	(AJ003197) adenine nucleotide translocator [Lupinus albus]

Seq. No.	220549
Seq. ID	LIB3149-054-Q1-K1-G1
Method	BLASTX
NCBI GI	g133808
BLAST score	177
E value	5.0e-13
Match length	44
% identity	80
NCBI Description	40S RIBOSOMAL PROTEIN S16 >gi_70921_pir__R3YL16 ribosomal protein S16, cytosolic - large-leaved lupine >gi_19512_emb_CAA36068_ (X51766) rps16 gene product (AA 1-145) [Lupinus polyphyllus]

Seq. No.	220550
Seq. ID	LIB3149-054-Q1-K1-G11
Method	BLASTX
NCBI GI	g728868
BLAST score	142
E value	6.0e-09
Match length	66
% identity	52
NCBI Description	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) >gi_99824_pir__S16748 proline-rich protein - rape (fragment) >gi_22597_emb_CAA42924_ (X60376) proline-rich protein [Brassica napus]

Seq. No.	220551
Seq. ID	LIB3149-054-Q1-K1-G9
Method	BLASTX
NCBI GI	g3033396
BLAST score	241
E value	2.0e-20
Match length	74
% identity	57
NCBI Description	(AC004238) unknown protein [Arabidopsis thaliana]

Seq. No.	220552
Seq. ID	LIB3149-054-Q1-K1-H1
Method	BLASTX
NCBI GI	g3687243
BLAST score	245
E value	4.0e-21
Match length	61
% identity	79
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	220553
Seq. ID	LIB3149-054-Q1-K1-H11
Method	BLASTX
NCBI GI	g4126399
BLAST score	438
E value	1.0e-43

Match length	108
% identity	80
NCBI Description	(AB011794) chalcone isomerase [Citrus sinensis]

Seq. No.	220554
Seq. ID	LIB3149-054-Q1-K1-H3
Method	BLASTX
NCBI GI	g3687243
BLAST score	188
E value	3.0e-14
Match length	57
% identity	68
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	220555
Seq. ID	LIB3149-054-Q1-K1-H4
Method	BLASTX
NCBI GI	g3510254
BLAST score	459
E value	6.0e-46
Match length	109
% identity	83
NCBI Description	(AC005310) putative zinc transporter [Arabidopsis thaliana]

Seq. No.	220556
Seq. ID	LIB3149-054-Q1-K1-H6
Method	BLASTX
NCBI GI	g2286153
BLAST score	563
E value	3.0e-58
Match length	119
% identity	92
NCBI Description	(AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No.	220557
Seq. ID	LIB3149-054-Q1-K1-H8
Method	BLASTX
NCBI GI	g951427
BLAST score	465
E value	1.0e-46
Match length	121
% identity	72
NCBI Description	(M59857) stearoyl-acyl-carrier protein desaturase [Ricinus communis]

Seq. No.	220558
Seq. ID	LIB3149-055-Q1-K1-A3
Method	BLASTX
NCBI GI	g3064039
BLAST score	136
E value	1.0e-08
Match length	62
% identity	48
NCBI Description	(AF054445) major latex protein homolog [Mesembryanthemum crystallinum]

Seq. No.	220559
Seq. ID	LIB3149-055-Q1-K1-A5
Method	BLASTX
NCBI GI	g2583108
BLAST score	190
E value	1.0e-14
Match length	59
% identity	56
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.	220560
Seq. ID	LIB3149-055-Q1-K1-A6
Method	BLASTX
NCBI GI	g2914700
BLAST score	140
E value	1.0e-08
Match length	78
% identity	47
NCBI Description	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No.	220561
Seq. ID	LIB3149-055-Q1-K1-B11
Method	BLASTX
NCBI GI	g2979553
BLAST score	174
E value	5.0e-13
Match length	65
% identity	51
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220562
Seq. ID	LIB3149-055-Q1-K1-B2
Method	BLASTX
NCBI GI	g3023847
BLAST score	315
E value	2.0e-29
Match length	74
% identity	58
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta subunit-like [Medicago sativa]

Seq. No.	220563
Seq. ID	LIB3149-055-Q1-K1-B3
Method	BLASTN
NCBI GI	g3108024
BLAST score	32
E value	1.0e-08
Match length	43
% identity	93
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T1F15 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	220564
Seq. ID	LIB3149-055-Q1-K1-B5
Method	BLASTX

NCBI GI	g1408471
BLAST score	170
E value	4.0e-12
Match length	39
% identity	85
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	220565
Seq. ID	LIB3149-055-Q1-K1-B8
Method	BLASTX
NCBI GI	g1708313
BLAST score	161
E value	4.0e-11
Match length	50
% identity	74
NCBI Description	HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi_999396_bbs_163637 (S77849) heat-shock Protein=HSP81-3 [Arabidopsis thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis thaliana]

Seq. No.	220566
Seq. ID	LIB3149-055-Q1-K1-C12
Method	BLASTX
NCBI GI	g167367
BLAST score	164
E value	2.0e-11
Match length	34
% identity	94
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	220567
Seq. ID	LIB3149-055-Q1-K1-C2
Method	BLASTX
NCBI GI	g4056497
BLAST score	296
E value	7.0e-27
Match length	93
% identity	69
NCBI Description	(AC005896) putative histone H2B [Arabidopsis thaliana]

Seq. No.	220568
Seq. ID	LIB3149-055-Q1-K1-C3
Method	BLASTX
NCBI GI	g3264767
BLAST score	142
E value	2.0e-16
Match length	93
% identity	52
NCBI Description	(AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No.	220569
Seq. ID	LIB3149-055-Q1-K1-C5
Method	BLASTX
NCBI GI	g1200205
BLAST score	543

E value 6.0e-56
Match length 109
% identity 94
NCBI Description (X95753) DAG [Antirrhinum majus]

Seq. No. 220570
Seq. ID LIB3149-055-Q1-K1-C6
Method BLASTN
NCBI GI g167366
BLAST score 325
E value 0.0e+00
Match length 394
% identity 96
NCBI Description Gossypium hirsutum peroxidase mRNA, complete cds

Seq. No. 220571
Seq. ID LIB3149-055-Q1-K1-C8
Method BLASTX
NCBI GI g2558962
BLAST score 293
E value 2.0e-26
Match length 60
% identity 98
NCBI Description (AF025667) histone H2B1 [Gossypium hirsutum]

Seq. No. 220572
Seq. ID LIB3149-055-Q1-K1-E1
Method BLASTX
NCBI GI g1172995
BLAST score 235
E value 1.0e-19
Match length 95
% identity 56
NCBI Description 60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal protein L22 - rat >gi_710295_emb_CAA55204_ (X78444) ribosomal protein L22 [Rattus norvegicus] >gi_1093952_prf__2105193A ribosomal protein L22 [Rattus norvegicus]

Seq. No. 220573
Seq. ID LIB3149-055-Q1-K1-E10
Method BLASTX
NCBI GI g4263712
BLAST score 268
E value 6.0e-24
Match length 71
% identity 66
NCBI Description (AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]

Seq. No. 220574
Seq. ID LIB3149-055-Q1-K1-E2
Method BLASTX
NCBI GI g1172995
BLAST score 136
E value 1.0e-08
Match length 48

% identity	65
NCBI Description	60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal protein L22 - rat >gi_710295_emb_CAA55204_ (X78444) ribosomal protein L22 [Rattus norvegicus] >gi_1093952_prf__2105193A ribosomal protein L22 [Rattus norvegicus]
Seq. No.	220575
Seq. ID	LIB3149-055-Q1-K1-E4
Method	BLASTX
NCBI GI	g728867
BLAST score	191
E value	1.0e-14
Match length	88
% identity	42
NCBI Description	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR >gi_99694_pir__S21961 proline-rich protein APG - Arabidopsis thaliana >gi_22599_emb_CAA42925_ (X60377) APG [Arabidopsis thaliana]
Seq. No.	220576
Seq. ID	LIB3149-055-Q1-K1-E5
Method	BLASTX
NCBI GI	g2239085
BLAST score	222
E value	3.0e-18
Match length	92
% identity	50
NCBI Description	(Z84384) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]
Seq. No.	220577
Seq. ID	LIB3149-055-Q1-K1-E7
Method	BLASTX
NCBI GI	g166878
BLAST score	196
E value	1.0e-19
Match length	94
% identity	57
NCBI Description	(M95796) St12p protein [Arabidopsis thaliana]
Seq. No.	220578
Seq. ID	LIB3149-055-Q1-K1-F12
Method	BLASTX
NCBI GI	g1173187
BLAST score	364
E value	5.0e-35
Match length	82
% identity	90
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]
Seq. No.	220579
Seq. ID	LIB3149-055-Q1-K1-F2
Method	BLASTX

NCBI GI	g4512698
BLAST score	197
E value	3.0e-15
Match length	107
% identity	41
NCBI Description	(AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220580
Seq. ID	LIB3149-055-Q1-K1-F4
Method	BLASTX
NCBI GI	g2244734
BLAST score	267
E value	2.0e-23
Match length	59
% identity	92
NCBI Description	(D88414) actin [Gossypium hirsutum]

Seq. No.	220581
Seq. ID	LIB3149-055-Q1-K1-F5
Method	BLASTX
NCBI GI	g2369714
BLAST score	264
E value	5.0e-23
Match length	72
% identity	74
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	220582
Seq. ID	LIB3149-055-Q1-K1-G4
Method	BLASTX
NCBI GI	g1173187
BLAST score	370
E value	1.0e-35
Match length	75
% identity	97
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]

Seq. No.	220583
Seq. ID	LIB3149-055-Q1-K1-G6
Method	BLASTX
NCBI GI	g2244811
BLAST score	194
E value	4.0e-17
Match length	113
% identity	56
NCBI Description	(Z97336) unnamed protein product [Arabidopsis thaliana]

Seq. No.	220584
Seq. ID	LIB3149-055-Q1-K1-G7
Method	BLASTX
NCBI GI	g3924597
BLAST score	146
E value	2.0e-09
Match length	57

% identity	47
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	220585
Seq. ID	LIB3149-055-Q1-K1-H1
Method	BLASTN
NCBI GI	g559547
BLAST score	97
E value	3.0e-47
Match length	153
% identity	91
NCBI Description	Transformation vector pPRV100B, plastid targeting segment

Seq. No.	220586
Seq. ID	LIB3149-056-Q1-K1-A9
Method	BLASTX
NCBI GI	g2494261
BLAST score	406
E value	1.0e-39
Match length	84
% identity	93
NCBI Description	ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >gi_99903_pir__S21567 translation elongation factor Tu precursor - soybean chloroplast >gi_18776_emb_CAA46864_ (X66062) EF-Tu [Glycine max] >gi_448921_prf__1918220A elongation factor Tu [Glycine max]

Seq. No.	220587
Seq. ID	LIB3149-056-Q1-K1-B10
Method	BLASTX
NCBI GI	g1710838
BLAST score	281
E value	1.0e-25
Match length	63
% identity	86
NCBI Description	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi_535584 (L36119) adenosylhomocysteinase [Medicago sativa]

Seq. No.	220588
Seq. ID	LIB3149-056-Q1-K1-C11
Method	BLASTX
NCBI GI	g81811
BLAST score	396
E value	1.0e-38
Match length	98
% identity	79
NCBI Description	ribosomal protein S11 - soybean (fragment) >gi_170054 (M31024) ribosomal protein S11 [Glycine max]

Seq. No.	220589
Seq. ID	LIB3149-056-Q1-K1-C7
Method	BLASTX
NCBI GI	g3335341
BLAST score	200
E value	9.0e-16
Match length	71

% identity	59
NCBI Description	(AC004512) T8F5.10 [Arabidopsis thaliana]

Seq. No.	220590
Seq. ID	LIB3149-056-Q1-K1-C9
Method	BLASTN
NCBI GI	g20419
BLAST score	35
E value	2.0e-10
Match length	95
% identity	15
NCBI Description	P.amygdalus mRNA for extensin

Seq. No.	220591
Seq. ID	LIB3149-056-Q1-K1-E12
Method	BLASTX
NCBI GI	g1170660
BLAST score	197
E value	3.0e-15
Match length	56
% identity	73
NCBI Description	MEVALONATE KINASE (MK) >gi_541880_pir__S42088 mevalonate kinase (EC 2.7.1.36) - Arabidopsis thaliana >gi_456614_emb_CAA54820_ (X77793) mevalonate kinase [Arabidopsis thaliana]

Seq. No.	220592
Seq. ID	LIB3149-056-Q1-K1-E4
Method	BLASTX
NCBI GI	g3287826
BLAST score	360
E value	1.0e-34
Match length	79
% identity	87
NCBI Description	(+)-DELTA-CADINENE SYNTHASE ISOZYME C2 (D-CADINENE SYNTHASE) >gi_2879841_emb_CAA76223.1_ (Y16432) (+)-delta-cadinene synthase [Gossypium arboreum]

Seq. No.	220593
Seq. ID	LIB3149-056-Q1-K1-E5
Method	BLASTX
NCBI GI	g3287824
BLAST score	171
E value	9.0e-13
Match length	38
% identity	82
NCBI Description	(+)-DELTA-CADINENE SYNTHASE ISOZYME XC1 (D-CADINENE SYNTHASE) >gi_2147015_pir__S68365 (+)-delta-cadinene synthase isozyme XC1 - Gossypium arboreum >gi_1045312 (U23206) (+)-delta-cadinene synthase isozyme XC1 [Gossypium arboreum]

Seq. No.	220594
Seq. ID	LIB3149-056-Q1-K1-E7
Method	BLASTX
NCBI GI	g3024516
BLAST score	341

E value	2.0e-32
Match length	70
% identity	97
NCBI Description	RAS-RELATED PROTEIN RAB11C >gi_2160157 (AC000132) Strong similarity to A. thaliana ara-2 (gb_ATHARA2). ESTs gb_ATTS2483,gb_ATTS2484,gb_AA042159 come from this gene. [Arabidopsis thaliana] >gi_2231303 (U74669) ras-related small GTPase [Arabidopsis thaliana]

Seq. No.	220595
Seq. ID	LIB3149-056-Q1-K1-E8
Method	BLASTX
NCBI GI	g1076510
BLAST score	607
E value	9.0e-64
Match length	142
% identity	85
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean >gi_829119_emb_CAA52414_ (X74403) cyclophilin [Phaseolus vulgaris]

Seq. No.	220596
Seq. ID	LIB3149-056-Q1-K1-F9
Method	BLASTX
NCBI GI	g2739366
BLAST score	244
E value	1.0e-20
Match length	125
% identity	42
NCBI Description	(AC002505) SF16 like protein [Arabidopsis thaliana]

Seq. No.	220597
Seq. ID	LIB3149-056-Q1-K1-G5
Method	BLASTX
NCBI GI	g3461848
BLAST score	137
E value	1.0e-08
Match length	34
% identity	85
NCBI Description	(AC005315) putative ATPase [Arabidopsis thaliana]

Seq. No.	220598
Seq. ID	LIB3149-056-Q1-K1-G9
Method	BLASTX
NCBI GI	g3080421
BLAST score	272
E value	6.0e-24
Match length	128
% identity	46
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	220599
Seq. ID	LIB3149-056-Q1-K1-H9
Method	BLASTX
NCBI GI	g4567207
BLAST score	216
E value	8.0e-18

Match length	79
% identity	57
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	220600
Seq. ID	LIB3149-057-Q1-K1-A1
Method	BLASTX
NCBI GI	g3107931
BLAST score	385
E value	1.0e-37
Match length	88
% identity	84
NCBI Description	(AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]

Seq. No.	220601
Seq. ID	LIB3149-057-Q1-K1-A3
Method	BLASTX
NCBI GI	g585963
BLAST score	170
E value	4.0e-12
Match length	49
% identity	73
NCBI Description	PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT

Seq. No.	220602
Seq. ID	LIB3149-057-Q1-K1-A8
Method	BLASTX
NCBI GI	g3549660
BLAST score	380
E value	8.0e-37
Match length	107
% identity	66
NCBI Description	(AL031394) carbonate dehydratase - like protein [Arabidopsis thaliana]

Seq. No.	220603
Seq. ID	LIB3149-057-Q1-K1-A9
Method	BLASTX
NCBI GI	g1841870
BLAST score	332
E value	3.0e-31
Match length	81
% identity	79
NCBI Description	(U87222) elongation factor 1-beta [Pimpinella brachycarpa]

Seq. No.	220604
Seq. ID	LIB3149-057-Q1-K1-B10
Method	BLASTN
NCBI GI	g1518539
BLAST score	44
E value	1.0e-15
Match length	76
% identity	89
NCBI Description	Glycine max UDP-glucose dehydrogenase mRNA, complete cds

Seq. No.	220605
Seq. ID	LIB3149-057-Q1-K1-B11

Method	BLASTX
NCBI GI	g1351017
BLAST score	232
E value	2.0e-19
Match length	46
% identity	93
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S4) >gi_629697_pir__S45375 ribosomal protein S4 - common tobacco (fragment) >gi_443960_emb_CAA78463_ (Z14085) RIBOSOMAL PROTEIN S4 [Nicotiana tabacum]

Seq. No.	220606
Seq. ID	LIB3149-057-Q1-K1-B12
Method	BLASTX
NCBI GI	g1669597
BLAST score	359
E value	2.0e-34
Match length	97
% identity	75
NCBI Description	(D88745) AR192 [Arabidopsis thaliana]

Seq. No.	220607
Seq. ID	LIB3149-057-Q1-K1-B3
Method	BLASTX
NCBI GI	g3287832
BLAST score	601
E value	1.0e-62
Match length	114
% identity	98
NCBI Description	(+)-DELTA-CADINENE SYNTHASE (D-CADINENE SYNTHASE) >gi_1843647 (U88318) (+)-delta-cadinene synthase [Gossypium hirsutum]

Seq. No.	220608
Seq. ID	LIB3149-057-Q1-K1-B7
Method	BLASTN
NCBI GI	g2687437
BLAST score	60
E value	4.0e-25
Match length	60
% identity	100
NCBI Description	Jepsonia parryi large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	220609
Seq. ID	LIB3149-057-Q1-K1-C1
Method	BLASTX
NCBI GI	g1703380
BLAST score	264
E value	2.0e-23
Match length	85
% identity	66
NCBI Description	ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607_ (D17760) ADP-ribosylation factor [Oryza sativa]

Seq. No.	220610
Seq. ID	LIB3149-057-Q1-K1-D1

Method	BLASTN
NCBI GI	g2351065
BLAST score	35
E value	3.0e-10
Match length	147
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	220611
Seq. ID	LIB3149-057-Q1-K1-D8
Method	BLASTX
NCBI GI	g1173234
BLAST score	327
E value	2.0e-30
Match length	72
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S25 >gi_481909_pir__S40089 ribosomal protein S25 - tomato >gi_435679_emb_CAA54132_ (X76714) ribosomal protein S25 [Lycopersicon esculentum] >gi_1584836_prf__2123431A ribosomal protein S25 [Lycopersicon esculentum]

Seq. No.	220612
Seq. ID	LIB3149-057-Q1-K1-D9
Method	BLASTN
NCBI GI	g409574
BLAST score	38
E value	4.0e-12
Match length	50
% identity	94
NCBI Description	Atriplex nummularia glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds. >gi_414606_emb_X75597_ANDAP3DH A.nummularia mRNA for glyceraldehyde-3-phosphate dehydrogenase

Seq. No.	220613
Seq. ID	LIB3149-057-Q1-K1-E12
Method	BLASTX
NCBI GI	g119354
BLAST score	146
E value	2.0e-09
Match length	32
% identity	91
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_82082_pir__JQ1185 phosphopyruvate hydratase (EC 4.2.1.11) - tomato >gi_19281_emb_CAA41115_ (X58108) enolase [Lycopersicon esculentum]

Seq. No.	220614
Seq. ID	LIB3149-057-Q1-K1-F11
Method	BLASTX
NCBI GI	g3925703
BLAST score	371
E value	8.0e-36
Match length	93

% identity	84
NCBI Description	(X95905) 14-3-3 protein [Lycopersicon esculentum]

Seq. No.	220615
Seq. ID	LIB3149-057-Q1-K1-F3
Method	BLASTX
NCBI GI	g2795807
BLAST score	187
E value	4.0e-14
Match length	81
% identity	49
NCBI Description	(AC003674) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220616
Seq. ID	LIB3149-057-Q1-K1-F6
Method	BLASTX
NCBI GI	g2119360
BLAST score	455
E value	1.0e-45
Match length	89
% identity	64
NCBI Description	calmodulin (clone PCM2) - potato (fragment) >gi_687698 (U20291) calmodulin [Solanum tuberosum] >gi_687702 (U20293) calmodulin [Solanum tuberosum]

Seq. No.	220617
Seq. ID	LIB3149-057-Q1-K1-F7
Method	BLASTX
NCBI GI	g2326231
BLAST score	620
E value	7.0e-65
Match length	125
% identity	93
NCBI Description	(AF012889) tousled-like kinase 4 [Zea mays]

Seq. No.	220618
Seq. ID	LIB3149-057-Q1-K1-F8
Method	BLASTX
NCBI GI	g3158474
BLAST score	481
E value	1.0e-48
Match length	106
% identity	89
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]

Seq. No.	220619
Seq. ID	LIB3149-057-Q1-K1-F9
Method	BLASTX
NCBI GI	g3158474
BLAST score	198
E value	1.0e-15
Match length	72
% identity	62
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]

Seq. No.	220620
Seq. ID	LIB3149-057-Q1-K1-G10

Method	BLASTX
NCBI GI	g3122785
BLAST score	458
E value	7.0e-46
Match length	102
% identity	88
NCBI Description	40S RIBOSOMAL PROTEIN S14 >gi_2565340 (AF026079) ribosomal protein S14 [Lupinus luteus]

Seq. No.	220621
Seq. ID	LIB3149-057-Q1-K1-G2
Method	BLASTX
NCBI GI	g1694976
BLAST score	458
E value	4.0e-46
Match length	103
% identity	85
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis thaliana]

Seq. No.	220622
Seq. ID	LIB3149-057-Q1-K1-G3
Method	BLASTX
NCBI GI	g3915189
BLAST score	193
E value	6.0e-15
Match length	79
% identity	53
NCBI Description	UBIQUITIN-CONJUGATING ENZYME X (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN)

Seq. No.	220623
Seq. ID	LIB3149-057-Q1-K1-G4
Method	BLASTX
NCBI GI	g225267
BLAST score	247
E value	3.0e-21
Match length	108
% identity	52
NCBI Description	ORF 1244 [Nicotiana tabacum]

Seq. No.	220624
Seq. ID	LIB3149-057-Q1-K1-G9
Method	BLASTX
NCBI GI	g3201613
BLAST score	457
E value	9.0e-46
Match length	121
% identity	70
NCBI Description	(AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	220625
Seq. ID	LIB3149-057-Q1-K1-H1
Method	BLASTX
NCBI GI	g3549691
BLAST score	504

E value	2.0e-51
Match length	102
% identity	81
NCBI Description	(AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]

Seq. No.	220626
Seq. ID	LIB3149-057-Q1-K1-H7
Method	BLASTX
NCBI GI	g2160694
BLAST score	282
E value	3.0e-25
Match length	94
% identity	55
NCBI Description	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq. No.	220627
Seq. ID	LIB3149-059-Q1-K1-A12
Method	BLASTX
NCBI GI	g3334320
BLAST score	634
E value	2.0e-66
Match length	123
% identity	98
NCBI Description	40S RIBOSOMAL PROTEIN SA (P40) >gi_2444420 (AF020553) ribosome-associated protein p40 [Glycine max]

Seq. No.	220628
Seq. ID	LIB3149-059-Q1-K1-A2
Method	BLASTX
NCBI GI	g3914535
BLAST score	389
E value	1.0e-37
Match length	93
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L13A >gi_2791948_emb_CAA11283_ (AJ223363) ribosomal protein L13a [Lupinus luteus]

Seq. No.	220629
Seq. ID	LIB3149-059-Q1-K1-A3
Method	BLASTX
NCBI GI	g3747050
BLAST score	434
E value	4.0e-43
Match length	100
% identity	85
NCBI Description	(AF093540) ribosomal protein L26 [Zea mays]

Seq. No.	220630
Seq. ID	LIB3149-059-Q1-K1-B11
Method	BLASTX
NCBI GI	g2493046
BLAST score	374
E value	5.0e-36
Match length	109
% identity	69
NCBI Description	ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR

>gi_82297_pir__A41740 H+-transporting ATP synthase (EC 3.6.1.34) delta' chain precursor - sweet potato
>gi_217938_dbj_BAA01511_ (D10660) mitochondrial F1-ATPase delta subunit [Ipomoea batatas]

Seq. No.	220631
Seq. ID	LIB3149-059-Q1-K1-B2
Method	BLASTX
NCBI GI	g3269289
BLAST score	368
E value	2.0e-35
Match length	113
% identity	67
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	220632
Seq. ID	LIB3149-059-Q1-K1-B4
Method	BLASTX
NCBI GI	g515377
BLAST score	209
E value	8.0e-17
Match length	45
% identity	93
NCBI Description	(X79715) histone H4 [Lolium temulentum]

Seq. No.	220633
Seq. ID	LIB3149-059-Q1-K1-B5
Method	BLASTX
NCBI GI	g4193382
BLAST score	209
E value	1.0e-16
Match length	39
% identity	100
NCBI Description	(AF083336) ribosomal protein S27 [Arabidopsis thaliana] >gi_4193384 (AF083337) ribosomal protein S27 [Arabidopsis thaliana]

Seq. No.	220634
Seq. ID	LIB3149-059-Q1-K1-B7
Method	BLASTX
NCBI GI	g2648032
BLAST score	391
E value	5.0e-38
Match length	119
% identity	65
NCBI Description	(AJ001374) alpha-glucosidase [Solanum tuberosum]

Seq. No.	220635
Seq. ID	LIB3149-059-Q1-K1-B9
Method	BLASTX
NCBI GI	g4056462
BLAST score	532
E value	1.0e-54
Match length	121
% identity	79
NCBI Description	(AC005990) Strong similarity to gb_Y09876 aldehyde dehydrogenase (NAD+) from Nicotiana tabacum and a member of

	the aldehyde dehydrogenase family PF_00171. ESTs gb_F15117, gb_R83958 and gb_586262 come from this gene. [Arabidopsis thaliana]
Seq. No.	220636
Seq. ID	LIB3149-059-Q1-K1-C1
Method	BLASTX
NCBI GI	g3212879
BLAST score	424
E value	7.0e-42
Match length	103
% identity	79
NCBI Description	(AC004005) putative ribosomal protein L7 [Arabidopsis thaliana]
Seq. No.	220637
Seq. ID	LIB3149-059-Q1-K1-C11
Method	BLASTX
NCBI GI	g2132388
BLAST score	166
E value	1.0e-11
Match length	112
% identity	37
NCBI Description	PHO85 protein - yeast (Saccharomyces cerevisiae) >gi_1163103 (U43503) Lph16p [Saccharomyces cerevisiae]
Seq. No.	220638
Seq. ID	LIB3149-059-Q1-K1-C3
Method	BLASTX
NCBI GI	g4455235
BLAST score	225
E value	2.0e-18
Match length	68
% identity	65
NCBI Description	(AL035523) PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT-like [Arabidopsis thaliana]
Seq. No.	220639
Seq. ID	LIB3149-059-Q1-K1-D10
Method	BLASTN
NCBI GI	g18506
BLAST score	161
E value	1.0e-85
Match length	215
% identity	94
NCBI Description	Cotton mRNA for malate synthase (EC 4.1.3.2)
Seq. No.	220640
Seq. ID	LIB3149-059-Q1-K1-D12
Method	BLASTX
NCBI GI	g913227
BLAST score	218
E value	1.0e-17
Match length	77
% identity	56
NCBI Description	transcription factor XlDP-1 [Xenopus laevis, embryos, Peptide, 409 aa]

Seq. No.	220641
Seq. ID	LIB3149-059-Q1-K1-D2
Method	BLASTX
NCBI GI	g3892055
BLAST score	212
E value	5.0e-17
Match length	90
% identity	52
NCBI Description	(AC002330) putative transport protein [Arabidopsis thaliana]

Seq. No.	220642
Seq. ID	LIB3149-059-Q1-K1-D9
Method	BLASTX
NCBI GI	g2492514
BLAST score	547
E value	3.0e-56
Match length	125
% identity	86
NCBI Description	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR >gi_1483215_emb_CAA68141_ (X99808) chloroplast FtsH protease [Arabidopsis thaliana]

Seq. No.	220643
Seq. ID	LIB3149-059-Q1-K1-E1
Method	BLASTX
NCBI GI	g4510428
BLAST score	264
E value	5.0e-23
Match length	133
% identity	47
NCBI Description	(AC006929) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	220644
Seq. ID	LIB3149-059-Q1-K1-E12
Method	BLASTX
NCBI GI	g2347054
BLAST score	218
E value	8.0e-18
Match length	82
% identity	52
NCBI Description	(X96791) arginine decarboxylase [Vitis vinifera]

Seq. No.	220645
Seq. ID	LIB3149-059-Q1-K1-E3
Method	BLASTX
NCBI GI	g1350720
BLAST score	390
E value	6.0e-38
Match length	99
% identity	74
NCBI Description	60S RIBOSOMAL PROTEIN L32

Seq. No.	220646
Seq. ID	LIB3149-059-Q1-K1-E4

Method	BLASTX
NCBI GI	g1346675
BLAST score	560
E value	7.0e-58
Match length	118
% identity	92
NCBI Description	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) >gi_499112 (U10283) nucleoside diphosphate kinase [Flaveria bidentis]

Seq. No.	220647
Seq. ID	LIB3149-059-Q1-K1-E5
Method	BLASTX
NCBI GI	g3901014
BLAST score	234
E value	8.0e-20
Match length	55
% identity	76
NCBI Description	(AJ130886) metallothionein-like protein class II [Fagus sylvatica]

Seq. No.	220648
Seq. ID	LIB3149-059-Q1-K1-E8
Method	BLASTX
NCBI GI	g3461822
BLAST score	285
E value	2.0e-25
Match length	72
% identity	68
NCBI Description	(AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220649
Seq. ID	LIB3149-059-Q1-K1-F10
Method	BLASTN
NCBI GI	g2618602
BLAST score	37
E value	2.0e-11
Match length	77
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	220650
Seq. ID	LIB3149-059-Q1-K1-F11
Method	BLASTX
NCBI GI	g3650030
BLAST score	240
E value	3.0e-20
Match length	79
% identity	56
NCBI Description	(AC005396) unknown protein [Arabidopsis thaliana]

Seq. No.	220651
Seq. ID	LIB3149-059-Q1-K1-F12
Method	BLASTX
NCBI GI	g495731
BLAST score	513

E value	2.0e-52
Match length	104
% identity	90
NCBI Description	(L16790) small ras-related protein [Arabidopsis thaliana]

Seq. No.	220652
Seq. ID	LIB3149-059-Q1-K1-F5
Method	BLASTX
NCBI GI	g4263720
BLAST score	195
E value	4.0e-15
Match length	86
% identity	47
NCBI Description	(AC006223) putative cysteine proteinase inhibitor [Arabidopsis thaliana]

Seq. No.	220653
Seq. ID	LIB3149-059-Q1-K1-F6
Method	BLASTX
NCBI GI	g3914394
BLAST score	604
E value	6.0e-63
Match length	128
% identity	89
NCBI Description	2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_2118335_pir__S60473 phosphoglycerate mutase (EC 5.4.2.1) - common ice plant >gi_602426 (U16021) phosphoglyceromutase [Mesembryanthemum crystallinum]

Seq. No.	220654
Seq. ID	LIB3149-059-Q1-K1-F7
Method	BLASTX
NCBI GI	g974782
BLAST score	632
E value	3.0e-66
Match length	126
% identity	95
NCBI Description	(Z49150) cobalamine-independent methionine synthase [Solenostemon scutellarioides]

Seq. No.	220655
Seq. ID	LIB3149-059-Q1-K1-F9
Method	BLASTX
NCBI GI	g2500518
BLAST score	307
E value	5.0e-49
Match length	107
% identity	96
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-11 (EIF-4A-11) >gi_485987_emb_CAA55737_ (X79136) NeIF-4A11 [Nicotiana tabacum]

Seq. No.	220656
Seq. ID	LIB3149-059-Q1-K1-G1
Method	BLASTX
NCBI GI	g3024426

BLAST score	476
E value	3.0e-52
Match length	117
% identity	92
NCBI Description	PYRUVATE,PHOSPHATE DIKINASE PRECURSOR (PYRUVATE,ORTHOPHOSPHATE DIKINASE) >gi_1084302_pir__S55478 pyruvate,orthophosphate dikinase (EC 2.7.9.1) - common ice plant >gi_854265_emb_CAA57872_ (X82489) pyruvate,orthophosphate dikinase [Mesembryanthemum crystallinum]

Seq. No.	220657
Seq. ID	LIB3149-059-Q1-K1-G10
Method	BLASTX
NCBI GI	g2746719
BLAST score	242
E value	1.0e-20
Match length	59
% identity	88
NCBI Description	(AF038386) histone H2B [Capsicum annuum]

Seq. No.	220658
Seq. ID	LIB3149-059-Q1-K1-G11
Method	BLASTX
NCBI GI	g3334200
BLAST score	624
E value	3.0e-65
Match length	140
% identity	84
NCBI Description	GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) >gi_2894362_emb_CAB16918_ (Z99770) P-Protein precursor [Solanum tuberosum]

Seq. No.	220659
Seq. ID	LIB3149-059-Q1-K1-G2
Method	BLASTX
NCBI GI	g1362093
BLAST score	271
E value	6.0e-24
Match length	94
% identity	62
NCBI Description	hypothetical protein (clone TPP15) - tomato (fragment) >gi_924632 (U20595) unknown [Solanum lycopersicum]

Seq. No.	220660
Seq. ID	LIB3149-059-Q1-K1-G6
Method	BLASTX
NCBI GI	g4103152
BLAST score	180
E value	3.0e-13
Match length	75
% identity	49
NCBI Description	(AF020716) histidyl-tRNA synthetase [Triticum aestivum]

Seq. No.	220661
Seq. ID	LIB3149-059-Q1-K1-G8

Method	BLASTX
NCBI GI	g133867
BLAST score	544
E value	5.0e-56
Match length	110
% identity	92
NCBI Description	40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays]

Seq. No.	220662
Seq. ID	LIB3149-059-Q1-K1-G9
Method	BLASTX
NCBI GI	g2497752
BLAST score	276
E value	2.0e-24
Match length	94
% identity	56
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1321911_emb_CAA65475_ (X96714) lipid transfer protein [Prunus dulcis]

Seq. No.	220663
Seq. ID	LIB3149-059-Q1-K1-H1
Method	BLASTX
NCBI GI	g2435518
BLAST score	255
E value	2.0e-22
Match length	62
% identity	84
NCBI Description	(AF024504) contains similarity to C3HC4-type zinc fingers [Arabidopsis thaliana]

Seq. No.	220664
Seq. ID	LIB3149-059-Q1-K1-H11
Method	BLASTX
NCBI GI	g2827992
BLAST score	268
E value	1.0e-23
Match length	102
% identity	53
NCBI Description	(AF034743) UDP-glucuronosyltransferase [Pisum sativum]

Seq. No.	220665
Seq. ID	LIB3149-059-Q1-K1-H8
Method	BLASTX
NCBI GI	g4263771
BLAST score	330
E value	9.0e-31
Match length	119
% identity	55
NCBI Description	(AC006218) putative nonspecific lipid-transfer protein precursor [Arabidopsis thaliana]

Seq. No.	220666
Seq. ID	LIB3149-059-Q1-K1-H9
Method	BLASTX

NCBI GI	g2982331
BLAST score	477
E value	3.0e-48
Match length	103
% identity	92
NCBI Description	(AF051251) TAT-binding protein homolog [Picea mariana]

Seq. No.	220667
Seq. ID	LIB3149-060-Q1-K1-A2
Method	BLASTX
NCBI GI	g2623300
BLAST score	241
E value	2.0e-20
Match length	60
% identity	80
NCBI Description	(AC002409) putative protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	220668
Seq. ID	LIB3149-060-Q1-K1-A4
Method	BLASTX
NCBI GI	g3915665
BLAST score	378
E value	2.0e-36
Match length	137
% identity	51
NCBI Description	ELONGATION FACTOR G (EF-G) >gi_2688449 (AE001155) translation elongation factor G (fus-1) [Borrelia burgdorferi]

Seq. No.	220669
Seq. ID	LIB3149-060-Q1-K1-A7
Method	BLASTX
NCBI GI	g2832682
BLAST score	210
E value	1.0e-16
Match length	119
% identity	46
NCBI Description	(AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220670
Seq. ID	LIB3149-060-Q1-K1-B11
Method	BLASTX
NCBI GI	g4103963
BLAST score	141
E value	1.0e-08
Match length	31
% identity	90
NCBI Description	(AF030035) calmodulin [Phaseolus vulgaris]

Seq. No.	220671
Seq. ID	LIB3149-060-Q1-K1-B12
Method	BLASTX
NCBI GI	g3687239
BLAST score	619
E value	1.0e-64
Match length	122

% identity	96
NCBI Description	(AC005169) putative clathrin coat assembly protein [Arabidopsis thaliana]

Seq. No.	220672
Seq. ID	LIB3149-060-Q1-K1-B2
Method	BLASTX
NCBI GI	g2495365
BLAST score	348
E value	5.0e-33
Match length	86
% identity	79
NCBI Description	HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B heat shock protein HSP81-2 [Arabidopsis thaliana]

Seq. No.	220673
Seq. ID	LIB3149-060-Q1-K1-B5
Method	BLASTX
NCBI GI	g2961300
BLAST score	546
E value	4.0e-56
Match length	125
% identity	85
NCBI Description	(AJ225027) ribosomal protein L24 [Cicer arietinum]

Seq. No.	220674
Seq. ID	LIB3149-060-Q1-K1-B8
Method	BLASTX
NCBI GI	g548852
BLAST score	361
E value	2.0e-34
Match length	82
% identity	80
NCBI Description	40S RIBOSOMAL PROTEIN S21 >gi_481227_pir__S38357 ribosomal protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S subunit ribosomal protein [Oryza sativa]

Seq. No.	220675
Seq. ID	LIB3149-060-Q1-K1-C1
Method	BLASTX
NCBI GI	g167367
BLAST score	255
E value	5.0e-22
Match length	49
% identity	100
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	220676
Seq. ID	LIB3149-060-Q1-K1-C10
Method	BLASTX
NCBI GI	g2499931
BLAST score	263
E value	6.0e-23
Match length	63
% identity	81
NCBI Description	ADENINE PHOSPHORIBOSYLTRANSFERASE 2 (APRT) >gi_2129534_pir__S71272 adenine phosphoribosyltransferase

(EC 2.4.2.7) - Arabidopsis thaliana
>gi_1321681_emb_CAA65609_ (X96866) adenine phosphoribosyltransferase [Arabidopsis thaliana]

Seq. No.	220677
Seq. ID	LIB3149-060-Q1-K1-C9
Method	BLASTX
NCBI GI	g4006886
BLAST score	367
E value	4.0e-35
Match length	119
% identity	61
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	220678
Seq. ID	LIB3149-060-Q1-K1-D1
Method	BLASTX
NCBI GI	g3063396
BLAST score	423
E value	7.0e-42
Match length	93
% identity	85
NCBI Description	(AB012947) vcCyP [Vicia faba]

Seq. No.	220679
Seq. ID	LIB3149-060-Q1-K1-D11
Method	BLASTX
NCBI GI	g2979553
BLAST score	297
E value	6.0e-27
Match length	130
% identity	45
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220680
Seq. ID	LIB3149-060-Q1-K1-D2
Method	BLASTX
NCBI GI	g2495365
BLAST score	414
E value	1.0e-40
Match length	118
% identity	75
NCBI Description	HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B heat shock protein HSP81-2 [Arabidopsis thaliana]

Seq. No.	220681
Seq. ID	LIB3149-060-Q1-K1-D3
Method	BLASTX
NCBI GI	g1710587
BLAST score	317
E value	1.0e-33
Match length	122
% identity	66
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P0 >gi_1196897 (L46848) acidic ribosomal protein P0 [Glycine max]

Seq. No.	220682

Seq. ID	LIB3149-060-Q1-K1-D4
Method	BLASTX
NCBI GI	g1173198
BLAST score	434
E value	4.0e-43
Match length	91
% identity	92
NCBI Description	40S RIBOSOMAL PROTEIN S13 >gi_480095_pir__S36423 ribosomal protein S13.e - garden pea >gi_396639_emb_CAA80974_ (Z25509) ribosomal protein S13 [Pisum sativum]

Seq. No.	220683
Seq. ID	LIB3149-060-Q1-K1-D5
Method	BLASTX
NCBI GI	g1710587
BLAST score	237
E value	5.0e-20
Match length	83
% identity	59
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P0 >gi_1196897 (L46848) acidic ribosomal protein P0 [Glycine max]

Seq. No.	220684
Seq. ID	LIB3149-060-Q1-K1-D7
Method	BLASTX
NCBI GI	g70753
BLAST score	482
E value	1.0e-48
Match length	117
% identity	84
NCBI Description	histone H3 - garden pea >gi_82610_pir__S00373 histone H3 - wheat

Seq. No.	220685
Seq. ID	LIB3149-060-Q1-K1-D8
Method	BLASTX
NCBI GI	g3377941
BLAST score	150
E value	1.0e-09
Match length	88
% identity	42
NCBI Description	(AL021960) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	220686
Seq. ID	LIB3149-060-Q1-K1-E12
Method	BLASTX
NCBI GI	g461729
BLAST score	394
E value	3.0e-38
Match length	94
% identity	74
NCBI Description	10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) >gi_2146744_pir__S65597 probable chaperonin, 10K - Arabidopsis thaliana >gi_166662 (L02843) 10 kDa chaperonin [Arabidopsis thaliana]

Seq. No.	220687
Seq. ID	LIB3149-060-Q1-K1-E3
Method	BLASTX
NCBI GI	g82200
BLAST score	375
E value	4.0e-36
Match length	137
% identity	55
NCBI Description	hypothetical protein 1244 - common tobacco chloroplast

Seq. No.	220688
Seq. ID	LIB3149-060-Q1-K1-E5
Method	BLASTX
NCBI GI	g2459412
BLAST score	235
E value	9.0e-20
Match length	91
% identity	49
NCBI Description	(AC002332) putative G9a protein [Arabidopsis thaliana]

Seq. No.	220689
Seq. ID	LIB3149-060-Q1-K1-F10
Method	BLASTX
NCBI GI	g2605932
BLAST score	519
E value	6.0e-53
Match length	133
% identity	76
NCBI Description	(AF029898) aspartate aminotransferase [Lotus corniculatus]

Seq. No.	220690
Seq. ID	LIB3149-060-Q1-K1-F11
Method	BLASTX
NCBI GI	g3047084
BLAST score	564
E value	3.0e-58
Match length	128
% identity	82
NCBI Description	(AF058914) similar to aminoacyl-tRNA synthetases [Arabidopsis thaliana]

Seq. No.	220691
Seq. ID	LIB3149-060-Q1-K1-F12
Method	BLASTX
NCBI GI	g2833390
BLAST score	624
E value	3.0e-65
Match length	129
% identity	88
NCBI Description	GLYCOGEN (STARCH) SYNTHASE PRECURSOR (GBSSII) (GRANULE-BOUND STARCH SYNTHASE II) >gi_887649_emb_CAA61241_ (X87988) glycogen (starch) synthase [Solanum tuberosum]

Seq. No.	220692
Seq. ID	LIB3149-060-Q1-K1-F2
Method	BLASTX
NCBI GI	g1336084

BLAST score	510
E value	5.0e-52
Match length	116
% identity	79
NCBI Description	(U56635) Arabidopsis thaliana glutamate dehydrogenase 2 (GDH2) mRNA, complete cds. [Arabidopsis thaliana]

Seq. No.	220693
Seq. ID	LIB3149-060-Q1-K1-F5
Method	BLASTX
NCBI GI	g2982432
BLAST score	335
E value	2.0e-31
Match length	76
% identity	80
NCBI Description	(AL022224) putative protein [Arabidopsis thaliana]

Seq. No.	220694
Seq. ID	LIB3149-060-Q1-K1-G11
Method	BLASTX
NCBI GI	g549732
BLAST score	189
E value	3.0e-14
Match length	78
% identity	47
NCBI Description	HYPOTHETICAL 16.2 KD PROTEIN IN PIR3-APE2 INTERGENIC REGION >gi_481110_pir__S37791 hypothetical protein YKL160w - yeast (Saccharomyces cerevisiae) >gi_407488_emb_CAA81494_ (Z26877) unknown [Saccharomyces cerevisiae] >gi_486279_emb_CAA82002_ (Z28160) ORF YKL160w [Saccharomyces cerevisiae] >gi_1582545_prf__2118404F ORF [Saccharomyces cerevisiae]

Seq. No.	220695
Seq. ID	LIB3149-060-Q1-K1-G5
Method	BLASTX
NCBI GI	g1351271
BLAST score	178
E value	5.0e-13
Match length	43
% identity	84
NCBI Description	TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) >gi_1084309_pir__S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi_806312 (L36387) triosephosphate isomerase, chloroplast isozyme [Spinacia oleracea]

Seq. No.	220696
Seq. ID	LIB3149-060-Q1-K1-G8
Method	BLASTX
NCBI GI	g1694976
BLAST score	221
E value	3.0e-24
Match length	92
% identity	62
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis

thaliana]

Seq. No.	220697
Seq. ID	LIB3149-060-Q1-K1-G9
Method	BLASTX
NCBI GI	g322639
BLAST score	229
E value	5.0e-19
Match length	68
% identity	56
NCBI Description	beta-1,3-glucanase homolog (clone A20) - rape (fragment) >gi_17734_emb_CAA49515_ (X69889) beta-1,3-glucanase homologue [Brassica napus]

Seq. No.	220698
Seq. ID	LIB3149-060-Q1-K1-H12
Method	BLASTX
NCBI GI	g3116020
BLAST score	165
E value	1.0e-11
Match length	46
% identity	76
NCBI Description	(Y15383) FtsZ protein [Pisum sativum]

Seq. No.	220699
Seq. ID	LIB3149-060-Q1-K1-H4
Method	BLASTX
NCBI GI	g3287696
BLAST score	512
E value	4.0e-52
Match length	131
% identity	71
NCBI Description	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]

Seq. No.	220700
Seq. ID	LIB3149-060-Q1-K1-H8
Method	BLASTX
NCBI GI	g1076524
BLAST score	269
E value	9.0e-24
Match length	78
% identity	59
NCBI Description	chloroplast outer envelope protein OEP86 precursor - garden pea >gi_599958_emb_CAA83453_ (Z31581) chloroplast outer envelope protein 86 [Pisum sativum]

Seq. No.	220701
Seq. ID	LIB3149-061-Q1-K1-A1
Method	BLASTX
NCBI GI	g312179
BLAST score	306
E value	4.0e-28
Match length	61
% identity	93

NCBI Description	(X73151) glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays] >gi_1185554 (U45858) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
Seq. No.	220702
Seq. ID	LIB3149-061-Q1-K1-A3
Method	BLASTX
NCBI GI	g120669
BLAST score	453
E value	3.0e-45
Match length	87
% identity	97
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.	220703
Seq. ID	LIB3149-061-Q1-K1-A5
Method	BLASTX
NCBI GI	g3367647
BLAST score	536
E value	6.0e-55
Match length	131
% identity	78
NCBI Description	(Y17298) enolase [Cunninghamella elegans]
Seq. No.	220704
Seq. ID	LIB3149-061-Q1-K1-B3
Method	BLASTX
NCBI GI	g2462834
BLAST score	234
E value	1.0e-19
Match length	87
% identity	53
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]
Seq. No.	220705
Seq. ID	LIB3149-061-Q1-K1-B5
Method	BLASTX
NCBI GI	g2499476
BLAST score	178
E value	5.0e-13
Match length	102
% identity	43
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR >gi_1498198_emb_CAA63909_ (X94218) 2-Cys peroxiredoxin bas1 [Arabidopsis thaliana] >gi_1783308_emb_CAA71503_ (Y10478) 2-Cys peroxiredoxin [Arabidopsis thaliana]
Seq. No.	220706
Seq. ID	LIB3149-061-Q1-K1-B7
Method	BLASTX
NCBI GI	g3493172

BLAST score	685
E value	2.0e-72
Match length	133
% identity	50
NCBI Description	(U89609) fiber annexin [Gossypium hirsutum]

Seq. No.	220707
Seq. ID	LIB3149-061-Q1-K1-B9
Method	BLASTX
NCBI GI	g4204294
BLAST score	330
E value	8.0e-31
Match length	105
% identity	67
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	220708
Seq. ID	LIB3149-061-Q1-K1-C3
Method	BLASTX
NCBI GI	g3850821
BLAST score	258
E value	1.0e-22
Match length	103
% identity	50
NCBI Description	(Y18350) U2 snRNP auxiliary factor, large subunit [Nicotiana plumbaginifolia]

Seq. No.	220709
Seq. ID	LIB3149-061-Q1-K1-C7
Method	BLASTX
NCBI GI	g1754997
BLAST score	146
E value	3.0e-09
Match length	31
% identity	94
NCBI Description	(U48690) calmodulin TaCaM2-1 [Triticum aestivum]

Seq. No.	220710
Seq. ID	LIB3149-061-Q1-K1-E11
Method	BLASTX
NCBI GI	g1172556
BLAST score	275
E value	2.0e-24
Match length	60
% identity	87
NCBI Description	36 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 36) >gi_629729_pir__S46925 porin II, 36K - potato >gi_1076681_pir__B55364 porin (clone pPOM 36.2) - potato mitochondrion >gi_515360_emb_CAA56600_ (X80387) 36kDA porin II [Solanum tuberosum]

Seq. No.	220711
Seq. ID	LIB3149-061-Q1-K1-F11
Method	BLASTX
NCBI GI	g4454032

BLAST score 282
E value 2.0e-25
Match length 81
% identity 69
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

Seq. No. 220712
Seq. ID LIB3149-061-Q1-K1-H9
Method BLASTX
NCBI GI g1477428
BLAST score 631
E value 4.0e-66
Match length 135
% identity 88
NCBI Description (X99623) alpha-tubulin 1 [Hordeum vulgare]

Seq. No. 220713
Seq. ID LIB3149-062-Q1-K1-A10
Method BLASTX
NCBI GI g3122053
BLAST score 117
E value 3.0e-10
Match length 71
% identity 58
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_1235582_emb_CAA65391_ (X96555) elongation factor 1-alpha [Pisum sativum]

Seq. No. 220714
Seq. ID LIB3149-062-Q1-K1-A11
Method BLASTX
NCBI GI g1350983
BLAST score 381
E value 3.0e-54
Match length 132
% identity 81
NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)

Seq. No. 220715
Seq. ID LIB3149-062-Q1-K1-A12
Method BLASTX
NCBI GI g2088652
BLAST score 442
E value 2.0e-44
Match length 115
% identity 77
NCBI Description (AF002109) 26S proteasome regulatory subunit S12 isolog [Arabidopsis thaliana] >gi_2351376 (U54561) translation initiation factor eIF2 p47 subunit homolog [Arabidopsis thaliana]

Seq. No. 220716
Seq. ID LIB3149-062-Q1-K1-A6
Method BLASTX
NCBI GI g4539335
BLAST score 373
E value 2.0e-47

Match length	136
% identity	62
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	220717
Seq. ID	LIB3149-062-Q1-K1-A7
Method	BLASTX
NCBI GI	g421843
BLAST score	317
E value	7.0e-36
Match length	125
% identity	60
NCBI Description	protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana >gi_217861_dbj_BAA01715_ (D10909) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	220718
Seq. ID	LIB3149-062-Q1-K1-A9
Method	BLASTX
NCBI GI	g2662343
BLAST score	508
E value	7.0e-67
Match length	133
% identity	98
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	220719
Seq. ID	LIB3149-062-Q1-K1-B11
Method	BLASTX
NCBI GI	g3785989
BLAST score	229
E value	7.0e-37
Match length	132
% identity	67
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	220720
Seq. ID	LIB3149-062-Q1-K1-C5
Method	BLASTX
NCBI GI	g3334405
BLAST score	437
E value	2.0e-50
Match length	118
% identity	95
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) >gi_2267583 (AF009338) vacuolar H+-ATPase subunit E [Gossypium hirsutum]

Seq. No.	220721
Seq. ID	LIB3149-062-Q1-K1-C9
Method	BLASTX
NCBI GI	g4454464
BLAST score	273
E value	3.0e-24
Match length	64
% identity	73
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	220722
Seq. ID	LIB3149-062-Q1-K1-D10
Method	BLASTX
NCBI GI	g3738285
BLAST score	192
E value	3.0e-15
Match length	99
% identity	43
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	220723
Seq. ID	LIB3149-062-Q1-K1-D12
Method	BLASTX
NCBI GI	g2369714
BLAST score	497
E value	2.0e-50
Match length	136
% identity	72
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	220724
Seq. ID	LIB3149-062-Q1-K1-D4
Method	BLASTX
NCBI GI	g100226
BLAST score	129
E value	9.0e-12
Match length	84
% identity	48
NCBI Description	hypothetical protein - tomato >gi_19275_emb_CAA78112_ (Z12127) protein of unknown function [Lycopersicon esculentum] >gi_445619_prf__1909366A Leu zipper protein [Lycopersicon esculentum]

Seq. No.	220725
Seq. ID	LIB3149-062-Q1-K1-D9
Method	BLASTX
NCBI GI	g585876
BLAST score	123
E value	2.0e-14
Match length	67
% identity	67
NCBI Description	60S RIBOSOMAL PROTEIN L23A (L25) >gi_1084424_pir__S48026 ribosomal protein L25 - common tobacco >gi_310935 (L18908) 60S ribosomal protein L25 [Nicotiana tabacum]

Seq. No.	220726
Seq. ID	LIB3149-062-Q1-K1-E11
Method	BLASTX
NCBI GI	g886116
BLAST score	197
E value	5.0e-25
Match length	69
% identity	77
NCBI Description	(U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473 (AF051338) xyloglucan endotransglycosylase related protein [Arabidopsis thaliana]

Seq. No.	220727
Seq. ID	LIB3149-062-Q1-K1-E6
Method	BLASTX
NCBI GI	g3075398
BLAST score	163
E value	1.0e-22
Match length	137
% identity	41
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]

Seq. No.	220728
Seq. ID	LIB3149-062-Q1-K1-F12
Method	BLASTX
NCBI GI	g113029
BLAST score	502
E value	2.0e-71
Match length	137
% identity	99
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68209_pir__WZCNIU isocitrate lyase (EC 4.1.3.1) - upland cotton >gi_18486_emb_CAA36381_ (X52136) isocitrate lyase (AA 1-576) [Gossypium hirsutum]

Seq. No.	220729
Seq. ID	LIB3149-062-Q1-K1-F2
Method	BLASTX
NCBI GI	g2661840
BLAST score	295
E value	1.0e-26
Match length	118
% identity	55
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]

Seq. No.	220730
Seq. ID	LIB3149-062-Q1-K1-F5
Method	BLASTX
NCBI GI	g3892058
BLAST score	194
E value	8.0e-15
Match length	98
% identity	43
NCBI Description	(AC002330) putative glutamate-/aspartate-binding peptide [Arabidopsis thaliana]

Seq. No.	220731
Seq. ID	LIB3149-062-Q1-K1-G2
Method	BLASTX
NCBI GI	g1498053
BLAST score	323
E value	3.0e-46
Match length	133
% identity	75
NCBI Description	(U64436) ribosomal protein S8 [Zea mays]

Seq. No.	220732
Seq. ID	LIB3149-062-Q1-K1-G5

Method	BLASTX
NCBI GI	g2827992
BLAST score	330
E value	2.0e-44
Match length	137
% identity	60
NCBI Description	(AF034743) UDP-glucuronosyltransferase [Pisum sativum]

Seq. No.	220733
Seq. ID	LIB3149-062-Q1-K1-G7
Method	BLASTX
NCBI GI	g2213862
BLAST score	207
E value	6.0e-20
Match length	126
% identity	45
NCBI Description	(AF003086) PfSNF2L [Plasmodium falciparum]

Seq. No.	220734
Seq. ID	LIB3149-062-Q1-K1-G8
Method	BLASTX
NCBI GI	g2664214
BLAST score	218
E value	1.0e-17
Match length	91
% identity	53
NCBI Description	(AJ222646) G2484-1 [Arabidopsis thaliana]

Seq. No.	220735
Seq. ID	LIB3149-062-Q1-K1-H10
Method	BLASTX
NCBI GI	g4204303
BLAST score	292
E value	3.0e-45
Match length	128
% identity	68
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	220736
Seq. ID	LIB3149-062-Q1-K1-H11
Method	BLASTX
NCBI GI	g2980767
BLAST score	305
E value	7.0e-28
Match length	111
% identity	63
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	220737
Seq. ID	LIB3149-062-Q1-K1-H3
Method	BLASTX
NCBI GI	g1174448
BLAST score	260
E value	6.0e-24
Match length	98
% identity	62

NCBI Description	TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) >gi_547391 (L32016) alpha-subunit; putative [Arabidopsis thaliana]

Seq. No.	220738
Seq. ID	LIB3149-062-Q1-K1-H7
Method	BLASTX
NCBI GI	g294060
BLAST score	169
E value	7.0e-12
Match length	96
% identity	40
NCBI Description	(L06467) major latex protein [Papaver somniferum]

Seq. No.	220739
Seq. ID	LIB3149-062-Q1-K1-H8
Method	BLASTX
NCBI GI	g886116
BLAST score	340
E value	2.0e-50
Match length	138
% identity	68
NCBI Description	(U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473 (AF051338) xyloglucan endotransglycosylase related protein [Arabidopsis thaliana]

Seq. No.	220740
Seq. ID	LIB3149-063-Q1-K1-A1
Method	BLASTX
NCBI GI	g3183640
BLAST score	329
E value	4.0e-31
Match length	66
% identity	94
NCBI Description	(AJ005869) transmembrane channel protein [Cicer arietinum]

Seq. No.	220741
Seq. ID	LIB3149-063-Q1-K1-A12
Method	BLASTX
NCBI GI	g3402703
BLAST score	150
E value	1.0e-09
Match length	92
% identity	35
NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220742
Seq. ID	LIB3149-063-Q1-K1-A2
Method	BLASTX
NCBI GI	g3183640
BLAST score	295
E value	1.0e-26
Match length	68
% identity	82
NCBI Description	(AJ005869) transmembrane channel protein [Cicer arietinum]

Seq. No.	220743
Seq. ID	LIB3149-063-Q1-K1-A3
Method	BLASTX
NCBI GI	g466160
BLAST score	364
E value	9.0e-35
Match length	84
% identity	83
NCBI Description	HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III >gi_630771_pir__S44903 ZK652.3 protein - Caenorhabditis elegans >gi_289769 (L14429) putative [Caenorhabditis elegans]

Seq. No.	220744
Seq. ID	LIB3149-063-Q1-K1-A4
Method	BLASTX
NCBI GI	g466160
BLAST score	287
E value	1.0e-25
Match length	82
% identity	71
NCBI Description	HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III >gi_630771_pir__S44903 ZK652.3 protein - Caenorhabditis elegans >gi_289769 (L14429) putative [Caenorhabditis elegans]

Seq. No.	220745
Seq. ID	LIB3149-063-Q1-K1-A7
Method	BLASTN
NCBI GI	g2558943
BLAST score	38
E value	6.0e-12
Match length	65
% identity	92
NCBI Description	Gossypium hirsutum histone 3 mRNA, complete cds

Seq. No.	220746
Seq. ID	LIB3149-063-Q1-K1-A9
Method	BLASTX
NCBI GI	g1174592
BLAST score	729
E value	1.0e-77
Match length	137
% identity	100
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	220747
Seq. ID	LIB3149-063-Q1-K1-B1
Method	BLASTX
NCBI GI	g4193382
BLAST score	386
E value	2.0e-37
Match length	86
% identity	83
NCBI Description	(AF083336) ribosomal protein S27 [Arabidopsis thaliana]

	>gi_4193384 (AF083337) ribosomal protein S27 [Arabidopsis thaliana]
Seq. No.	220748
Seq. ID	LIB3149-063-Q1-K1-B11
Method	BLASTX
NCBI GI	g3024017
BLAST score	552
E value	6.0e-57
Match length	112
% identity	94
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C) >gi_2565421 (AF026804) eukaryotic translation initiation factor eIF-1A [Onobrychis viciifolia]
Seq. No.	220749
Seq. ID	LIB3149-063-Q1-K1-B12
Method	BLASTX
NCBI GI	g4371293
BLAST score	253
E value	9.0e-22
Match length	96
% identity	64
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]
Seq. No.	220750
Seq. ID	LIB3149-063-Q1-K1-B2
Method	BLASTX
NCBI GI	g2065531
BLAST score	429
E value	2.0e-42
Match length	118
% identity	64
NCBI Description	(U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
Seq. No.	220751
Seq. ID	LIB3149-063-Q1-K1-B4
Method	BLASTX
NCBI GI	g2244750
BLAST score	599
E value	2.0e-62
Match length	137
% identity	82
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]
Seq. No.	220752
Seq. ID	LIB3149-063-Q1-K1-B5
Method	BLASTX
NCBI GI	g2244750
BLAST score	444
E value	3.0e-44
Match length	108
% identity	80
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase

[Arabidopsis thaliana]

Seq. No.	220753
Seq. ID	LIB3149-063-Q1-K1-B7
Method	BLASTX
NCBI GI	g4204265
BLAST score	156
E value	2.0e-10
Match length	49
% identity	65
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	220754
Seq. ID	LIB3149-063-Q1-K1-C12
Method	BLASTX
NCBI GI	g1762945
BLAST score	323
E value	5.0e-30
Match length	120
% identity	53
NCBI Description	(U66269) ORF; able to induce HR-like lesions [Nicotiana tabacum]

Seq. No.	220755
Seq. ID	LIB3149-063-Q1-K1-C2
Method	BLASTX
NCBI GI	g4218120
BLAST score	357
E value	5.0e-34
Match length	106
% identity	66
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	220756
Seq. ID	LIB3149-063-Q1-K1-C9
Method	BLASTX
NCBI GI	g2244970
BLAST score	430
E value	1.0e-42
Match length	117
% identity	65
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana] >gi_2326365_emb_CAA74765_ (Y14423) putative cell wall protein [Arabidopsis thaliana]

Seq. No.	220757
Seq. ID	LIB3149-063-Q1-K1-D1
Method	BLASTX
NCBI GI	g2828296
BLAST score	323
E value	4.0e-30
Match length	67
% identity	88
NCBI Description	(AL021687) RNase L inhibitor [Arabidopsis thaliana]

Seq. No.	220758

Seq. ID	LIB3149-063-Q1-K1-D11
Method	BLASTX
NCBI GI	g3377797
BLAST score	497
E value	2.0e-50
Match length	125
% identity	76
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	220759
Seq. ID	LIB3149-063-Q1-K1-D6
Method	BLASTX
NCBI GI	g1419088
BLAST score	666
E value	3.0e-70
Match length	127
% identity	94
NCBI Description	(Z71395) calreticulin [Nicotiana plumbaginifolia]

Seq. No.	220760
Seq. ID	LIB3149-063-Q1-K1-D8
Method	BLASTX
NCBI GI	g4432857
BLAST score	181
E value	3.0e-18
Match length	115
% identity	46
NCBI Description	(AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220761
Seq. ID	LIB3149-063-Q1-K1-D9
Method	BLASTX
NCBI GI	g1710546
BLAST score	116
E value	2.0e-14
Match length	100
% identity	48
NCBI Description	60S RIBOSOMAL PROTEIN L36 >gi_1276967 (U47095) putative ribosomal protein [Daucus carota]

Seq. No.	220762
Seq. ID	LIB3149-063-Q1-K1-E10
Method	BLASTX
NCBI GI	g531829
BLAST score	166
E value	4.0e-12
Match length	46
% identity	72
NCBI Description	(U12390) beta-galactosidase alpha peptide [cloning vector pSport1]

Seq. No.	220763
Seq. ID	LIB3149-063-Q1-K1-E11

Method	BLASTX
NCBI GI	g3021485
BLAST score	261
E value	8.0e-23
Match length	63
% identity	83
NCBI Description	(AJ224932) histone H2B-3 [Lycopersicon esculentum]

Seq. No.	220764
Seq. ID	LIB3149-063-Q1-K1-E2
Method	BLASTX
NCBI GI	g3142291
BLAST score	445
E value	2.0e-44
Match length	112
% identity	70
NCBI Description	(AC002411) Contains similarity to adenylate cyclase gb_AF012921 from Magnaporthe grisae. EST gb_Z24512 comes from this gene. [Arabidopsis thaliana]

Seq. No.	220765
Seq. ID	LIB3149-063-Q1-K1-E4
Method	BLASTX
NCBI GI	g1174592
BLAST score	341
E value	3.0e-32
Match length	116
% identity	60
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	220766
Seq. ID	LIB3149-063-Q1-K1-E6
Method	BLASTX
NCBI GI	g266972
BLAST score	204
E value	5.0e-16
Match length	54
% identity	65
NCBI Description	40S RIBOSOMAL PROTEIN S29 >gi_631884_pir__S30298 ribosomal protein S29 - rat >gi_1362934_pir__S55919 ribosomal protein S29 - human >gi_57133_emb_CAA41778_ (X59051) ribosomal protein S29 [Rattus norvegicus] >gi_550027 (U14973) ribosomal protein S29 [Homo sapiens] >gi_1220361 (L31610) homologous to antisense sequence of krev-1, anti oncogene [Homo sapiens] >gi_1220418 (L31609) S29 ribosomal protein [Mus musculus] >gi_1513230 (U66372) ribosomal protein S29 [Bos taurus] >gi_1096945_prf__2113200H ribosomal protein S29 [Homo sapiens] >gi_4506717_ref_NP_001023.1_pRPS29_ ribosomal protein S29

Seq. No.	220767
Seq. ID	LIB3149-063-Q1-K1-E7
Method	BLASTX
NCBI GI	g120669
BLAST score	454

E value	2.0e-45
Match length	105
% identity	81
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	220768
Seq. ID	LIB3149-063-Q1-K1-E8
Method	BLASTX
NCBI GI	g2459429
BLAST score	470
E value	3.0e-47
Match length	112
% identity	73
NCBI Description	(AC002332) unknown protein [Arabidopsis thaliana]

Seq. No.	220769
Seq. ID	LIB3149-063-Q1-K1-F10
Method	BLASTX
NCBI GI	g1174448
BLAST score	285
E value	2.0e-25
Match length	113
% identity	56
NCBI Description	TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA). (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) >gi_547391 (L32016) alpha-subunit; putative [Arabidopsis thaliana]

Seq. No.	220770
Seq. ID	LIB3149-063-Q1-K1-F11
Method	BLASTX
NCBI GI	g1399380
BLAST score	662
E value	9.0e-70
Match length	131
% identity	92
NCBI Description	(U43683) S-adenosyl-L-methionine:delta24-sterol-C-methyltransferase [Glycine max]

Seq. No.	220771
Seq. ID	LIB3149-063-Q1-K1-F12
Method	BLASTX
NCBI GI	g3560474
BLAST score	259
E value	1.0e-22
Match length	96
% identity	52
NCBI Description	(U81312) S-adenosyl-methionine-sterol-C- methyltransferase [Nicotiana tabacum]

Seq. No.	220772
Seq. ID	LIB3149-063-Q1-K1-F2
Method	BLASTX

NCBI GI	g1431629
BLAST score	459
E value	5.0e-46
Match length	122
% identity	68
NCBI Description	(X99348) pectinacetylesterase precursor [Vigna radiata]

Seq. No.	220773
Seq. ID	LIB3149-063-Q1-K1-F6
Method	BLASTX
NCBI GI	g1172977
BLAST score	531
E value	2.0e-54
Match length	122
% identity	84
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	220774
Seq. ID	LIB3149-063-Q1-K1-F8
Method	BLASTX
NCBI GI	g3004560
BLAST score	145
E value	3.0e-09
Match length	47
% identity	66
NCBI Description	(AC003673) putative ATP binding protein [Arabidopsis thaliana]

Seq. No.	220775
Seq. ID	LIB3149-063-Q1-K1-G10
Method	BLASTX
NCBI GI	g4027891
BLAST score	339
E value	7.0e-32
Match length	117
% identity	62
NCBI Description	(AF049350) alpha-expansin precursor [Nicotiana tabacum]

Seq. No.	220776
Seq. ID	LIB3149-063-Q1-K1-G11
Method	BLASTX
NCBI GI	g4204293
BLAST score	493
E value	6.0e-50
Match length	115
% identity	81
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	220777
Seq. ID	LIB3149-063-Q1-K1-G3
Method	BLASTX
NCBI GI	g1928981
BLAST score	392
E value	4.0e-38
Match length	85

% identity	92
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	220778
Seq. ID	LIB3149-063-Q1-K1-G7
Method	BLASTX
NCBI GI	g1173234
BLAST score	327
E value	2.0e-30
Match length	72
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S25 >gi_481909_pir__S40089 ribosomal protein S25 - tomato >gi_435679_emb_CAA54132_ (X76714) ribosomal protein S25 [Lycopersicon esculentum] >gi_1584836_prf__2123431A ribosomal protein S25 [Lycopersicon esculentum]

Seq. No.	220779
Seq. ID	LIB3149-063-Q1-K1-G9
Method	BLASTX
NCBI GI	g1052973
BLAST score	342
E value	3.0e-32
Match length	87
% identity	76
NCBI Description	(U37838) fructokinase [Beta vulgaris]

Seq. No.	220780
Seq. ID	LIB3149-063-Q1-K1-H12
Method	BLASTX
NCBI GI	g3885339
BLAST score	239
E value	5.0e-23
Match length	110
% identity	54
NCBI Description	(AC005623) putative bzip protein [Arabidopsis thaliana]

Seq. No.	220781
Seq. ID	LIB3149-063-Q1-K1-H4
Method	BLASTX
NCBI GI	g4056420
BLAST score	307
E value	4.0e-28
Match length	81
% identity	73
NCBI Description	(AC005322) ESTs gb_T144077 and gb_T43352 come from this gene. [Arabidopsis thaliana]

Seq. No.	220782
Seq. ID	LIB3149-063-Q1-K1-H5
Method	BLASTX
NCBI GI	g20559
BLAST score	647
E value	6.0e-68
Match length	140
% identity	91

NCBI Description (X13301) hsp70 (AA 6 - 651) [Petunia x hybrida]

Seq. No. 220783
Seq. ID LIB3149-063-Q1-K1-H7
Method BLASTX
NCBI GI g4415934
BLAST score 261
E value 1.0e-22
Match length 87
% identity 55
NCBI Description (AC006418) putative auxin response factor 1 [Arabidopsis thaliana]

Seq. No. 220784
Seq. ID LIB3149-063-Q1-K1-H8
Method BLASTX
NCBI GI g3645985
BLAST score 438
E value 2.0e-43
Match length 77
% identity 96
NCBI Description (AL031581) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=23.36; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=AA141041; 2-match_description=CK01110.3prime CK Drosophila melanogaster

Seq. No. 220785
Seq. ID LIB3149-063-Q1-K1-H9
Method BLASTX
NCBI GI g1477428
BLAST score 565
E value 2.0e-58
Match length 126
% identity 89
NCBI Description (X99623) alpha-tubulin 1 [Hordeum vulgare]

Seq. No. 220786
Seq. ID LIB3149-064-Q1-K1-A11
Method BLASTX
NCBI GI g3647355
BLAST score 329
E value 1.0e-30
Match length 134
% identity 49
NCBI Description (Z97348) predicted using hexExon; MAL3P1.12 (PFC0150w), Human hypothetical protein KIAA0249-related protein len: 1160 aa; Similarity to 2 human and an yeast hypothetical gene. Human hypothetical protein KIAA0249 (SW:Y249_HUMA

Seq. No. 220787
Seq. ID LIB3149-064-Q1-K1-A12
Method BLASTX
NCBI GI g4115377
BLAST score 611
E value 1.0e-63

Match length	143
% identity	80
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	220788
Seq. ID	LIB3149-064-Q1-K1-A7
Method	BLASTX
NCBI GI	g3426051
BLAST score	309
E value	2.0e-28
Match length	105
% identity	55
NCBI Description	(AC005168) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220789
Seq. ID	LIB3149-064-Q1-K1-A8
Method	BLASTX
NCBI GI	g4539417
BLAST score	498
E value	2.0e-50
Match length	111
% identity	79
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]

Seq. No.	220790
Seq. ID	LIB3149-064-Q1-K1-B11
Method	BLASTN
NCBI GI	g2826742
BLAST score	170
E value	5.0e-91
Match length	194
% identity	96
NCBI Description	Gossypium arboreum ribosomal protein L16 (rpl16) gene, chloroplast gene encoding chloroplast protein, partial cds, and intron sequence

Seq. No.	220791
Seq. ID	LIB3149-064-Q1-K1-B12
Method	BLASTX
NCBI GI	g544134
BLAST score	160
E value	5.0e-11
Match length	64
% identity	50
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR >gi_99720_pir__S22863 hypothetical protein - Arabidopsis thaliana >gi_421844_pir__A46260 RecA functional analog DRT100 - Arabidopsis thaliana (fragment)

Seq. No.	220792
Seq. ID	LIB3149-064-Q1-K1-B2
Method	BLASTX
NCBI GI	g2341034
BLAST score	560
E value	9.0e-58
Match length	114
% identity	97

NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	220793
Seq. ID	LIB3149-064-Q1-K1-B3
Method	BLASTX
NCBI GI	g2688820
BLAST score	174
E value	1.0e-12
Match length	85
% identity	42
NCBI Description	(U93271) enoyl-CoA hydratase [Prunus armeniaca]

Seq. No.	220794
Seq. ID	LIB3149-064-Q1-K1-B7
Method	BLASTX
NCBI GI	g3600052
BLAST score	116
E value	6.0e-14
Match length	100
% identity	43
NCBI Description	(AF080120) contains similarity to glycosyl hydrolases family 9 (Pfam: glycosyl_hydro5.hmm, score: 88.03) [Arabidopsis thaliana]

Seq. No.	220795
Seq. ID	LIB3149-064-Q1-K1-B8
Method	BLASTX
NCBI GI	g974782
BLAST score	589
E value	3.0e-61
Match length	129
% identity	90
NCBI Description	(Z49150) cobalamine-independent methionine synthase [Solenostemon scutellarioides]

Seq. No.	220796
Seq. ID	LIB3149-064-Q1-K1-B9
Method	BLASTX
NCBI GI	g218157
BLAST score	459
E value	5.0e-46
Match length	116
% identity	80
NCBI Description	(D13512) cytoplasmic aldolase [Oryza sativa]

Seq. No.	220797
Seq. ID	LIB3149-064-Q1-K1-C1
Method	BLASTX
NCBI GI	g1856971
BLAST score	554
E value	5.0e-57
Match length	117
% identity	89
NCBI Description	(D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	220798
Seq. ID	LIB3149-064-Q1-K1-C12
Method	BLASTX
NCBI GI	g2501433
BLAST score	359
E value	3.0e-34
Match length	87
% identity	72
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-24 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2-EPF5) >gi_181916 (M91670) ubiquitin carrier protein [Homo sapiens]

Seq. No.	220799
Seq. ID	LIB3149-064-Q1-K1-C2
Method	BLASTX
NCBI GI	g1856971
BLAST score	304
E value	1.0e-27
Match length	136
% identity	56
NCBI Description	(D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	220800
Seq. ID	LIB3149-064-Q1-K1-C3
Method	BLASTX
NCBI GI	g1706319
BLAST score	282
E value	4.0e-25
Match length	103
% identity	53
NCBI Description	HISTIDINE DECARBOXYLASE (HDC) (TOM92) >gi_481829_pir__S39554 histidine decarboxylase (EC 4.1.1.22) - tomato >gi_416534_emb_CAA50719_ (X71900) histidine decarboxylase [Lycopersicon esculentum]

Seq. No.	220801
Seq. ID	LIB3149-064-Q1-K1-C5
Method	BLASTX
NCBI GI	g3395440
BLAST score	231
E value	3.0e-19
Match length	105
% identity	46
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220802
Seq. ID	LIB3149-064-Q1-K1-C7
Method	BLASTX
NCBI GI	g4127660
BLAST score	462
E value	3.0e-46
Match length	138
% identity	64
NCBI Description	(Y11124) invertase [Cichorium intybus]

Seq. No.	220803
Seq. ID	LIB3149-064-Q1-K1-C8
Method	BLASTX
NCBI GI	g232031
BLAST score	278
E value	1.0e-24
Match length	95
% identity	58
NCBI Description	ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224 translation elongation factor eEF-1 beta' chain - rice >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta' [Oryza sativa]

Seq. No.	220804
Seq. ID	LIB3149-064-Q1-K1-D10
Method	BLASTX
NCBI GI	g3152660
BLAST score	204
E value	5.0e-16
Match length	119
% identity	33
NCBI Description	(AF064603) GA17 protein [Homo sapiens]

Seq. No.	220805
Seq. ID	LIB3149-064-Q1-K1-D11
Method	BLASTN
NCBI GI	g2501849
BLAST score	36
E value	6.0e-11
Match length	56
% identity	91
NCBI Description	Nicotiana tabacum GDP dissociation inhibitor (GDI) mRNA, complete cds

Seq. No.	220806
Seq. ID	LIB3149-064-Q1-K1-D12
Method	BLASTN
NCBI GI	g531251
BLAST score	34
E value	1.0e-09
Match length	34
% identity	100
NCBI Description	Apple mitochondrial atp9 gene for F0-ATPase subunit 9 (complete cds) and nad5 gene for NADH dehydrogehase subunit 5 (exon a and b)

Seq. No.	220807
Seq. ID	LIB3149-064-Q1-K1-D2
Method	BLASTX
NCBI GI	g3236238
BLAST score	263
E value	7.0e-23
Match length	143
% identity	46
NCBI Description	(AC004684) putative ARF1 GTPase activating protein [Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_ (AB017876) Asp1 [Arabidopsis thaliana]

Seq. No.	220808
Seq. ID	LIB3149-064-Q1-K1-D9
Method	BLASTX
NCBI GI	g1173256
BLAST score	664
E value	6.0e-70
Match length	128
% identity	99
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal protein S4 - upland cotton >gi_488739_emb_CAA55882_ (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]

Seq. No.	220809
Seq. ID	LIB3149-064-Q1-K1-E11
Method	BLASTX
NCBI GI	g1856971
BLAST score	443
E value	5.0e-44
Match length	95
% identity	88
NCBI Description	(D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	220810
Seq. ID	LIB3149-064-Q1-K1-E6
Method	BLASTX
NCBI GI	g3377820
BLAST score	393
E value	4.0e-38
Match length	98
% identity	77
NCBI Description	(AF076275) contains similarity to coatomer zeta chains [Arabidopsis thaliana]

Seq. No.	220811
Seq. ID	LIB3149-064-Q1-K1-F11
Method	BLASTX
NCBI GI	g629483
BLAST score	357
E value	6.0e-34
Match length	125
% identity	58
NCBI Description	gene 1-Sc3 protein - European white birch >gi_534898_emb_CAA54696_ (X77601) 1 Sc-3 [Betula pendula] >gi_1584322_prf__2122374C allergen Bet v 1-Sc3 [Betula pendula]

Seq. No.	220812
Seq. ID	LIB3149-064-Q1-K1-F2
Method	BLASTX
NCBI GI	g2088654
BLAST score	357
E value	8.0e-42
Match length	117

% identity	83
NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]

Seq. No.	220813
Seq. ID	LIB3149-064-Q1-K1-F6
Method	BLASTX
NCBI GI	g1673344
BLAST score	166
E value	2.0e-11
Match length	53
% identity	55
NCBI Description	(D64002) hypothetical protein [Synechocystis sp.]

Seq. No.	220814
Seq. ID	LIB3149-064-Q1-K1-G10
Method	BLASTX
NCBI GI	g1256830
BLAST score	578
E value	7.0e-60
Match length	141
% identity	77
NCBI Description	(U52970) cysteine endopeptidase 1 [Phaseolus vulgaris] >gi_2959418_emb_CAA12118_ (AJ224766) cysteine protease [Phaseolus vulgaris]

Seq. No.	220815
Seq. ID	LIB3149-064-Q1-K1-G7
Method	BLASTX
NCBI GI	g1684857
BLAST score	572
E value	4.0e-59
Match length	116
% identity	39
NCBI Description	(U77940) polyubiquitin [Phaseolus vulgaris]

Seq. No.	220816
Seq. ID	LIB3149-064-Q1-K1-G9
Method	BLASTX
NCBI GI	g4455174
BLAST score	189
E value	3.0e-14
Match length	52
% identity	62
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	220817
Seq. ID	LIB3149-064-Q1-K1-H10
Method	BLASTX
NCBI GI	g4406780
BLAST score	543
E value	9.0e-56
Match length	125
% identity	78
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	220818
Seq. ID	LIB3149-064-Q1-K1-H11
Method	BLASTX
NCBI GI	g4406780
BLAST score	141
E value	3.0e-09
Match length	52
% identity	58
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	220819
Seq. ID	LIB3149-064-Q1-K1-H12
Method	BLASTX
NCBI GI	g2507222
BLAST score	404
E value	2.0e-39
Match length	105
% identity	69
NCBI Description	KINASE ASSOCIATED PROTEIN PHOSPHATASE >gi_1709236 (U09505) kinase associated protein phosphatase [Arabidopsis thaliana]

Seq. No.	220820
Seq. ID	LIB3165-001-Q1-K1-A11
Method	BLASTX
NCBI GI	g3914603
BLAST score	734
E value	4.0e-78
Match length	151
% identity	89
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No.	220821
Seq. ID	LIB3165-001-Q1-K1-A2
Method	BLASTX
NCBI GI	g131385
BLAST score	484
E value	7.0e-49
Match length	122
% identity	83
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN)

Seq. No.	220822
Seq. ID	LIB3165-001-Q1-K1-A3
Method	BLASTX
NCBI GI	g131397
BLAST score	376
E value	3.0e-36
Match length	133
% identity	62
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD

SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_81480_pir__S00008 photosystem II oxygen-evolving complex protein 3 precursor - spinach >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi_225597_prf__1307179B luminal protein 16kD [Spinacia oleracea]

Seq. No.	220823
Seq. ID	LIB3165-001-Q1-K1-A6
Method	BLASTX
NCBI GI	g4406530
BLAST score	423
E value	1.0e-41
Match length	118
% identity	75
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	220824
Seq. ID	LIB3165-001-Q1-K1-A7
Method	BLASTX
NCBI GI	g100616
BLAST score	294
E value	1.0e-26
Match length	67
% identity	84
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	220825
Seq. ID	LIB3165-001-Q1-K1-A8
Method	BLASTX
NCBI GI	g100616
BLAST score	294
E value	1.0e-26
Match length	67
% identity	84
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	220826
Seq. ID	LIB3165-001-Q1-K1-B12
Method	BLASTX
NCBI GI	g1352821
BLAST score	729
E value	2.0e-77
Match length	145
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	220827
Seq. ID	LIB3165-001-Q1-K1-B2
Method	BLASTX
NCBI GI	g136707
BLAST score	443
E value	4.0e-44
Match length	123
% identity	69
NCBI Description	CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_280397_pir__S26199 plastoquinol--plastocyanin reductase (EC 1.10.99.1) iron-sulfur protein precursor - garden pea >gi_20832_emb_CAA45151_ (X63605) chloroplast Rieske FeS protein [Pisum sativum]

Seq. No.	220828
Seq. ID	LIB3165-001-Q1-K1-B3
Method	BLASTX
NCBI GI	g3183088
BLAST score	205
E value	4.0e-16
Match length	70
% identity	56
NCBI Description	PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer like protein [Vigna unguiculata]

Seq. No.	220829
Seq. ID	LIB3165-001-Q1-K1-B4
Method	BLASTX
NCBI GI	g100454
BLAST score	648
E value	4.0e-68
Match length	138
% identity	89
NCBI Description	photosystem II oxygen-evolving complex protein 1 - potato >gi_809113_emb_CAA35601_ (X17578) 33kDa precursor protein of oxygen-evolving complex [Solanum tuberosum]

Seq. No.	220830
Seq. ID	LIB3165-001-Q1-K1-B5
Method	BLASTX
NCBI GI	g1352821
BLAST score	593
E value	1.0e-61
Match length	111
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	220831
Seq. ID	LIB3165-001-Q1-K1-B7
Method	BLASTX
NCBI GI	g4126403
BLAST score	503
E value	5.0e-51
Match length	144
% identity	64
NCBI Description	(AB011796) flavonol synthase [Citrus unshiu]

Seq. No.	220832
Seq. ID	LIB3165-001-Q1-K1-B9
Method	BLASTX
NCBI GI	g1172664
BLAST score	265
E value	4.0e-23
Match length	56
% identity	93
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_419791_pir__S31165 photosystem I chain III precursor - Flaveria trinervia >gi_298482_bbs_127083 photosystem I reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem I subunit III [Flaveria trinervia]

Seq. No.	220833
Seq. ID	LIB3165-001-Q1-K1-C1
Method	BLASTX
NCBI GI	g100196
BLAST score	584
E value	1.0e-60
Match length	127
% identity	83
NCBI Description	chlorophyll a/b-binding protein (cab-11) - tomato

Seq. No.	220834
Seq. ID	LIB3165-001-Q1-K1-C10
Method	BLASTX
NCBI GI	g3600059
BLAST score	354
E value	1.0e-33
Match length	84
% identity	79
NCBI Description	(AF080120) contains similarity to WB domains, G-beta repeats (Pfam: G-beta.hmm, score: 14.83 and 23.03) [Arabidopsis thaliana]

Seq. No.	220835
Seq. ID	LIB3165-001-Q1-K1-C11
Method	BLASTN
NCBI GI	g4049332
BLAST score	40
E value	4.0e-13
Match length	64
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4

(ESSAII project)

Seq. No.	220836
Seq. ID	LIB3165-001-Q1-K1-C2
Method	BLASTX
NCBI GI	g120661
BLAST score	547
E value	2.0e-56
Match length	115
% identity	93
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_170237 (M14417) glyceraldehyde-3-phosphate dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No.	220837
Seq. ID	LIB3165-001-Q1-K1-C3
Method	BLASTX
NCBI GI	g4027897
BLAST score	351
E value	2.0e-33
Match length	72
% identity	88
NCBI Description	(AF049353) alpha-expansin precursor [Nicotiana tabacum]

Seq. No.	220838
Seq. ID	LIB3165-001-Q1-K1-C4
Method	BLASTX
NCBI GI	g4204267
BLAST score	220
E value	8.0e-18
Match length	131
% identity	45
NCBI Description	(AC005223) 55585 [Arabidopsis thaliana]

Seq. No.	220839
Seq. ID	LIB3165-001-Q1-K1-C7
Method	BLASTX
NCBI GI	g266936
BLAST score	432
E value	1.0e-42
Match length	120
% identity	76
NCBI Description	50S RIBOSOMAL PROTEIN L27, CHLOROPLAST PRECURSOR (CL27) >gi_282960_pir__A42840 ribosomal protein L27 - common tobacco >gi_170306 (M98473) ribosomal protein L27 [Nicotiana tabacum] >gi_170326 (M75731) ribosomal protein L27 [Nicotiana tabacum]

Seq. No.	220840
Seq. ID	LIB3165-001-Q1-K1-C8
Method	BLASTX
NCBI GI	g1527191
BLAST score	431
E value	1.0e-42
Match length	97
% identity	81
NCBI Description	(U67861) 1-aminocyclopropane-1-carboxylate oxidase

[Pelargonium x hortorum]

Seq. No.	220841
Seq. ID	LIB3165-001-Q1-K1-C9
Method	BLASTX
NCBI GI	g4006858
BLAST score	362
E value	2.0e-34
Match length	95
% identity	66
NCBI Description	(Z99707) cold acclimation protein homolog [Arabidopsis thaliana]

Seq. No.	220842
Seq. ID	LIB3165-001-Q1-K1-D10
Method	BLASTX
NCBI GI	g430947
BLAST score	431
E value	1.0e-42
Match length	105
% identity	81
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	220843
Seq. ID	LIB3165-001-Q1-K1-D11
Method	BLASTX
NCBI GI	g226263
BLAST score	232
E value	1.0e-19
Match length	43
% identity	100
NCBI Description	chlorophyll a/b binding protein [Glycine max]

Seq. No.	220844
Seq. ID	LIB3165-001-Q1-K1-D12
Method	BLASTX
NCBI GI	g1532118
BLAST score	241
E value	2.0e-20
Match length	127
% identity	45
NCBI Description	(U36268) beta-prime-adaptin [Homo sapiens]

Seq. No.	220845
Seq. ID	LIB3165-001-Q1-K1-D3
Method	BLASTX
NCBI GI	g1352821
BLAST score	626
E value	2.0e-65
Match length	117
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	220846
Seq. ID	LIB3165-001-Q1-K1-D4
Method	BLASTX
NCBI GI	g1352821
BLAST score	612
E value	8.0e-64
Match length	114
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	220847
Seq. ID	LIB3165-001-Q1-K1-D6
Method	BLASTX
NCBI GI	g2190992
BLAST score	229
E value	6.0e-19
Match length	79
% identity	58
NCBI Description	(AF004358) glutathione S-transferase TSI-1 [Aegilops tauschii]

Seq. No.	220848
Seq. ID	LIB3165-001-Q1-K1-D7
Method	BLASTX
NCBI GI	g2754849
BLAST score	209
E value	1.0e-17
Match length	55
% identity	89
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

Seq. No.	220849
Seq. ID	LIB3165-001-Q1-K1-E1
Method	BLASTX
NCBI GI	g3747111
BLAST score	369
E value	3.0e-35
Match length	114
% identity	61
NCBI Description	(AF095641) MTN3 homolog [Arabidopsis thaliana]

Seq. No.	220850
Seq. ID	LIB3165-001-Q1-K1-E10
Method	BLASTX
NCBI GI	g4406530
BLAST score	409
E value	5.0e-40
Match length	115
% identity	75
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No. 220851
Seq. ID LIB3165-001-Q1-K1-E11
Method BLASTX
NCBI GI g2815246
BLAST score 225
E value 2.0e-18
Match length 55
% identity 73
NCBI Description (X95709) class I type 2 metallothionein [Cicer arietinum]

Seq. No. 220852
Seq. ID LIB3165-001-Q1-K1-E2
Method BLASTN
NCBI GI g18058
BLAST score 108
E value 3.0e-54
Match length 136
% identity 95
NCBI Description Citrus limon cistron for 26S ribosomal RNA

Seq. No. 220853
Seq. ID LIB3165-001-Q1-K1-E5
Method BLASTX
NCBI GI g3426051
BLAST score 159
E value 1.0e-10
Match length 63
% identity 56
NCBI Description (AC005168) hypothetical protein [Arabidopsis thaliana]

Seq. No. 220854
Seq. ID LIB3165-001-Q1-K1-E6
Method BLASTX
NCBI GI g3790567
BLAST score 180
E value 4.0e-13
Match length 115
% identity 33
NCBI Description (AF078821) RING-H2 finger protein RHA1b [Arabidopsis thaliana]

Seq. No. 220855
Seq. ID LIB3165-001-Q1-K1-E8
Method BLASTX
NCBI GI g1352821
BLAST score 637
E value 9.0e-67
Match length 120
% identity 97
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 220856
Seq. ID LIB3165-001-Q1-K1-F1

Method	BLASTX
NCBI GI	g166834
BLAST score	307
E value	4.0e-28
Match length	71
% identity	79
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	220857
Seq. ID	LIB3165-001-Q1-K1-F2
Method	BLASTX
NCBI GI	g557084
BLAST score	159
E value	1.0e-10
Match length	103
% identity	3
NCBI Description	(L35601) ankyrin [Drosophila melanogaster] >gi_1092123_prf__2022340A ankyrin [Drosophila melanogaster]

Seq. No.	220858
Seq. ID	LIB3165-001-Q1-K1-F5
Method	BLASTX
NCBI GI	g441457
BLAST score	591
E value	2.0e-61
Match length	112
% identity	98
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]

Seq. No.	220859
Seq. ID	LIB3165-001-Q1-K1-F9
Method	BLASTX
NCBI GI	g2496789
BLAST score	500
E value	1.0e-50
Match length	148
% identity	68
NCBI Description	1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE (DXP REDUCTOISOMERASE) >gi_1001556_dbj_BAA10183_ (D64000) hypothetical protein [Synechocystis sp.]

Seq. No.	220860
Seq. ID	LIB3165-001-Q1-K1-G4
Method	BLASTX
NCBI GI	g2702281
BLAST score	407
E value	5.0e-40
Match length	101
% identity	56
NCBI Description	(AC003033) putative protein disulfide isomerase precursor [Arabidopsis thaliana]

Seq. No.	220861
Seq. ID	LIB3165-001-Q1-K1-G5

Method	BLASTX
NCBI GI	g1354515
BLAST score	303
E value	1.0e-27
Match length	136
% identity	53
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	220862
Seq. ID	LIB3165-001-Q1-K1-G7
Method	BLASTX
NCBI GI	g4512018
BLAST score	614
E value	4.0e-64
Match length	131
% identity	84
NCBI Description	(AF106660) mRNA binding protein precursor [Lycopersicon esculentum]

Seq. No.	220863
Seq. ID	LIB3165-001-Q1-K1-G8
Method	BLASTX
NCBI GI	g1928981
BLAST score	580
E value	4.0e-60
Match length	123
% identity	93
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	220864
Seq. ID	LIB3165-001-Q1-K1-G9
Method	BLASTX
NCBI GI	g131225
BLAST score	390
E value	5.0e-52
Match length	149
% identity	71
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	220865
Seq. ID	LIB3165-001-Q1-K1-H1
Method	BLASTX
NCBI GI	g166834
BLAST score	378
E value	2.0e-36
Match length	88
% identity	80
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	220866

Seq. ID	LIB3165-001-Q1-K1-H10
Method	BLASTX
NCBI GI	g4406530
BLAST score	360
E value	3.0e-34
Match length	98
% identity	76
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	220867
Seq. ID	LIB3165-001-Q1-K1-H11
Method	BLASTX
NCBI GI	g3914472
BLAST score	291
E value	2.0e-26
Match length	97
% identity	62
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10) >gi_322764_pir__S32021 photosystem II 10K protein - common tobacco >gi_22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana tabacum]

Seq. No.	220868
Seq. ID	LIB3165-001-Q1-K1-H2
Method	BLASTX
NCBI GI	g125578
BLAST score	444
E value	4.0e-44
Match length	116
% identity	74
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_167266 (M73707) phosphoribulokinase [Mesembryanthemum crystallinum]

Seq. No.	220869
Seq. ID	LIB3165-001-Q1-K1-H4
Method	BLASTX
NCBI GI	g400890
BLAST score	229
E value	5.0e-19
Match length	110
% identity	48
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_282837_pir__S26953 photosystem II 22K protein precursor - spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864) photosystem II 22 kda polypeptide [spinach, Peptide, 274 aa] [Spinacia oleracea]

Seq. No.	220870
Seq. ID	LIB3165-002-Q1-K1-A1
Method	BLASTX
NCBI GI	g4406530
BLAST score	347
E value	8.0e-33
Match length	92
% identity	77

NCBI Description	(AF126870) rubisco activase [Vigna radiata]
Seq. No.	220871
Seq. ID	LIB3165-002-Q1-K1-A10
Method	BLASTX
NCBI GI	g3901268
BLAST score	224
E value	2.0e-18
Match length	132
% identity	35
NCBI Description	(AF060173) SV2 related protein [Rattus norvegicus]
Seq. No.	220872
Seq. ID	LIB3165-002-Q1-K1-A12
Method	BLASTX
NCBI GI	g505482
BLAST score	457
E value	1.0e-45
Match length	114
% identity	82
NCBI Description	(X64349) 33 kDa polypeptide of water-oxidizing complex of photosystem II [Nicotiana tabacum]
Seq. No.	220873
Seq. ID	LIB3165-002-Q1-K1-A3
Method	BLASTX
NCBI GI	g4210948
BLAST score	495
E value	4.0e-50
Match length	99
% identity	93
NCBI Description	(AF085275) DnaJ protein [Hevea brasiliensis]
Seq. No.	220874
Seq. ID	LIB3165-002-Q1-K1-A4
Method	BLASTX
NCBI GI	g3869088
BLAST score	574
E value	2.0e-59
Match length	110
% identity	99
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]
Seq. No.	220875
Seq. ID	LIB3165-002-Q1-K1-A8
Method	BLASTN
NCBI GI	g4519194
BLAST score	41
E value	1.0e-13
Match length	193
% identity	80
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence
Seq. No.	220876
Seq. ID	LIB3165-002-Q1-K1-A9
Method	BLASTX

NCBI GI	g3738261
BLAST score	563
E value	4.0e-58
Match length	130
% identity	86
NCBI Description	(AB018412) chloroplast phosphoglycerate kinase [Populus nigra]

Seq. No.	220877
Seq. ID	LIB3165-002-Q1-K1-B11
Method	BLASTX
NCBI GI	g4510345
BLAST score	161
E value	5.0e-11
Match length	53
% identity	53
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	220878
Seq. ID	LIB3165-002-Q1-K1-B4
Method	BLASTX
NCBI GI	g4545262
BLAST score	239
E value	4.0e-20
Match length	44
% identity	100
NCBI Description	(AF118230) metallothionein-like protein [Gossypium hirsutum]

Seq. No.	220879
Seq. ID	LIB3165-002-Q1-K1-B5
Method	BLASTX
NCBI GI	g2864617
BLAST score	251
E value	2.0e-21
Match length	121
% identity	46
NCBI Description	(AL021811) H+-transporting ATP synthase chain9 - like protein [Arabidopsis thaliana]

Seq. No.	220880
Seq. ID	LIB3165-002-Q1-K1-B6
Method	BLASTX
NCBI GI	g2765081
BLAST score	455
E value	2.0e-45
Match length	128
% identity	71
NCBI Description	(Y10557) g5bf [Arabidopsis thaliana]

Seq. No.	220881
Seq. ID	LIB3165-002-Q1-K1-B7
Method	BLASTX
NCBI GI	g4185515
BLAST score	441
E value	8.0e-44
Match length	104

% identity	78
NCBI Description	(AF102824) actin depolymerizing factor 6 [Arabidopsis thaliana]

Seq. No.	220882
Seq. ID	LIB3165-002-Q1-K1-B8
Method	BLASTX
NCBI GI	g2244905
BLAST score	364
E value	8.0e-35
Match length	121
% identity	57
NCBI Description	(Z97339) indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	220883
Seq. ID	LIB3165-002-Q1-K1-B9
Method	BLASTX
NCBI GI	g3643192
BLAST score	268
E value	1.0e-23
Match length	122
% identity	51
NCBI Description	(AF087435) unknown [Arabidopsis thaliana]

Seq. No.	220884
Seq. ID	LIB3165-002-Q1-K1-C1
Method	BLASTX
NCBI GI	g289920
BLAST score	682
E value	4.0e-72
Match length	128
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	220885
Seq. ID	LIB3165-002-Q1-K1-C10
Method	BLASTX
NCBI GI	g1781348
BLAST score	609
E value	2.0e-63
Match length	122
% identity	94
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No.	220886
Seq. ID	LIB3165-002-Q1-K1-C11
Method	BLASTX
NCBI GI	g1843527
BLAST score	654
E value	8.0e-69
Match length	129
% identity	57
NCBI Description	(U73747) annexin [Gossypium hirsutum]

Seq. No.	220887
Seq. ID	LIB3165-002-Q1-K1-C12
Method	BLASTX
NCBI GI	g68200
BLAST score	528
E value	5.0e-54
Match length	131
% identity	82
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	220888
Seq. ID	LIB3165-002-Q1-K1-C3
Method	BLASTX
NCBI GI	g505482
BLAST score	209
E value	1.0e-23
Match length	102
% identity	69
NCBI Description	(X64349) 33 kDa polypeptide of water-oxidizing complex of photosystem II [Nicotiana tabacum]

Seq. No.	220889
Seq. ID	LIB3165-002-Q1-K1-C6
Method	BLASTX
NCBI GI	g1750404
BLAST score	209
E value	1.0e-16
Match length	56
% identity	62
NCBI Description	(U80953) Similar to 40S ribosomal protein S29; coded for by C. elegans cDNA cm10c2; coded for by C. elegans cDNA yk61d8.5; coded for by C. elegans cDNA yk107e8.5; coded for by C. elegans cDNA CEESF55F; coded for by C. elegans cDNA yk107e8.3;

Seq. No.	220890
Seq. ID	LIB3165-002-Q1-K1-C8
Method	BLASTX
NCBI GI	g418854
BLAST score	538
E value	3.0e-55
Match length	109
% identity	18
NCBI Description	ubiquitin precursor - parsley >gi_288112_emb_CAA45621_ (X64344) polyubiquitin [Petroselinum crispum] >gi_288114_emb_CAA45622_ (X64345) polyubiquitin [Petroselinum crispum]

Seq. No.	220891
Seq. ID	LIB3165-002-Q1-K1-D1
Method	BLASTX
NCBI GI	g1352821
BLAST score	570
E value	6.0e-59
Match length	108

% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	220892
Seq. ID	LIB3165-002-Q1-K1-D11
Method	BLASTN
NCBI GI	g3821780
BLAST score	33
E value	6.0e-09
Match length	33
% identity	58
NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	220893
Seq. ID	LIB3165-002-Q1-K1-D12
Method	BLASTX
NCBI GI	g4263710
BLAST score	364
E value	8.0e-35
Match length	74
% identity	59
NCBI Description	(AC006223) putative pur-alpha transcriptional activator protein [Arabidopsis thaliana]
Seq. No.	220894
Seq. ID	LIB3165-002-Q1-K1-D2
Method	BLASTX
NCBI GI	g1170567
BLAST score	512
E value	4.0e-52
Match length	102
% identity	90
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1085960_pir__S52648 INO1 protein - Citrus paradisi >gi_602565_emb_CAA83565_ (Z32632) INO1 [Citrus x paradisi]
Seq. No.	220895
Seq. ID	LIB3165-002-Q1-K1-D3
Method	BLASTX
NCBI GI	g3157952
BLAST score	245
E value	8.0e-21
Match length	100
% identity	55
NCBI Description	(AC002131) F12F1.11 [Arabidopsis thaliana]
Seq. No.	220896
Seq. ID	LIB3165-002-Q1-K1-D5
Method	BLASTX
NCBI GI	g1655536
BLAST score	256
E value	4.0e-22
Match length	88

% identity	56
NCBI Description	(Y09095) chloride channel [Arabidopsis thaliana] >gi_1742957_emb_CAA96059_ (Z71447) CLC-c chloride channel protein [Arabidopsis thaliana]

Seq. No.	220897
Seq. ID	LIB3165-002-Q1-K1-D6
Method	BLASTX
NCBI GI	g1352821
BLAST score	553
E value	6.0e-57
Match length	105
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	220898
Seq. ID	LIB3165-002-Q1-K1-D8
Method	BLASTX
NCBI GI	g2618686
BLAST score	209
E value	1.0e-16
Match length	118
% identity	42
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220899
Seq. ID	LIB3165-002-Q1-K1-E1
Method	BLASTX
NCBI GI	g3913018
BLAST score	624
E value	3.0e-65
Match length	125
% identity	94
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No.	220900
Seq. ID	LIB3165-002-Q1-K1-E10
Method	BLASTX
NCBI GI	g2493694
BLAST score	316
E value	4.0e-29
Match length	126
% identity	56
NCBI Description	PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII 6.1 KD PROTEIN) >gi_1076268_pir__S53025 photosystem II protein - spinach >gi_728716_emb_CAA59409_ (X85038) protein of photosystem II [Spinacia oleracea]

Seq. No.	220901
Seq. ID	LIB3165-002-Q1-K1-E3
Method	BLASTX

NCBI GI	g3426043
BLAST score	436
E value	3.0e-43
Match length	135
% identity	66
NCBI Description	(AC005168) putative choline kinase [Arabidopsis thaliana]

Seq. No.	220902
Seq. ID	LIB3165-002-Q1-K1-E4
Method	BLASTX
NCBI GI	g2511691
BLAST score	274
E value	3.0e-24
Match length	80
% identity	69
NCBI Description	(Z99953) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No.	220903
Seq. ID	LIB3165-002-Q1-K1-E5
Method	BLASTX
NCBI GI	g2764574
BLAST score	302
E value	2.0e-27
Match length	128
% identity	52
NCBI Description	(AJ001009) pore protein of 24 kD (OEP24) [Pisum sativum]

Seq. No.	220904
Seq. ID	LIB3165-002-Q1-K1-E7
Method	BLASTX
NCBI GI	g2765081
BLAST score	455
E value	2.0e-45
Match length	128
% identity	71
NCBI Description	(Y10557) g5bf [Arabidopsis thaliana]

Seq. No.	220905
Seq. ID	LIB3165-002-Q1-K1-E8
Method	BLASTX
NCBI GI	g4406530
BLAST score	349
E value	5.0e-33
Match length	93
% identity	76
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	220906
Seq. ID	LIB3165-002-Q1-K1-F1
Method	BLASTX
NCBI GI	g3355486
BLAST score	494
E value	5.0e-50
Match length	131
% identity	72
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.	220907
Seq. ID	LIB3165-002-Q1-K1-F10
Method	BLASTX
NCBI GI	g3687652
BLAST score	537
E value	1.0e-62
Match length	129
% identity	95
NCBI Description	(AF047352) rubisco activase precursor [Datisca glomerata]

Seq. No.	220908
Seq. ID	LIB3165-002-Q1-K1-F11
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	9.0e-11
Match length	37
% identity	61
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	220909
Seq. ID	LIB3165-002-Q1-K1-F2
Method	BLASTX
NCBI GI	g1495251
BLAST score	244
E value	9.0e-21
Match length	126
% identity	44
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	220910
Seq. ID	LIB3165-002-Q1-K1-F3
Method	BLASTX
NCBI GI	g2505872
BLAST score	144
E value	5.0e-09
Match length	63
% identity	52
NCBI Description	(Y12227) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220911
Seq. ID	LIB3165-002-Q1-K1-F4
Method	BLASTX
NCBI GI	g3201969
BLAST score	450
E value	7.0e-45
Match length	110
% identity	70
NCBI Description	(AF068332) submergence induced protein 2A [Oryza sativa]

Seq. No.	220912
Seq. ID	LIB3165-002-Q1-K1-F5
Method	BLASTX
NCBI GI	g3694811
BLAST score	434
E value	4.0e-43
Match length	109

% identity	76
NCBI Description	(AF060481) p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana]

Seq. No.	220913
Seq. ID	LIB3165-002-Q1-K1-F6
Method	BLASTX
NCBI GI	g289920
BLAST score	601
E value	1.0e-62
Match length	115
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	220914
Seq. ID	LIB3165-002-Q1-K1-F7
Method	BLASTX
NCBI GI	g4096662
BLAST score	569
E value	8.0e-59
Match length	111
% identity	98
NCBI Description	(U35026) Rab1-like small GTP-binding protein [Petunia x hybrida]

Seq. No.	220915
Seq. ID	LIB3165-002-Q1-K1-G1
Method	BLASTX
NCBI GI	g1352821
BLAST score	398
E value	8.0e-39
Match length	75
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	220916
Seq. ID	LIB3165-002-Q1-K1-G10
Method	BLASTX
NCBI GI	g1657948
BLAST score	468
E value	5.0e-47
Match length	103
% identity	87
NCBI Description	(U73466) MipC [Mesembryanthemum crystallinum]

Seq. No.	220917
Seq. ID	LIB3165-002-Q1-K1-G12
Method	BLASTN
NCBI GI	g1399549
BLAST score	41
E value	8.0e-14
Match length	61

% identity	92
NCBI Description	Anemone trifolia nuclear 26S ribosomal RNA gene, partial sequence

Seq. No.	220918
Seq. ID	LIB3165-002-Q1-K1-G2
Method	BLASTX
NCBI GI	g2160185
BLAST score	298
E value	5.0e-27
Match length	90
% identity	61
NCBI Description	(AC000132) Similar to S. pombe ISP4 (gb_D83992). [Arabidopsis thaliana]

Seq. No.	220919
Seq. ID	LIB3165-002-Q1-K1-G4
Method	BLASTX
NCBI GI	g2995384
BLAST score	167
E value	8.0e-12
Match length	59
% identity	57
NCBI Description	(AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No.	220920
Seq. ID	LIB3165-002-Q1-K1-G6
Method	BLASTX
NCBI GI	g3065814
BLAST score	250
E value	2.0e-21
Match length	124
% identity	46
NCBI Description	(AF058714) sodium-dicarboxylate cotransporter SDCT1 [Rattus norvegicus] >gi_3168585_dbj_BAA28609_ (AB001321) sodium-dependent dicarboxylate transporter [Rattus norvegicus]

Seq. No.	220921
Seq. ID	LIB3165-002-Q1-K1-G7
Method	BLASTX
NCBI GI	g1170897
BLAST score	483
E value	1.0e-48
Match length	113
% identity	84
NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi_1076276_pir__S52039 NAD-malate dehydrogenase - cucumber >gi_695311 (L31900) glyoxysomal malate dehydrogenase [Cucumis sativus]

Seq. No.	220922
Seq. ID	LIB3165-002-Q1-K1-G8
Method	BLASTX
NCBI GI	g1168408
BLAST score	638
E value	6.0e-67

Match length	135
% identity	92
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1 >gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828) fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No.	220923
Seq. ID	LIB3165-002-Q1-K1-G9
Method	BLASTX
NCBI GI	g1181599
BLAST score	518
E value	7.0e-53
Match length	133
% identity	77
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.	220924
Seq. ID	LIB3165-002-Q1-K1-H10
Method	BLASTX
NCBI GI	g1168411
BLAST score	507
E value	1.0e-51
Match length	126
% identity	82
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	220925
Seq. ID	LIB3165-002-Q1-K1-H11
Method	BLASTX
NCBI GI	g2661021
BLAST score	593
E value	1.0e-61
Match length	113
% identity	96
NCBI Description	(AF035255) catalase [Glycine max]

Seq. No.	220926
Seq. ID	LIB3165-002-Q1-K1-H12
Method	BLASTX
NCBI GI	g3738316
BLAST score	235
E value	1.0e-19
Match length	65
% identity	69
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	220927
Seq. ID	LIB3165-002-Q1-K1-H3
Method	BLASTX
NCBI GI	g3123745
BLAST score	285
E value	1.0e-25
Match length	125
% identity	46
NCBI Description	(AB013447) aluminum-induced [Brassica napus]

Seq. No.	220928
Seq. ID	LIB3165-002-Q1-K1-H4
Method	BLASTX
NCBI GI	g4455356
BLAST score	207
E value	2.0e-16
Match length	98
% identity	41
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	220929
Seq. ID	LIB3165-002-Q1-K1-H5
Method	BLASTX
NCBI GI	g166834
BLAST score	281
E value	3.0e-25
Match length	65
% identity	78
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	220930
Seq. ID	LIB3165-002-Q1-K1-H6
Method	BLASTX
NCBI GI	g120658
BLAST score	424
E value	8.0e-42
Match length	114
% identity	75
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_66025_pir__DEPMNA glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - garden pea >gi_12159_emb_CAA36396_ (X52148) GAPA [Pisum sativum]

Seq. No.	220931
Seq. ID	LIB3165-002-Q1-K1-H7
Method	BLASTX
NCBI GI	g4490321
BLAST score	428
E value	3.0e-42
Match length	95
% identity	87
NCBI Description	(AJ011604) nitrate transporter [Arabidopsis thaliana]

Seq. No.	220932
Seq. ID	LIB3165-002-Q1-K1-H8
Method	BLASTX
NCBI GI	g1345698
BLAST score	637
E value	8.0e-67
Match length	126
% identity	94
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR (CAB-151) (LHCP) >gi_99601_pir__S20917 chlorophyll

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a/b-binding protein - upland cotton
>gi_452314_emb_CAA38025_ (X54090) chlorophyll ab binding protein [Gossypium hirsutum]

Seq. No.	220933
Seq. ID	LIB3165-003-P1-K1-A1
Method	BLASTX
NCBI GI	g1703129
BLAST score	471
E value	2.0e-47
Match length	91
% identity	96
NCBI Description	ACTIN 11 >gi_2129522_pir__S68109 actin 11 - Arabidopsis thaliana >gi_1002533 (U27981) actin-11 [Arabidopsis thaliana]

Seq. No.	220934
Seq. ID	LIB3165-003-P1-K1-A12
Method	BLASTX
NCBI GI	g1352821
BLAST score	305
E value	3.0e-28
Match length	61
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	220935
Seq. ID	LIB3165-003-P1-K1-A3
Method	BLASTX
NCBI GI	g3603401
BLAST score	321
E value	7.0e-30
Match length	82
% identity	70
NCBI Description	(AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No.	220936
Seq. ID	LIB3165-003-P1-K1-A4
Method	BLASTX
NCBI GI	g3510256
BLAST score	150
E value	9.0e-10
Match length	89
% identity	40
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	220937
Seq. ID	LIB3165-003-P1-K1-A5
Method	BLASTX
NCBI GI	g3687237
BLAST score	246
E value	4.0e-24
Match length	113

% identity	53
NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No.	220938
Seq. ID	LIB3165-003-P1-K1-A6
Method	BLASTX
NCBI GI	g68200
BLAST score	282
E value	3.0e-25
Match length	62
% identity	92
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	220939
Seq. ID	LIB3165-003-P1-K1-A7
Method	BLASTN
NCBI GI	g18058
BLAST score	188
E value	1.0e-102
Match length	212
% identity	98
NCBI Description	Citrus limon cistron for 26S ribosomal RNA

Seq. No.	220940
Seq. ID	LIB3165-003-P1-K1-A9
Method	BLASTX
NCBI GI	g228403
BLAST score	527
E value	6.0e-54
Match length	120
% identity	85
NCBI Description	glycolate oxidase [Lens culinaris]

Seq. No.	220941
Seq. ID	LIB3165-003-P1-K1-B1
Method	BLASTX
NCBI GI	g441457
BLAST score	624
E value	3.0e-65
Match length	118
% identity	97
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]

Seq. No.	220942
Seq. ID	LIB3165-003-P1-K1-B12
Method	BLASTX
NCBI GI	g1352821
BLAST score	311
E value	7.0e-29
Match length	61
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	220943
Seq. ID	LIB3165-003-P1-K1-B3
Method	BLASTX
NCBI GI	g462187
BLAST score	634
E value	2.0e-66
Match length	125
% identity	96
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_282928_pir__A42906 serine hydroxymethyltransferase - garden pea >gi_169158 (M87649) serine hydroxymethyltransferase [Pisum sativum]

Seq. No.	220944
Seq. ID	LIB3165-003-P1-K1-B6
Method	BLASTX
NCBI GI	g70644
BLAST score	547
E value	3.0e-56
Match length	113
% identity	19
NCBI Description	ubiquitin precursor - common sunflower (fragment)

Seq. No.	220945
Seq. ID	LIB3165-003-P1-K1-B7
Method	BLASTX
NCBI GI	g115813
BLAST score	377
E value	2.0e-36
Match length	109
% identity	69
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE III PRECURSOR (CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	220946
Seq. ID	LIB3165-003-P1-K1-C1
Method	BLASTX
NCBI GI	g131393
BLAST score	292
E value	2.0e-26
Match length	61
% identity	92
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_100360_pir__S15005 photosystem II oxygen-evolving complex protein 2 - common tobacco >gi_19911_emb_CAA39039.1_ (X55354) photosystem II 23kDa polypeptide [Nicotiana tabacum]

Seq. No.	220947
Seq. ID	LIB3165-003-P1-K1-C10

Method	BLASTX
NCBI GI	g3063392
BLAST score	338
E value	8.0e-32
Match length	98
% identity	72
NCBI Description	(AB012932) Ca2+/H+ exchanger [Vigna radiata]

Seq. No.	220948
Seq. ID	LIB3165-003-P1-K1-C12
Method	BLASTX
NCBI GI	g136707
BLAST score	222
E value	2.0e-18
Match length	65
% identity	68
NCBI Description	CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_280397_pir__S26199 plastoquinol--plastocyanin reductase (EC 1.10.99.1) iron-sulfur protein precursor - garden pea >gi_20832_emb_CAA45151_ (X63605) chloroplast Rieske FeS protein [Pisum sativum]

Seq. No.	220949
Seq. ID	LIB3165-003-P1-K1-C3
Method	BLASTX
NCBI GI	g3288821
BLAST score	416
E value	6.0e-41
Match length	101
% identity	79
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana]

Seq. No.	220950
Seq. ID	LIB3165-003-P1-K1-C4
Method	BLASTX
NCBI GI	g3033513
BLAST score	220
E value	2.0e-21
Match length	92
% identity	66
NCBI Description	(AF041068) rubisco activase [Phaseolus vulgaris]

Seq. No.	220951
Seq. ID	LIB3165-003-P1-K1-C6
Method	BLASTX
NCBI GI	g461501
BLAST score	377
E value	1.0e-36
Match length	81
% identity	88
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE 2, CHLOROPLAST >gi_418803_pir__S29048 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea (fragment)

Seq. No.	220952

Seq. ID	LIB3165-003-P1-K1-C7
Method	BLASTX
NCBI GI	g2864617
BLAST score	360
E value	2.0e-34
Match length	102
% identity	75
NCBI Description	(AL021811) H+-transporting ATP synthase chain9 - like protein [Arabidopsis thaliana]

Seq. No.	220953
Seq. ID	LIB3165-003-P1-K1-C9
Method	BLASTX
NCBI GI	g166708
BLAST score	186
E value	3.0e-14
Match length	68
% identity	54
NCBI Description	(M64118) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	220954
Seq. ID	LIB3165-003-P1-K1-E1
Method	BLASTX
NCBI GI	g1168411
BLAST score	396
E value	1.0e-38
Match length	101
% identity	81
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	220955
Seq. ID	LIB3165-003-P1-K1-E2
Method	BLASTN
NCBI GI	g18058
BLAST score	212
E value	1.0e-116
Match length	264
% identity	96
NCBI Description	Citrus limon cistron for 26S ribosomal RNA

Seq. No.	220956
Seq. ID	LIB3165-003-P1-K1-E3
Method	BLASTX
NCBI GI	g119932
BLAST score	361
E value	1.0e-34
Match length	96
% identity	69
NCBI Description	FERREDOXIN I >gi_65749_pir__FEFW1 ferredoxin [2Fe-2S] I - Virginian pokeweed

Seq. No.	220957
Seq. ID	LIB3165-003-P1-K1-E4
Method	BLASTX
NCBI GI	g1352821
BLAST score	472

E value	2.0e-47
Match length	96
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	220958
Seq. ID	LIB3165-003-P1-K1-E6
Method	BLASTX
NCBI GI	g3913651
BLAST score	324
E value	3.0e-30
Match length	97
% identity	65
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR (FNR) >gi_2225993_emb_CAA74359_ (Y14032) ferredoxin--NADP(+) reductase [Nicotiana tabacum]

Seq. No.	220959
Seq. ID	LIB3165-003-P1-K1-E8
Method	BLASTX
NCBI GI	g1881585
BLAST score	146
E value	3.0e-09
Match length	71
% identity	59
NCBI Description	(U72489) remorin [Solanum tuberosum]

Seq. No.	220960
Seq. ID	LIB3165-003-P1-K1-F1
Method	BLASTX
NCBI GI	g1531758
BLAST score	223
E value	3.0e-18
Match length	45
% identity	89
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	220961
Seq. ID	LIB3165-003-P1-K1-F11
Method	BLASTX
NCBI GI	g3288821
BLAST score	445
E value	3.0e-44
Match length	107
% identity	78
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana]

Seq. No.	220962
Seq. ID	LIB3165-003-P1-K1-F3
Method	BLASTX
NCBI GI	g1362086

BLAST score	515
E value	1.0e-52
Match length	106
% identity	92
NCBI Description	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir__S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]

Seq. No.	220963
Seq. ID	LIB3165-003-P1-K1-F4
Method	BLASTX
NCBI GI	g120663
BLAST score	472
E value	2.0e-47
Match length	121
% identity	74
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR, CHLOROPLAST >gi_66027_pir__DEPMNB glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast - garden pea >gi_309671 (M55147) glyceraldehyde-3-phosphate dehydrogenase B subunit [Pisum sativum]

Seq. No.	220964
Seq. ID	LIB3165-003-P1-K1-F5
Method	BLASTX
NCBI GI	g282995
BLAST score	180
E value	3.0e-13
Match length	85
% identity	52
NCBI Description	seed protein B32E - barley (fragment) >gi_1345530_emb_CAA45538_ (X64254) B32E [Hordeum vulgare]

Seq. No.	220965
Seq. ID	LIB3165-003-P1-K1-F8
Method	BLASTN
NCBI GI	g3298532
BLAST score	44
E value	1.0e-15
Match length	80
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	220966
Seq. ID	LIB3165-003-P1-K1-F9
Method	BLASTN
NCBI GI	g3108248
BLAST score	287
E value	1.0e-160
Match length	338
% identity	96

NCBI Description	Gossypium barbadense clone pXP027 repetitive DNA sequence
Seq. No.	220967
Seq. ID	LIB3165-003-P1-K1-G10
Method	BLASTX
NCBI GI	g1709651
BLAST score	215
E value	1.0e-23
Match length	114
% identity	53
NCBI Description	PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209 plastocyanin a precursor - black poplar >gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus nigra]
Seq. No.	220968
Seq. ID	LIB3165-003-P1-K1-G11
Method	BLASTX
NCBI GI	g20729
BLAST score	452
E value	4.0e-45
Match length	124
% identity	75
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]
Seq. No.	220969
Seq. ID	LIB3165-003-P1-K1-G6
Method	BLASTX
NCBI GI	g68200
BLAST score	499
E value	1.0e-50
Match length	123
% identity	83
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]
Seq. No.	220970
Seq. ID	LIB3165-003-P1-K1-H12
Method	BLASTX
NCBI GI	g4406530
BLAST score	244
E value	1.0e-20
Match length	54
% identity	85
NCBI Description	(AF126870) rubisco activase [Vigna radiata]
Seq. No.	220971
Seq. ID	LIB3165-003-P1-K1-H5
Method	BLASTX
NCBI GI	g4006884
BLAST score	139
E value	1.0e-08
Match length	44
% identity	68
NCBI Description	(Z99707) BEL1-like homeodomain protein [Arabidopsis thaliana]

Seq. No.	220972
Seq. ID	LIB3165-004-P1-K1-A11
Method	BLASTX
NCBI GI	g1709825
BLAST score	267
E value	2.0e-23
Match length	126
% identity	49
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No.	220973
Seq. ID	LIB3165-004-P1-K1-A12
Method	BLASTX
NCBI GI	g1588365
BLAST score	171
E value	3.0e-12
Match length	82
% identity	40
NCBI Description	signal peptidase:SUBUNIT=12kD [Homo sapiens]

Seq. No.	220974
Seq. ID	LIB3165-004-P1-K1-A6
Method	BLASTX
NCBI GI	g1781348
BLAST score	151
E value	4.0e-10
Match length	42
% identity	74
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No.	220975
Seq. ID	LIB3165-004-P1-K1-A7
Method	BLASTX
NCBI GI	g343369
BLAST score	561
E value	6.0e-58
Match length	108
% identity	95
NCBI Description	(M27308) 44 kd photosystem II protein [Spinacia oleracea]

Seq. No.	220976
Seq. ID	LIB3165-004-P1-K1-A8
Method	BLASTX
NCBI GI	g400890
BLAST score	235
E value	1.0e-19
Match length	110
% identity	45
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_282837_pir__S26953 photosystem II 22K protein precursor - spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864) photosystem II 22 kda polypeptide [spinach, Peptide, 274 aa] [Spinacia oleracea]

Seq. No.	220977
Seq. ID	LIB3165-004-P1-K1-A9
Method	BLASTX
NCBI GI	g1617274
BLAST score	514
E value	2.0e-52
Match length	123
% identity	75
NCBI Description	(Z72152) AMP-binding protein [Brassica napus]

Seq. No.	220978
Seq. ID	LIB3165-004-P1-K1-B1
Method	BLASTX
NCBI GI	g1345698
BLAST score	640
E value	3.0e-67
Match length	121
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR (CAB-151) (LHCP) >gi_99601_pir__S20917 chlorophyll a/b-binding protein - upland cotton >gi_452314_emb_CAA38025_ (X54090) chlorophyll ab binding protein [Gossypium hirsutum]

Seq. No.	220979
Seq. ID	LIB3165-004-P1-K1-B4
Method	BLASTX
NCBI GI	g100196
BLAST score	178
E value	1.0e-13
Match length	46
% identity	74
NCBI Description	chlorophyll a/b-binding protein (cab-11) - tomato

Seq. No.	220980
Seq. ID	LIB3165-004-P1-K1-B5
Method	BLASTX
NCBI GI	g1170897
BLAST score	558
E value	1.0e-57
Match length	123
% identity	89
NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi_1076276_pir__S52039 NAD-malate dehydrogenase - cucumber >gi_695311 (L31900) glyoxysomal malate dehydrogenase [Cucumis sativus]

Seq. No.	220981
Seq. ID	LIB3165-004-P1-K1-B6
Method	BLASTX
NCBI GI	g2677828
BLAST score	286
E value	2.0e-30
Match length	114
% identity	60
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	220982
Seq. ID	LIB3165-004-P1-K1-B8
Method	BLASTX
NCBI GI	g507275
BLAST score	165
E value	2.0e-11
Match length	108
% identity	35
NCBI Description	(L34159) NADPH:quinone oxidoreductase/zeta crystallin [Lama guanicoe]

Seq. No.	220983
Seq. ID	LIB3165-004-P1-K1-B9
Method	BLASTX
NCBI GI	g2501568
BLAST score	157
E value	1.0e-10
Match length	97
% identity	38
NCBI Description	HYPOTHETICAL 28.8 KD PROTEIN SLL0506 >gi_1001342_dbj_BAA10829_ (D64006) hypothetical protein [Synechocystis sp.]

Seq. No.	220984
Seq. ID	LIB3165-004-P1-K1-C1
Method	BLASTX
NCBI GI	g231688
BLAST score	555
E value	5.0e-61
Match length	127
% identity	96
NCBI Description	CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC 1.11.1.6) - upland cotton >gi_18488_emb_CAA39998_ (X56675) subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No.	220985
Seq. ID	LIB3165-004-P1-K1-C10
Method	BLASTX
NCBI GI	g2970051
BLAST score	380
E value	1.0e-36
Match length	95
% identity	74
NCBI Description	(AB012110) ARG10 [Vigna radiata]

Seq. No.	220986
Seq. ID	LIB3165-004-P1-K1-C11
Method	BLASTX
NCBI GI	g1354515
BLAST score	234
E value	1.0e-19
Match length	125
% identity	46
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	220987
Seq. ID	LIB3165-004-P1-K1-C12
Method	BLASTX
NCBI GI	g1458245
BLAST score	252
E value	1.0e-21
Match length	123
% identity	46
NCBI Description	(U64834) coded for by C. elegans cDNA cm17a1; coded for by C. elegans cDNA cm7g1; coded for by C. elegans cDNA CEMSE26F; similar to methyltransferases [Caenorhabditis elegans]

Seq. No.	220988
Seq. ID	LIB3165-004-P1-K1-C3
Method	BLASTX
NCBI GI	g400890
BLAST score	224
E value	2.0e-18
Match length	94
% identity	44
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_282837_pir__S26953 photosystem II 22K protein precursor - spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864) photosystem II 22 kda polypeptide [spinach, Peptide, 274 aa] [Spinacia oleracea]

Seq. No.	220989
Seq. ID	LIB3165-004-P1-K1-C4
Method	BLASTX
NCBI GI	g3128176
BLAST score	316
E value	3.0e-29
Match length	86
% identity	65
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	220990
Seq. ID	LIB3165-004-P1-K1-C5
Method	BLASTX
NCBI GI	g231610
BLAST score	274
E value	3.0e-24
Match length	101
% identity	60
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]

Seq. No.	220991
Seq. ID	LIB3165-004-P1-K1-C7
Method	BLASTX
NCBI GI	g2864617
BLAST score	227

E value	9.0e-19
Match length	94
% identity	54
NCBI Description	(AL021811) H+-transporting ATP synthase chain9 - like protein [Arabidopsis thaliana]

Seq. No.	220992
Seq. ID	LIB3165-004-P1-K1-C8
Method	BLASTX
NCBI GI	g2984709
BLAST score	426
E value	4.0e-42
Match length	83
% identity	98
NCBI Description	(AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No.	220993
Seq. ID	LIB3165-004-P1-K1-C9
Method	BLASTN
NCBI GI	g2687434
BLAST score	320
E value	1.0e-180
Match length	375
% identity	97
NCBI Description	Eucryphia lucida large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	220994
Seq. ID	LIB3165-004-P1-K1-D1
Method	BLASTX
NCBI GI	g974782
BLAST score	374
E value	5.0e-36
Match length	78
% identity	95
NCBI Description	(Z49150) cobalamine-independent methionine synthase [Solenostemon scutellarioides]

Seq. No.	220995
Seq. ID	LIB3165-004-P1-K1-D10
Method	BLASTX
NCBI GI	g136636
BLAST score	286
E value	1.0e-25
Match length	56
% identity	95
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	220996

Seq. ID	LIB3165-004-P1-K1-D12
Method	BLASTX
NCBI GI	g3242704
BLAST score	302
E value	1.0e-27
Match length	113
% identity	53
NCBI Description	(AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No.	220997
Seq. ID	LIB3165-004-P1-K1-D4
Method	BLASTX
NCBI GI	g1168411
BLAST score	462
E value	2.0e-46
Match length	116
% identity	81
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	220998
Seq. ID	LIB3165-004-P1-K1-D5
Method	BLASTX
NCBI GI	g1781348
BLAST score	512
E value	6.0e-55
Match length	124
% identity	90
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No.	220999
Seq. ID	LIB3165-004-P1-K1-D6
Method	BLASTX
NCBI GI	g118564
BLAST score	622
E value	4.0e-65
Match length	125
% identity	94
NCBI Description	GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE REDUCTASE) (HPR) (GDH) >gi_65955_pir__DEKVG glycerate dehydrogenase (EC 1.1.1.29) - cucumber >gi_18264_emb_CAA41434_ (X58542) NADH-dependent hydroxypyruvate reductase [Cucumis sativus] >gi_18275_emb_CAA32764_ (X14609) NAPH-dependent hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

Seq. No.	221000
Seq. ID	LIB3165-004-P1-K1-D7
Method	BLASTX
NCBI GI	g541951
BLAST score	313
E value	7.0e-29
Match length	63
% identity	50
NCBI Description	SPCP2 protein - soybean >gi_310578 (L12258) nodulin-26 [Glycine max]

Seq. No.	221001
Seq. ID	LIB3165-004-P1-K1-E1
Method	BLASTX
NCBI GI	g131397
BLAST score	320
E value	1.0e-29
Match length	120
% identity	58
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_81480_pir__S00008 photosystem II oxygen-evolving complex protein 3 precursor - spinach >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi_225597_prf__1307179B luminal protein 16kD [Spinacia oleracea]

Seq. No.	221002
Seq. ID	LIB3165-004-P1-K1-E10
Method	BLASTX
NCBI GI	g289920
BLAST score	616
E value	2.0e-64
Match length	116
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221003
Seq. ID	LIB3165-004-P1-K1-E11
Method	BLASTX
NCBI GI	g2493146
BLAST score	396
E value	1.0e-38
Match length	94
% identity	56
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_755148 (U13669) vacuolar H+-ATPase proteolipid (16 kDa) subunit [Gossypium hirsutum] >gi_4519415_dbj_BAA75542.1_ (AB024275) vacuolar H+-ATPase c subunit [Citrus unshiu]

Seq. No.	221004
Seq. ID	LIB3165-004-P1-K1-E2
Method	BLASTN
NCBI GI	g18058
BLAST score	211
E value	1.0e-115
Match length	274
% identity	94
NCBI Description	Citrus limon cistron for 26S ribosomal RNA

Seq. No.	221005
Seq. ID	LIB3165-004-P1-K1-E4
Method	BLASTN
NCBI GI	g2687437
BLAST score	33
E value	2.0e-09

Match length	90
% identity	82
NCBI Description	Jepsonia parryi large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	221006
Seq. ID	LIB3165-004-P1-K1-E6
Method	BLASTX
NCBI GI	g2623881
BLAST score	223
E value	3.0e-18
Match length	48
% identity	94
NCBI Description	(AF031318) catalase [Raphanus sativus]

Seq. No.	221007
Seq. ID	LIB3165-004-P1-K1-E7
Method	BLASTX
NCBI GI	g487046
BLAST score	304
E value	8.0e-28
Match length	118
% identity	55
NCBI Description	photosystem I chain II precursor - wood tobacco >gi_407769_dbj_BAA02871_ (D13718) PSI-D1 precursor [Nicotiana sylvestris]

Seq. No.	221008
Seq. ID	LIB3165-004-P1-K1-F11
Method	BLASTX
NCBI GI	g166834
BLAST score	557
E value	5.0e-60
Match length	127
% identity	89
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	221009
Seq. ID	LIB3165-004-P1-K1-F12
Method	BLASTX
NCBI GI	g68200
BLAST score	351
E value	3.0e-33
Match length	93
% identity	80
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	221010
Seq. ID	LIB3165-004-P1-K1-F4
Method	BLASTX
NCBI GI	g2864617
BLAST score	283
E value	2.0e-25

Match length	127
% identity	48
NCBI Description	(AL021811) H+-transporting ATP synthase chain9 - like protein [Arabidopsis thaliana]

Seq. No.	221011
Seq. ID	LIB3165-004-P1-K1-F6
Method	BLASTX
NCBI GI	g4106696
BLAST score	264
E value	4.0e-23
Match length	64
% identity	81
NCBI Description	(AB021872) ribosome-sedimenting protein [Pisum sativum]

Seq. No.	221012
Seq. ID	LIB3165-004-P1-K1-F7
Method	BLASTX
NCBI GI	g2894306
BLAST score	466
E value	8.0e-47
Match length	121
% identity	80
NCBI Description	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]

Seq. No.	221013
Seq. ID	LIB3165-004-P1-K1-F8
Method	BLASTX
NCBI GI	g1053047
BLAST score	506
E value	2.0e-51
Match length	102
% identity	100
NCBI Description	(U38425) histone H3 [Glycine max] >gi_1053049 (U38426) histone H3 [Glycine max] >gi_1053051 (U38427) histone H3 [Glycine max]

Seq. No.	221014
Seq. ID	LIB3165-004-P1-K1-G10
Method	BLASTX
NCBI GI	g1170897
BLAST score	343
E value	1.0e-32
Match length	82
% identity	83
NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi_1076276_pir__S52039 NAD-malate dehydrogenase - cucumber >gi_695311 (L31900) glyoxysomal malate dehydrogenase [Cucumis sativus]

Seq. No.	221015
Seq. ID	LIB3165-004-P1-K1-G4
Method	BLASTX
NCBI GI	g4376650
BLAST score	268
E value	1.0e-23
Match length	81

% identity	59
NCBI Description	(AE001621) GcpE Protein [Chlamydia pneumoniae]

Seq. No.	221016
Seq. ID	LIB3165-004-P1-K1-G5
Method	BLASTX
NCBI GI	g1129145
BLAST score	225
E value	1.0e-18
Match length	73
% identity	62
NCBI Description	(X75329) acetyl-CoA C-acyltransferase [Mangifera indica]

Seq. No.	221017
Seq. ID	LIB3165-004-P1-K1-G6
Method	BLASTX
NCBI GI	g131385
BLAST score	525
E value	1.0e-53
Match length	125
% identity	86
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN)

Seq. No.	221018
Seq. ID	LIB3165-004-P1-K1-G7
Method	BLASTX
NCBI GI	g228403
BLAST score	456
E value	1.0e-45
Match length	108
% identity	81
NCBI Description	glycolate oxidase [Lens culinaris]

Seq. No.	221019
Seq. ID	LIB3165-004-P1-K1-G8
Method	BLASTX
NCBI GI	g486827
BLAST score	236
E value	8.0e-20
Match length	104
% identity	60
NCBI Description	translation elongation factor Tu.B precursor, chloroplast - wood tobacco

Seq. No.	221020
Seq. ID	LIB3165-004-P1-K1-G9
Method	BLASTX
NCBI GI	g1632831
BLAST score	426
E value	4.0e-42
Match length	95
% identity	87
NCBI Description	(Z49698) orf [Ricinus communis]

Seq. No.	221021

Seq. ID	LIB3165-004-P1-K1-H1
Method	BLASTX
NCBI GI	g1256595
BLAST score	283
E value	2.0e-25
Match length	87
% identity	60
NCBI Description	(U38915) LytB [Synechocystis PCC6803]

Seq. No.	221022
Seq. ID	LIB3165-004-P1-K1-H2
Method	BLASTX
NCBI GI	g1172664
BLAST score	180
E value	2.0e-13
Match length	39
% identity	90
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_419791_pir__S31165 photosystem I chain III precursor - Flaveria trinervia >gi_298482_bbs_127083 photosystem I reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem I subunit III [Flaveria trinervia]

Seq. No.	221023
Seq. ID	LIB3165-004-P1-K1-H5
Method	BLASTX
NCBI GI	g3024127
BLAST score	311
E value	3.0e-50
Match length	119
% identity	92
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1655578_emb_CAA95857_ (Z71272) S-adenosyl-L-methionine synthetase 2 [Catharanthus roseus]

Seq. No.	221024
Seq. ID	LIB3165-004-P1-K1-H9
Method	BLASTX
NCBI GI	g289920
BLAST score	566
E value	2.0e-58
Match length	103
% identity	100
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221025
Seq. ID	LIB3165-005-P1-K1-A12
Method	BLASTX
NCBI GI	g1354515
BLAST score	235
E value	9.0e-20
Match length	121
% identity	47

NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	221026
Seq. ID	LIB3165-005-P1-K1-A2
Method	BLASTN
NCBI GI	g2062691
BLAST score	35
E value	3.0e-10
Match length	35
% identity	100
NCBI Description	Human sodium phosphate transporter (NPT4) mRNA, complete cds

Seq. No.	221027
Seq. ID	LIB3165-005-P1-K1-A4
Method	BLASTX
NCBI GI	g4106657
BLAST score	315
E value	4.0e-31
Match length	122
% identity	60
NCBI Description	(AL035064) activator 1 subunit (replication factor subunit) [Schizosaccharomyces pombe]

Seq. No.	221028
Seq. ID	LIB3165-005-P1-K1-A5
Method	BLASTX
NCBI GI	g2505876
BLAST score	349
E value	5.0e-33
Match length	103
% identity	66
NCBI Description	(Y12776) MYB-related protein [Arabidopsis thaliana]

Seq. No.	221029
Seq. ID	LIB3165-005-P1-K1-A6
Method	BLASTX
NCBI GI	g3193285
BLAST score	236
E value	5.0e-27
Match length	115
% identity	54
NCBI Description	(AF069298) T14P8.18 gene product [Arabidopsis thaliana]

Seq. No.	221030
Seq. ID	LIB3165-005-P1-K1-A8
Method	BLASTX
NCBI GI	g100200
BLAST score	243
E value	9.0e-21
Match length	82
% identity	61
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	221031
Seq. ID	LIB3165-005-P1-K1-A9

Method	BLASTX
NCBI GI	g2501353
BLAST score	243
E value	1.0e-20
Match length	52
% identity	90
NCBI Description	TRANSKETOLASE, CHLOROPLAST (TK) >gi_1084440_pir__S54300 transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) >gi_664901_emb_CAA86607_ (Z46646) transketolase [Craterostigma plantagineum]

Seq. No.	221032
Seq. ID	LIB3165-005-P1-K1-B10
Method	BLASTX
NCBI GI	g2764396
BLAST score	476
E value	4.0e-51
Match length	109
% identity	90
NCBI Description	(AJ000004) starch branching enzyme II, SBE-II [Solanum tuberosum]

Seq. No.	221033
Seq. ID	LIB3165-005-P1-K1-B11
Method	BLASTX
NCBI GI	g3036945
BLAST score	449
E value	6.0e-45
Match length	104
% identity	90
NCBI Description	(AB012637) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	221034
Seq. ID	LIB3165-005-P1-K1-B12
Method	BLASTX
NCBI GI	g1352821
BLAST score	488
E value	2.0e-49
Match length	94
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221035
Seq. ID	LIB3165-005-P1-K1-B3
Method	BLASTX
NCBI GI	g3023752
BLAST score	298
E value	4.0e-27
Match length	108
% identity	59
NCBI Description	FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520) ferredoxin-I [Lycopersicon esculentum]

Seq. No.	221036
Seq. ID	LIB3165-005-P1-K1-B4
Method	BLASTX
NCBI GI	g1352821
BLAST score	535
E value	7.0e-55
Match length	102
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221037
Seq. ID	LIB3165-005-P1-K1-B5
Method	BLASTX
NCBI GI	g1352821
BLAST score	563
E value	4.0e-58
Match length	108
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221038
Seq. ID	LIB3165-005-P1-K1-B6
Method	BLASTX
NCBI GI	g289920
BLAST score	563
E value	3.0e-58
Match length	104
% identity	100
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221039
Seq. ID	LIB3165-005-P1-K1-C10
Method	BLASTX
NCBI GI	g3785986
BLAST score	162
E value	4.0e-11
Match length	78
% identity	53
NCBI Description	(AC005560) RGA1 protein [Arabidopsis thaliana]

Seq. No.	221040
Seq. ID	LIB3165-005-P1-K1-C12
Method	BLASTX
NCBI GI	g125578
BLAST score	495
E value	4.0e-50
Match length	128

% identity	74
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_167266 (M73707) phosphoribulokinase [Mesembryanthemum crystallinum]

Seq. No.	221041
Seq. ID	LIB3165-005-P1-K1-C2
Method	BLASTX
NCBI GI	g3202030
BLAST score	395
E value	2.0e-38
Match length	126
% identity	67
NCBI Description	(AF069318) geranylgeranyl hydrogenase [Mesembryanthemum crystallinum]

Seq. No.	221042
Seq. ID	LIB3165-005-P1-K1-C3
Method	BLASTX
NCBI GI	g1352821
BLAST score	506
E value	2.0e-51
Match length	96
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221043
Seq. ID	LIB3165-005-P1-K1-C4
Method	BLASTX
NCBI GI	g289920
BLAST score	653
E value	1.0e-68
Match length	122
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221044
Seq. ID	LIB3165-005-P1-K1-C7
Method	BLASTX
NCBI GI	g505482
BLAST score	472
E value	2.0e-47
Match length	117
% identity	83
NCBI Description	(X64349) 33 kDa polypeptide of water-oxidizing complex of photosystem II [Nicotiana tabacum]

Seq. No.	221045
Seq. ID	LIB3165-005-P1-K1-C8
Method	BLASTX
NCBI GI	g289920
BLAST score	577

E value	7.0e-60
Match length	109
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221046
Seq. ID	LIB3165-005-P1-K1-C9
Method	BLASTX
NCBI GI	g289920
BLAST score	674
E value	4.0e-71
Match length	128
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221047
Seq. ID	LIB3165-005-P1-K1-D1
Method	BLASTN
NCBI GI	g18058
BLAST score	305
E value	1.0e-171
Match length	344
% identity	97
NCBI Description	Citrus limon cistron for 26S ribosomal RNA

Seq. No.	221048
Seq. ID	LIB3165-005-P1-K1-D10
Method	BLASTX
NCBI GI	g289920
BLAST score	593
E value	1.0e-61
Match length	112
% identity	97
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221049
Seq. ID	LIB3165-005-P1-K1-D11
Method	BLASTX
NCBI GI	g4406530
BLAST score	337
E value	1.0e-31
Match length	88
% identity	78
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221050
Seq. ID	LIB3165-005-P1-K1-D4
Method	BLASTX
NCBI GI	g100616
BLAST score	437
E value	2.0e-43
Match length	117
% identity	68
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor -

	barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]
Seq. No.	221051
Seq. ID	LIB3165-005-P1-K1-D7
Method	BLASTX
NCBI GI	g4454459
BLAST score	552
E value	7.0e-57
Match length	126
% identity	82
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]
Seq. No.	221052
Seq. ID	LIB3165-005-P1-K1-D9
Method	BLASTX
NCBI GI	g4210948
BLAST score	597
E value	4.0e-62
Match length	115
% identity	97
NCBI Description	(AF085275) DnaJ protein [Hevea brasiliensis]
Seq. No.	221053
Seq. ID	LIB3165-005-P1-K1-E1
Method	BLASTN
NCBI GI	g2687435
BLAST score	74
E value	6.0e-34
Match length	82
% identity	98
NCBI Description	Hamamelis virginiana large subunit 26S ribosomal RNA gene, partial sequence
Seq. No.	221054
Seq. ID	LIB3165-005-P1-K1-E10
Method	BLASTX
NCBI GI	g1352821
BLAST score	365
E value	5.0e-35
Match length	75
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	221055
Seq. ID	LIB3165-005-P1-K1-E11
Method	BLASTX
NCBI GI	g4406530
BLAST score	330
E value	8.0e-31
Match length	90

% identity	76
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221056
Seq. ID	LIB3165-005-P1-K1-E6
Method	BLASTX
NCBI GI	g4539351
BLAST score	166
E value	1.0e-11
Match length	59
% identity	63
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	221057
Seq. ID	LIB3165-005-P1-K1-E8
Method	BLASTX
NCBI GI	g100200
BLAST score	419
E value	3.0e-41
Match length	112
% identity	73
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	221058
Seq. ID	LIB3165-005-P1-K1-E9
Method	BLASTX
NCBI GI	g267120
BLAST score	189
E value	2.0e-14
Match length	83
% identity	54
NCBI Description	THIOREDOXIN F-TYPE PRECURSOR (TRX-F) >gi_100070_pir__S20929 thioredoxin f precursor - garden pea >gi_20907_emb_CAA45098_ (X63537) thioredoxin F [Pisum sativum] >gi_1388086 (U35830) thioredoxin f [Pisum sativum]

Seq. No.	221059
Seq. ID	LIB3165-005-P1-K1-F1
Method	BLASTX
NCBI GI	g289920
BLAST score	520
E value	2.0e-53
Match length	95
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221060
Seq. ID	LIB3165-005-P1-K1-F10
Method	BLASTX
NCBI GI	g3869088
BLAST score	639
E value	5.0e-67
Match length	126
% identity	98
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No.	221061
Seq. ID	LIB3165-005-P1-K1-F12
Method	BLASTX
NCBI GI	g1352821
BLAST score	516
E value	1.0e-52
Match length	100
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221062
Seq. ID	LIB3165-005-P1-K1-F2
Method	BLASTX
NCBI GI	g289920
BLAST score	447
E value	1.0e-44
Match length	121
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221063
Seq. ID	LIB3165-005-P1-K1-F3
Method	BLASTX
NCBI GI	g417103
BLAST score	355
E value	2.0e-56
Match length	119
% identity	99
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	221064
Seq. ID	LIB3165-005-P1-K1-F4
Method	BLASTX
NCBI GI	g2760834

BLAST score	502
E value	5.0e-51
Match length	127
% identity	76
NCBI Description	(AC003105) putative nitrate transporter [Arabidopsis thaliana]

Seq. No.	221065
Seq. ID	LIB3165-005-P1-K1-F5
Method	BLASTX
NCBI GI	g2827715
BLAST score	335
E value	2.0e-31
Match length	79
% identity	84
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	221066
Seq. ID	LIB3165-005-P1-K1-F6
Method	BLASTX
NCBI GI	g1168411
BLAST score	358
E value	4.0e-34
Match length	94
% identity	80
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	221067
Seq. ID	LIB3165-005-P1-K1-F8
Method	BLASTX
NCBI GI	g2677828
BLAST score	370
E value	2.0e-35
Match length	101
% identity	67
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	221068
Seq. ID	LIB3165-005-P1-K1-G10
Method	BLASTX
NCBI GI	g1352821
BLAST score	538
E value	3.0e-55
Match length	106
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221069
Seq. ID	LIB3165-005-P1-K1-G2
Method	BLASTX
NCBI GI	g1353352
BLAST score	322

E value	7.0e-30
Match length	87
% identity	75
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	221070
Seq. ID	LIB3165-005-P1-K1-G4
Method	BLASTX
NCBI GI	g3075488
BLAST score	325
E value	3.0e-30
Match length	110
% identity	58
NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.	221071
Seq. ID	LIB3165-005-P1-K1-G6
Method	BLASTX
NCBI GI	g167367
BLAST score	607
E value	3.0e-63
Match length	131
% identity	91
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	221072
Seq. ID	LIB3165-005-P1-K1-G7
Method	BLASTX
NCBI GI	g1168411
BLAST score	345
E value	8.0e-33
Match length	89
% identity	81
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	221073
Seq. ID	LIB3165-005-P1-K1-G9
Method	BLASTX
NCBI GI	g1352821
BLAST score	324
E value	2.0e-30
Match length	63
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221074
Seq. ID	LIB3165-005-P1-K1-H1
Method	BLASTX
NCBI GI	g2829916
BLAST score	267
E value	2.0e-23
Match length	55

% identity	85
NCBI Description	(AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No.	221075
Seq. ID	LIB3165-005-P1-K1-H10
Method	BLASTX
NCBI GI	g2811025
BLAST score	318
E value	2.0e-29
Match length	98
% identity	67
NCBI Description	ASPARTIC PROTEINASE PRECURSOR >gi_1944181_dbj_BAA19607_ (AB002695) aspartic endopeptidase [Cucurbita pepo]

Seq. No.	221076
Seq. ID	LIB3165-005-P1-K1-H2
Method	BLASTX
NCBI GI	g4406530
BLAST score	306
E value	5.0e-28
Match length	85
% identity	74
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221077
Seq. ID	LIB3165-005-P1-K1-H4
Method	BLASTX
NCBI GI	g3738295
BLAST score	282
E value	3.0e-25
Match length	119
% identity	54
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	221078
Seq. ID	LIB3165-005-P1-K1-H5
Method	BLASTX
NCBI GI	g4210948
BLAST score	416
E value	6.0e-41
Match length	83
% identity	96
NCBI Description	(AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No.	221079
Seq. ID	LIB3165-005-P1-K1-H6
Method	BLASTX
NCBI GI	g551047
BLAST score	364
E value	4.0e-35
Match length	93
% identity	76
NCBI Description	(X79277) type II LHCI [Lolium temulentum]

Seq. No.	221080
Seq. ID	LIB3165-005-P1-K1-H7
Method	BLASTX

NCBI GI	g3158476
BLAST score	547
E value	3.0e-56
Match length	120
% identity	87
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	221081
Seq. ID	LIB3165-006-P1-K1-A10
Method	BLASTX
NCBI GI	g1084372
BLAST score	637
E value	7.0e-67
Match length	126
% identity	96
NCBI Description	glyceraldehyde-3-phosphate dehydrogenase (NADP+) (EC 1.2.1.9) - garden pea

Seq. No.	221082
Seq. ID	LIB3165-006-P1-K1-A11
Method	BLASTX
NCBI GI	g2239089
BLAST score	223
E value	3.0e-18
Match length	108
% identity	40
NCBI Description	(Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] >gi_3288180_emb_CAB11466_ (Z98758) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]

Seq. No.	221083
Seq. ID	LIB3165-006-P1-K1-A12
Method	BLASTX
NCBI GI	g3882081
BLAST score	579
E value	5.0e-60
Match length	120
% identity	37
NCBI Description	(AJ012552) polyubiquitin [Vicia faba]

Seq. No.	221084
Seq. ID	LIB3165-006-P1-K1-A2
Method	BLASTX
NCBI GI	g1353352
BLAST score	196
E value	3.0e-15
Match length	53
% identity	74
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	221085
Seq. ID	LIB3165-006-P1-K1-A6
Method	BLASTX
NCBI GI	g136707
BLAST score	415

E value	8.0e-41
Match length	116
% identity	70
NCBI Description	CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_280397_pir__S26199 plastoquinol--plastocyanin reductase (EC 1.10.99.1) iron-sulfur protein precursor - garden pea >gi_20832_emb_CAA45151_ (X63605) chloroplast Rieske FeS protein [Pisum sativum]

Seq. No.	221086
Seq. ID	LIB3165-006-P1-K1-B11
Method	BLASTX
NCBI GI	g115765
BLAST score	394
E value	2.0e-38
Match length	92
% identity	77
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	221087
Seq. ID	LIB3165-006-P1-K1-B12
Method	BLASTX
NCBI GI	g4406530
BLAST score	280
E value	5.0e-25
Match length	101
% identity	61
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221088
Seq. ID	LIB3165-006-P1-K1-B2
Method	BLASTX
NCBI GI	g1657617
BLAST score	334
E value	3.0e-31
Match length	82
% identity	77
NCBI Description	(U72503) G2p [Arabidopsis thaliana] >gi_3068707 (AF049236) putative nuclear DNA-binding protein G2p [Arabidopsis thaliana]

Seq. No.	221089
Seq. ID	LIB3165-006-P1-K1-B3
Method	BLASTX
NCBI GI	g3822036
BLAST score	215
E value	2.0e-17
Match length	110
% identity	46

NCBI Description	(AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]

Seq. No.	221090
Seq. ID	LIB3165-006-P1-K1-B4
Method	BLASTX
NCBI GI	g1928981
BLAST score	485
E value	5.0e-49
Match length	107
% identity	89
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	221091
Seq. ID	LIB3165-006-P1-K1-B6
Method	BLASTX
NCBI GI	g2529342
BLAST score	237
E value	1.0e-22
Match length	100
% identity	58
NCBI Description	(L76554) transketolase [Spinacia oleracea]

Seq. No.	221092
Seq. ID	LIB3165-006-P1-K1-C1
Method	BLASTX
NCBI GI	g4406814
BLAST score	303
E value	1.0e-27
Match length	75
% identity	77
NCBI Description	(AC006201) putative peptidyl-prolyl isomerase [Arabidopsis thaliana]

Seq. No.	221093
Seq. ID	LIB3165-006-P1-K1-C10
Method	BLASTX
NCBI GI	g121080
BLAST score	496
E value	3.0e-50
Match length	115
% identity	83
NCBI Description	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_1070638_pir__GCPMH glycine cleavage system protein H precursor - garden pea >gi_20737_emb_CAA45978_ (X64726) H protein [Pisum sativum] >gi_169093 (J05164) H-protein of glycine decarboxylase precursor (EC 2.1.2.10) [Pisum sativum] >gi_287815_emb_CAA37704_ (X53656) H-protein [Pisum sativum]

Seq. No.	221094
Seq. ID	LIB3165-006-P1-K1-C11
Method	BLASTN
NCBI GI	g602358
BLAST score	35
E value	3.0e-10
Match length	75

% identity	87
NCBI Description	P.sativum mRNA for type II chlorophyll a/b binding protein

Seq. No.	221095
Seq. ID	LIB3165-006-P1-K1-C2
Method	BLASTX
NCBI GI	g2911085
BLAST score	328
E value	1.0e-30
Match length	118
% identity	62
NCBI Description	(AL021960) photosystem II oxygen-evolving complex protein 3 - like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_ (AL031187) photosystem II oxygen-evolving complex protein 3 - like [Arabidopsis thaliana]

Seq. No.	221096
Seq. ID	LIB3165-006-P1-K1-C6
Method	BLASTX
NCBI GI	g115765
BLAST score	248
E value	3.0e-21
Match length	74
% identity	66
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	221097
Seq. ID	LIB3165-006-P1-K1-C9
Method	BLASTX
NCBI GI	g2369714
BLAST score	565
E value	2.0e-58
Match length	118
% identity	88
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	221098
Seq. ID	LIB3165-006-P1-K1-D2
Method	BLASTX
NCBI GI	g115765
BLAST score	528
E value	5.0e-54
Match length	123
% identity	49
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A

chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	221099
Seq. ID	LIB3165-006-P1-K1-D3
Method	BLASTX
NCBI GI	g1172664
BLAST score	190
E value	2.0e-14
Match length	41
% identity	90
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_419791_pir__S31165 photosystem I chain III precursor - Flaveria trinervia >gi_298482_bbs_127083 photosystem I reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem I subunit III [Flaveria trinervia]

Seq. No.	221100
Seq. ID	LIB3165-006-P1-K1-D4
Method	BLASTN
NCBI GI	g4545261
BLAST score	331
E value	0.0e+00
Match length	375
% identity	97
NCBI Description	Gossypium hirsutum metallothionein-like protein mRNA, complete cds

Seq. No.	221101
Seq. ID	LIB3165-006-P1-K1-D6
Method	BLASTX
NCBI GI	g3894183
BLAST score	168
E value	7.0e-12
Match length	107
% identity	39
NCBI Description	(AC005662) calmodulin-like protein [Arabidopsis thaliana]

Seq. No.	221102
Seq. ID	LIB3165-006-P1-K1-D7
Method	BLASTX
NCBI GI	g1709651
BLAST score	364
E value	6.0e-35
Match length	97
% identity	71
NCBI Description	PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209 plastocyanin a precursor - black poplar >gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus nigra]

Seq. No.	221103
Seq. ID	LIB3165-006-P1-K1-E10
Method	BLASTX
NCBI GI	g1362086

BLAST score	632
E value	3.0e-66
Match length	122
% identity	97
NCBI Description	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir__S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]

Seq. No.	221104
Seq. ID	LIB3165-006-P1-K1-E11
Method	BLASTX
NCBI GI	g549063
BLAST score	321
E value	8.0e-30
Match length	102
% identity	63
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]

Seq. No.	221105
Seq. ID	LIB3165-006-P1-K1-E2
Method	BLASTX
NCBI GI	g2511691
BLAST score	385
E value	2.0e-37
Match length	119
% identity	64
NCBI Description	(Z99953) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No.	221106
Seq. ID	LIB3165-006-P1-K1-E3
Method	BLASTX
NCBI GI	g167097
BLAST score	610
E value	1.0e-63
Match length	126
% identity	92
NCBI Description	(M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	221107
Seq. ID	LIB3165-006-P1-K1-E4
Method	BLASTX
NCBI GI	g1168411
BLAST score	292
E value	2.0e-26
Match length	92
% identity	72
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	221108

Seq. ID	LIB3165-006-P1-K1-E8
Method	BLASTX
NCBI GI	g3914136
BLAST score	240
E value	3.0e-20
Match length	107
% identity	45
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) >gi_2632171_emb_CAA05771_ (AJ002958) lipid transfer protein [Cicer arietinum]

Seq. No.	221109
Seq. ID	LIB3165-006-P1-K1-E9
Method	BLASTX
NCBI GI	g1619602
BLAST score	314
E value	5.0e-29
Match length	90
% identity	61
NCBI Description	(Y08726) MtN3 [Medicago truncatula]

Seq. No.	221110
Seq. ID	LIB3165-006-P1-K1-F1
Method	BLASTX
NCBI GI	g3928543
BLAST score	387
E value	2.0e-37
Match length	103
% identity	66
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	221111
Seq. ID	LIB3165-006-P1-K1-F12
Method	BLASTX
NCBI GI	g1352821
BLAST score	468
E value	5.0e-47
Match length	91
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221112
Seq. ID	LIB3165-006-P1-K1-F2
Method	BLASTX
NCBI GI	g3928089
BLAST score	358
E value	4.0e-34
Match length	116
% identity	65
NCBI Description	(AC005770) putative osr40 [Arabidopsis thaliana]

Seq. No.	221113

Seq. ID	LIB3165-006-P1-K1-F4
Method	BLASTX
NCBI GI	g1352821
BLAST score	510
E value	6.0e-52
Match length	98
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221114
Seq. ID	LIB3165-006-P1-K1-F5
Method	BLASTX
NCBI GI	g1771778
BLAST score	551
E value	9.0e-57
Match length	127
% identity	79
NCBI Description	(X99320) 23 kDa oxygen evolving protein of photosystem II [Solanum tuberosum]

Seq. No.	221115
Seq. ID	LIB3165-006-P1-K1-F9
Method	BLASTX
NCBI GI	g4406530
BLAST score	311
E value	1.0e-28
Match length	85
% identity	75
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221116
Seq. ID	LIB3165-006-P1-K1-G1
Method	BLASTX
NCBI GI	g231610
BLAST score	167
E value	1.0e-11
Match length	67
% identity	54
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]

Seq. No.	221117
Seq. ID	LIB3165-006-P1-K1-G11
Method	BLASTX
NCBI GI	g2935298
BLAST score	328
E value	1.0e-30
Match length	98
% identity	66
NCBI Description	(AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase

1 [Gossypium hirsutum]

Seq. No.	221118
Seq. ID	LIB3165-006-P1-K1-G12
Method	BLASTX
NCBI GI	g231610
BLAST score	274
E value	3.0e-24
Match length	101
% identity	60
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]

Seq. No.	221119
Seq. ID	LIB3165-006-P1-K1-G4
Method	BLASTX
NCBI GI	g100203
BLAST score	361
E value	2.0e-34
Match length	91
% identity	77
NCBI Description	cysteine proteinase (EC 3.4.22.-) precursor - tomato >gi_19195_emb_CAA78403_ (Z14028) pre-pro-cysteine proteinase [Lycopersicon esculentum]

Seq. No.	221120
Seq. ID	LIB3165-006-P1-K1-G5
Method	BLASTX
NCBI GI	g445116
BLAST score	571
E value	4.0e-59
Match length	122
% identity	89
NCBI Description	light-harvesting complex IIa protein; [Hordeum vulgare]

Seq. No.	221121
Seq. ID	LIB3165-006-P1-K1-G6
Method	BLASTX
NCBI GI	g430947
BLAST score	589
E value	3.0e-61
Match length	123
% identity	88
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	221122
Seq. ID	LIB3165-006-P1-K1-G7
Method	BLASTX
NCBI GI	g3033513
BLAST score	380
E value	1.0e-36
Match length	109
% identity	70

NCBI Description (AF041068) rubisco activase [Phaseolus vulgaris]

Seq. No. 221123
Seq. ID LIB3165-006-P1-K1-G8
Method BLASTX
NCBI GI g585322
BLAST score 151
E value 7.0e-10
Match length 58
% identity 45
NCBI Description INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi_539751_pir__A45153 inorganic pyrophosphatase (EC 3.6.1.1) - bovine

Seq. No. 221124
Seq. ID LIB3165-006-P1-K1-H1
Method BLASTX
NCBI GI g4512667
BLAST score 550
E value 1.0e-56
Match length 127
% identity 79
NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No. 221125
Seq. ID LIB3165-006-P1-K1-H11
Method BLASTX
NCBI GI g4406530
BLAST score 317
E value 3.0e-29
Match length 109
% identity 62
NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 221126
Seq. ID LIB3165-006-P1-K1-H3
Method BLASTX
NCBI GI g3582333
BLAST score 466
E value 9.0e-47
Match length 119
% identity 76
NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No. 221127
Seq. ID LIB3165-006-P1-K1-H5
Method BLASTX
NCBI GI g1352821
BLAST score 468
E value 6.0e-47
Match length 91
% identity 99
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221128
Seq. ID	LIB3165-006-P1-K1-H6
Method	BLASTX
NCBI GI	g131385
BLAST score	512
E value	3.0e-52
Match length	128
% identity	81
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN)

Seq. No.	221129
Seq. ID	LIB3165-006-P1-K1-H8
Method	BLASTX
NCBI GI	g2244811
BLAST score	226
E value	1.0e-18
Match length	107
% identity	56
NCBI Description	(Z97336) unnamed protein product [Arabidopsis thaliana]

Seq. No.	221130
Seq. ID	LIB3165-006-P1-K1-H9
Method	BLASTX
NCBI GI	g100200
BLAST score	345
E value	1.0e-32
Match length	98
% identity	68
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	221131
Seq. ID	LIB3165-006-P1-K2-A10
Method	BLASTX
NCBI GI	g1084372
BLAST score	741
E value	7.0e-79
Match length	145
% identity	97
NCBI Description	glyceraldehyde-3-phosphate dehydrogenase (NADP+) (EC 1.2.1.9) - garden pea

Seq. No.	221132
Seq. ID	LIB3165-006-P1-K2-A11
Method	BLASTX
NCBI GI	g2239089
BLAST score	293
E value	3.0e-26
Match length	137
% identity	41
NCBI Description	(Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] >gi_3288180_emb_CAB11466_ (Z98758) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]

Seq. No.	221133
Seq. ID	LIB3165-006-P1-K2-A12
Method	BLASTX
NCBI GI	g1076708
BLAST score	669
E value	2.0e-70
Match length	138
% identity	27
NCBI Description	seed tetraubiquitin - common sunflower >gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max] >gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max] >gi_556688_emb_CAA84440_ (Z34988) seed tetraubiquitin [Helianthus annuus] >gi_994785_dbj_BAA05085_ (D26092) Ubiquitin [Glycine max] >gi_4263514_gb_AAD15340_ (AC004044) putative polyubiquitin [Arabidopsis thaliana] >gi_1096513_prf__2111434A tetraubiquitin [Helianthus annuus]

Seq. No.	221134
Seq. ID	LIB3165-006-P1-K2-A3
Method	BLASTN
NCBI GI	g1498381
BLAST score	37
E value	7.0e-12
Match length	68
% identity	90
NCBI Description	Zea mays actin (Maz95) gene, partial cds

Seq. No.	221135
Seq. ID	LIB3165-006-P1-K2-A6
Method	BLASTX
NCBI GI	g136707
BLAST score	651
E value	3.0e-68
Match length	162
% identity	75
NCBI Description	CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_280397_pir__S26199 plastoquinol--plastocyanin reductase (EC 1.10.99.1) iron-sulfur protein precursor - garden pea >gi_20832_emb_CAA45151_ (X63605) chloroplast Rieske FeS protein [Pisum sativum]

Seq. No.	221136
Seq. ID	LIB3165-006-P1-K2-A9
Method	BLASTX
NCBI GI	g121344
BLAST score	259
E value	2.0e-22
Match length	87
% identity	57
NCBI Description	GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR (GLUTAMATE-AMMONIA LIGASE) (CHLOROPLAST GS2) >gi_68597_pir__AJPMQ2 glutamate--ammonia ligase (EC 6.3.1.2) delta precursor, chloroplast - garden pea >gi_169059 (M20664) glutamine synthetase (chloroplast GS2) (EC 6.3.1.2) [Pisum sativum]

Seq. No.	221137
Seq. ID	LIB3165-006-P1-K2-B1
Method	BLASTX
NCBI GI	g1351208
BLAST score	175
E value	6.0e-13
Match length	61
% identity	67
NCBI Description	T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA) >gi_1046266 (U25632) CCT-2 [Caenorhabditis elegans]

Seq. No.	221138
Seq. ID	LIB3165-006-P1-K2-B11
Method	BLASTX
NCBI GI	g115765
BLAST score	809
E value	1.0e-86
Match length	174
% identity	83
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	221139
Seq. ID	LIB3165-006-P1-K2-B12
Method	BLASTX
NCBI GI	g3914605
BLAST score	354
E value	4.0e-43
Match length	156
% identity	64
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase - apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica]

Seq. No.	221140
Seq. ID	LIB3165-006-P1-K2-B4
Method	BLASTX
NCBI GI	g1928981
BLAST score	858
E value	2.0e-92
Match length	189
% identity	91
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	221141
Seq. ID	LIB3165-006-P1-K2-B7

Method	BLASTX
NCBI GI	g1657617
BLAST score	600
E value	3.0e-62
Match length	138
% identity	82
NCBI Description	(U72503) G2p [Arabidopsis thaliana] >gi_3068707 (AF049236) putative nuclear DNA-binding protein G2p [Arabidopsis thaliana]

Seq. No.	221142
Seq. ID	LIB3165-006-P1-K2-B8
Method	BLASTX
NCBI GI	g3822036
BLAST score	286
E value	2.0e-25
Match length	157
% identity	42
NCBI Description	(AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]

Seq. No.	221143
Seq. ID	LIB3165-006-P1-K2-B9
Method	BLASTX
NCBI GI	g4406814
BLAST score	303
E value	8.0e-43
Match length	115
% identity	79
NCBI Description	(AC006201) putative peptidyl-prolyl isomerase [Arabidopsis thaliana]

Seq. No.	221144
Seq. ID	LIB3165-006-P1-K2-C10
Method	BLASTX
NCBI GI	g542100
BLAST score	723
E value	1.0e-76
Match length	165
% identity	84
NCBI Description	H-protein - Flaveria pringlei >gi_2147453_pir__S60195 H-protein precursor (clone HFC1) - Flaveria cronquistii >gi_437993_emb_CAA81073_ (Z25854) H-protein [Flaveria cronquistii] >gi_437999_emb_CAA81074_ (Z25855) H-protein [Flaveria pringlei] >gi_3688299_emb_CAB16912_ (Z99763) H-protein [Flaveria pringlei]

Seq. No.	221145
Seq. ID	LIB3165-006-P1-K2-C11
Method	BLASTX
NCBI GI	g115765
BLAST score	681
E value	9.0e-72
Match length	153
% identity	53
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_

	(X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]
Seq. No.	221146
Seq. ID	LIB3165-006-P1-K2-C7
Method	BLASTX
NCBI GI	g131397
BLAST score	441
E value	1.0e-43
Match length	172
% identity	57
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_81480_pir__S00008 photosystem II oxygen-evolving complex protein 3 precursor - spinach >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi_225597_prf__1307179B luminal protein 16kD [Spinacia oleracea]
Seq. No.	221147
Seq. ID	LIB3165-006-P1-K2-C8
Method	BLASTX
NCBI GI	g1352821
BLAST score	304
E value	5.0e-28
Match length	61
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	221148
Seq. ID	LIB3165-006-P1-K2-D2
Method	BLASTX
NCBI GI	g115765
BLAST score	712
E value	2.0e-75
Match length	162
% identity	55
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]
Seq. No.	221149
Seq. ID	LIB3165-006-P1-K2-D4
Method	BLASTN

NCBI GI	g4545261
BLAST score	150
E value	8.0e-79
Match length	200
% identity	95
NCBI Description	Gossypium hirsutum metallothionein-like protein mRNA, complete cds

Seq. No.	221150
Seq. ID	LIB3165-006-P1-K2-D6
Method	BLASTX
NCBI GI	g3894183
BLAST score	309
E value	4.0e-28
Match length	170
% identity	30
NCBI Description	(AC005662) calmodulin-like protein [Arabidopsis thaliana]

Seq. No.	221151
Seq. ID	LIB3165-006-P1-K2-D7
Method	BLASTX
NCBI GI	g1709651
BLAST score	515
E value	3.0e-52
Match length	132
% identity	73
NCBI Description	PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209 plastocyanin a precursor - black poplar >gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus nigra]

Seq. No.	221152
Seq. ID	LIB3165-006-P1-K2-E10
Method	BLASTX
NCBI GI	g974782
BLAST score	960
E value	1.0e-104
Match length	188
% identity	96
NCBI Description	(Z49150) cobalamine-independent methionine synthase [Solenostemon scutellarioides]

Seq. No.	221153
Seq. ID	LIB3165-006-P1-K2-E11
Method	BLASTX
NCBI GI	g4193388
BLAST score	529
E value	5.0e-54
Match length	147
% identity	73
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	221154
Seq. ID	LIB3165-006-P1-K2-E2
Method	BLASTX
NCBI GI	g2511691

BLAST score	737
E value	3.0e-78
Match length	193
% identity	73
NCBI Description	(Z99953) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No.	221155
Seq. ID	LIB3165-006-P1-K2-E3
Method	BLASTX
NCBI GI	g266893
BLAST score	523
E value	1.0e-53
Match length	103
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__S28172 ribulose-bisphosphate carboxylase activase - cucumber >gi_18284_emb_CAA47906_ (X67674) rubisco activase [Cucumis sativus]

Seq. No.	221156
Seq. ID	LIB3165-006-P1-K2-E4
Method	BLASTX
NCBI GI	g1168411
BLAST score	635
E value	2.0e-66
Match length	157
% identity	82
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	221157
Seq. ID	LIB3165-006-P1-K2-E9
Method	BLASTX
NCBI GI	g3747111
BLAST score	197
E value	2.0e-15
Match length	67
% identity	54
NCBI Description	(AF095641) MTN3 homolog [Arabidopsis thaliana]

Seq. No.	221158
Seq. ID	LIB3165-006-P1-K2-F1
Method	BLASTX
NCBI GI	g3928543
BLAST score	534
E value	2.0e-54
Match length	166
% identity	57
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	221159
Seq. ID	LIB3165-006-P1-K2-F10
Method	BLASTX
NCBI GI	g3894183
BLAST score	314
E value	1.0e-28

Match length	191
% identity	29
NCBI Description	(AC005662) calmodulin-like protein [Arabidopsis thaliana]

Seq. No.	221160
Seq. ID	LIB3165-006-P1-K2-F12
Method	BLASTX
NCBI GI	g1352821
BLAST score	858
E value	2.0e-92
Match length	163
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221161
Seq. ID	LIB3165-006-P1-K2-F2
Method	BLASTX
NCBI GI	g3928089
BLAST score	358
E value	5.0e-34
Match length	116
% identity	65
NCBI Description	(AC005770) putative osr40 [Arabidopsis thaliana]

Seq. No.	221162
Seq. ID	LIB3165-006-P1-K2-F4
Method	BLASTX
NCBI GI	g1352821
BLAST score	848
E value	3.0e-91
Match length	162
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221163
Seq. ID	LIB3165-006-P1-K2-F5
Method	BLASTX
NCBI GI	g1771778
BLAST score	824
E value	2.0e-88
Match length	183
% identity	83
NCBI Description	(X99320) 23 kDa oxygen evolving protein of photosystem II [Solanum tuberosum]

Seq. No.	221164
Seq. ID	LIB3165-006-P1-K2-F9
Method	BLASTX
NCBI GI	g4406530

BLAST score	484
E value	1.0e-48
Match length	132
% identity	75
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221165
Seq. ID	LIB3165-006-P1-K2-G11
Method	BLASTX
NCBI GI	g2935298
BLAST score	415
E value	1.0e-40
Match length	132
% identity	64
NCBI Description	(AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 [Gossypium hirsutum]

Seq. No.	221166
Seq. ID	LIB3165-006-P1-K2-G12
Method	BLASTX
NCBI GI	g231610
BLAST score	489
E value	3.0e-49
Match length	152
% identity	68
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]

Seq. No.	221167
Seq. ID	LIB3165-006-P1-K2-G3
Method	BLASTX
NCBI GI	g2511693
BLAST score	481
E value	3.0e-48
Match length	156
% identity	63
NCBI Description	(Z99954) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No.	221168
Seq. ID	LIB3165-006-P1-K2-G4
Method	BLASTX
NCBI GI	g2511691
BLAST score	521
E value	4.0e-63
Match length	154
% identity	78
NCBI Description	(Z99953) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No.	221169
Seq. ID	LIB3165-006-P1-K2-G5
Method	BLASTX
NCBI GI	g445116
BLAST score	947
E value	1.0e-103

Match length 195
% identity 92
NCBI Description light-harvesting complex IIa protein; [Hordeum vulgare]

Seq. No. 221170
Seq. ID LIB3165-006-P1-K2-G7
Method BLASTX
NCBI GI g4406530
BLAST score 661
E value 2.0e-69
Match length 162
% identity 82
NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 221171
Seq. ID LIB3165-006-P1-K2-G8
Method BLASTX
NCBI GI g585322
BLAST score 283
E value 4.0e-25
Match length 111
% identity 51
NCBI Description INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi_539751_pir__A45153 inorganic pyrophosphatase (EC 3.6.1.1) - bovine

Seq. No. 221172
Seq. ID LIB3165-006-P1-K2-H1
Method BLASTX
NCBI GI g4512667
BLAST score 750
E value 7.0e-80
Match length 176
% identity 78
NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No. 221173
Seq. ID LIB3165-006-P1-K2-H10
Method BLASTX
NCBI GI g286001
BLAST score 194
E value 1.0e-14
Match length 149
% identity 32
NCBI Description (D13630) KIAA0005 [Homo sapiens]

Seq. No. 221174
Seq. ID LIB3165-006-P1-K2-H11
Method BLASTX
NCBI GI g3914605
BLAST score 507
E value 3.0e-51
Match length 155
% identity 65
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase -

apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica]

Seq. No.	221175
Seq. ID	LIB3165-006-P1-K2-H2
Method	BLASTX
NCBI GI	g3482918
BLAST score	146
E value	3.0e-18
Match length	108
% identity	59
NCBI Description	(AC003970) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	221176
Seq. ID	LIB3165-006-P1-K2-H3
Method	BLASTX
NCBI GI	g3582333
BLAST score	820
E value	5.0e-88
Match length	175
% identity	86
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	221177
Seq. ID	LIB3165-006-P1-K2-H5
Method	BLASTX
NCBI GI	g1352821
BLAST score	837
E value	5.0e-90
Match length	159
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221178
Seq. ID	LIB3165-006-P1-K2-H6
Method	BLASTX
NCBI GI	g100454
BLAST score	603
E value	9.0e-63
Match length	144
% identity	84
NCBI Description	photosystem II oxygen-evolving complex protein 1 - potato >gi_809113_emb_CAA35601_ (X17578) 33kDa precursor protein of oxygen-evolving complex [Solanum tuberosum]

Seq. No.	221179
Seq. ID	LIB3165-006-P1-K2-H7
Method	BLASTX
NCBI GI	g4103635
BLAST score	321
E value	2.0e-29

Match length	142
% identity	50
NCBI Description	(AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. No.	221180
Seq. ID	LIB3165-006-P1-K2-H8
Method	BLASTX
NCBI GI	g2244811
BLAST score	238
E value	6.0e-20
Match length	129
% identity	51
NCBI Description	(Z97336) unnamed protein product [Arabidopsis thaliana]

Seq. No.	221181
Seq. ID	LIB3165-006-P1-K2-H9
Method	BLASTX
NCBI GI	g100200
BLAST score	634
E value	3.0e-66
Match length	152
% identity	64
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	221182
Seq. ID	LIB3165-006-P1-K3-A10
Method	BLASTX
NCBI GI	g3914605
BLAST score	745
E value	4.0e-79
Match length	204
% identity	72
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase - apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica]

Seq. No.	221183
Seq. ID	LIB3165-006-P1-K3-A11
Method	BLASTX
NCBI GI	g121344
BLAST score	248
E value	3.0e-21
Match length	87
% identity	59
NCBI Description	GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR (GLUTAMATE-AMMONIA LIGASE) (CHLOROPLAST GS2) >gi_68597_pir__AJPMQ2 glutamate--ammonia ligase (EC 6.3.1.2) delta precursor, chloroplast - garden pea >gi_169059 (M20664) glutamine synthetase (chloroplast GS2) (EC 6.3.1.2) [Pisum sativum]

Seq. No.	221184
Seq. ID	LIB3165-006-P1-K3-A12
Method	BLASTX

NCBI GI	g1084372
BLAST score	952
E value	1.0e-103
Match length	208
% identity	88
NCBI Description	glyceraldehyde-3-phosphate dehydrogenase (NADP+) (EC 1.2.1.9) - garden pea

Seq. No.	221185
Seq. ID	LIB3165-006-P1-K3-A2
Method	BLASTX
NCBI GI	g1353352
BLAST score	424
E value	1.0e-41
Match length	121
% identity	71
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	221186
Seq. ID	LIB3165-006-P1-K3-A3
Method	BLASTX
NCBI GI	g1531672
BLAST score	642
E value	3.0e-67
Match length	130
% identity	94
NCBI Description	(U68461) actin [Striga asiatica]

Seq. No.	221187
Seq. ID	LIB3165-006-P1-K3-A6
Method	BLASTX
NCBI GI	g136707
BLAST score	702
E value	3.0e-74
Match length	177
% identity	75
NCBI Description	CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_280397_pir__S26199 plastoquinol--plastocyanin reductase (EC 1.10.99.1) iron-sulfur protein precursor - garden pea >gi_20832_emb_CAA45151_ (X63605) chloroplast Rieske FeS protein [Pisum sativum]

Seq. No.	221188
Seq. ID	LIB3165-006-P1-K3-A8
Method	BLASTX
NCBI GI	g4206122
BLAST score	321
E value	1.0e-29
Match length	174
% identity	45
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No.	221189
Seq. ID	LIB3165-006-P1-K3-B1

Method	BLASTX
NCBI GI	g3024702
BLAST score	600
E value	3.0e-62
Match length	192
% identity	64
NCBI Description	T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) >gi_1871210 (U91327) T-complex protein 1, Beta subunit (TCP-1-BETA) [Homo sapiens]

Seq. No.	221190
Seq. ID	LIB3165-006-P1-K3-B10
Method	BLASTX
NCBI GI	g3603456
BLAST score	711
E value	3.0e-75
Match length	144
% identity	30
NCBI Description	(AF088848) polyubiquitin [Capsicum chinense]

Seq. No.	221191
Seq. ID	LIB3165-006-P1-K3-B11
Method	BLASTX
NCBI GI	g4406814
BLAST score	303
E value	1.0e-42
Match length	115
% identity	79
NCBI Description	(AC006201) putative peptidyl-prolyl isomerase [Arabidopsis thaliana]

Seq. No.	221192
Seq. ID	LIB3165-006-P1-K3-B4
Method	BLASTX
NCBI GI	g1928981
BLAST score	834
E value	1.0e-89
Match length	178
% identity	69
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	221193
Seq. ID	LIB3165-006-P1-K3-B6
Method	BLASTX
NCBI GI	g2583125
BLAST score	682
E value	7.0e-72
Match length	173
% identity	76
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	221194
Seq. ID	LIB3165-006-P1-K3-B7
Method	BLASTX
NCBI GI	g1657617

BLAST score	600
E value	3.0e-62
Match length	138
% identity	82
NCBI Description	(U72503) G2p [Arabidopsis thaliana] >gi_3068707 (AF049236) putative nuclear DNA-binding protein G2p [Arabidopsis thaliana]

Seq. No.	221195
Seq. ID	LIB3165-006-P1-K3-B8
Method	BLASTX
NCBI GI	g3822036
BLAST score	349
E value	9.0e-33
Match length	185
% identity	42
NCBI Description	(AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]

Seq. No.	221196
Seq. ID	LIB3165-006-P1-K3-B9
Method	BLASTX
NCBI GI	g2239089
BLAST score	249
E value	3.0e-21
Match length	117
% identity	41
NCBI Description	(Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] >gi_3288180_emb_CAB11466_ (Z98758) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]

Seq. No.	221197
Seq. ID	LIB3165-006-P1-K3-C10
Method	BLASTX
NCBI GI	g3914605
BLAST score	681
E value	1.0e-71
Match length	192
% identity	70
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase - apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica]

Seq. No.	221198
Seq. ID	LIB3165-006-P1-K3-C11
Method	BLASTX
NCBI GI	g2369714
BLAST score	1035
E value	1.0e-113
Match length	219
% identity	90
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	221199

Seq. ID	LIB3165-006-P1-K3-C12
Method	BLASTX
NCBI GI	g121080
BLAST score	444
E value	3.0e-44
Match length	108
% identity	81
NCBI Description	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_1070638_pir__GCPMH glycine cleavage system protein H precursor - garden pea >gi_20737_emb_CAA45978_ (X64726) H protein [Pisum sativum] >gi_169093 (J05164) H-protein of glycine decarboxylase precursor (EC 2.1.2.10) [Pisum sativum] >gi_287815_emb_CAA37704_ (X53656) H-protein [Pisum sativum]

Seq. No.	221200
Seq. ID	LIB3165-006-P1-K3-C7
Method	BLASTX
NCBI GI	g131397
BLAST score	443
E value	7.0e-44
Match length	172
% identity	56
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_81480_pir__S00008 photosystem II oxygen-evolving complex protein 3 precursor - spinach >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi_225597_prf__1307179B luminal protein 16kD [Spinacia oleracea]

Seq. No.	221201
Seq. ID	LIB3165-006-P1-K3-C8
Method	BLASTX
NCBI GI	g1352821
BLAST score	848
E value	3.0e-91
Match length	162
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221202
Seq. ID	LIB3165-006-P1-K3-C9
Method	BLASTX
NCBI GI	g115765
BLAST score	849
E value	2.0e-91
Match length	182
% identity	83
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_

(X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	221203
Seq. ID	LIB3165-006-P1-K3-D2
Method	BLASTX
NCBI GI	g115765
BLAST score	872
E value	4.0e-94
Match length	188
% identity	59
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	221204
Seq. ID	LIB3165-006-P1-K3-D3
Method	BLASTX
NCBI GI	g3885892
BLAST score	202
E value	4.0e-30
Match length	97
% identity	75
NCBI Description	(AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No.	221205
Seq. ID	LIB3165-006-P1-K3-D4
Method	BLASTX
NCBI GI	g4545262
BLAST score	239
E value	4.0e-20
Match length	44
% identity	100
NCBI Description	(AF118230) metallothionein-like protein [Gossypium hirsutum]

Seq. No.	221206
Seq. ID	LIB3165-006-P1-K3-D6
Method	BLASTX
NCBI GI	g3894183
BLAST score	358
E value	8.0e-34
Match length	191
% identity	32
NCBI Description	(AC005662) calmodulin-like protein [Arabidopsis thaliana]

Seq. No.	221207
Seq. ID	LIB3165-006-P1-K3-D7
Method	BLASTX

NCBI GI	g1709651
BLAST score	500
E value	2.0e-50
Match length	129
% identity	74
NCBI Description	PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209 plastocyanin a precursor - black poplar >gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus nigra]

Seq. No.	221208
Seq. ID	LIB3165-006-P1-K3-D8
Method	BLASTN
NCBI GI	g3869069
BLAST score	36
E value	1.0e-10
Match length	87
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	221209
Seq. ID	LIB3165-006-P1-K3-D9
Method	BLASTX
NCBI GI	g115765
BLAST score	795
E value	4.0e-85
Match length	172
% identity	83
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	221210
Seq. ID	LIB3165-006-P1-K3-E11
Method	BLASTX
NCBI GI	g3747111
BLAST score	364
E value	8.0e-42
Match length	167
% identity	56
NCBI Description	(AF095641) MTN3 homolog [Arabidopsis thaliana]

Seq. No.	221211
Seq. ID	LIB3165-006-P1-K3-E12
Method	BLASTX
NCBI GI	g974782
BLAST score	995
E value	1.0e-108
Match length	195
% identity	96
NCBI Description	(Z49150) cobalamine-independent methionine synthase

[Solenostemon scutellarioides]

Seq. No.	221212
Seq. ID	LIB3165-006-P1-K3-E2
Method	BLASTX
NCBI GI	g2511691
BLAST score	839
E value	3.0e-90
Match length	224
% identity	70
NCBI Description	(Z99953) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No.	221213
Seq. ID	LIB3165-006-P1-K3-E3
Method	BLASTX
NCBI GI	g3687652
BLAST score	992
E value	1.0e-108
Match length	192
% identity	97
NCBI Description	(AF047352) rubisco activase precursor [Datisca glomerata]

Seq. No.	221214
Seq. ID	LIB3165-006-P1-K3-E4
Method	BLASTX
NCBI GI	g68200
BLAST score	747
E value	2.0e-79
Match length	179
% identity	83
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	221215
Seq. ID	LIB3165-006-P1-K3-E8
Method	BLASTX
NCBI GI	g3914136
BLAST score	268
E value	3.0e-23
Match length	116
% identity	46
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) >gi_2632171_emb_CAA05771_ (AJ002958) lipid transfer protein [Cicer arietinum]

Seq. No.	221216
Seq. ID	LIB3165-006-P1-K3-F1
Method	BLASTX
NCBI GI	g3928543
BLAST score	659
E value	4.0e-69
Match length	201
% identity	59
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	221217
Seq. ID	LIB3165-006-P1-K3-F11
Method	BLASTX
NCBI GI	g4406530
BLAST score	701
E value	5.0e-74
Match length	173
% identity	81
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221218
Seq. ID	LIB3165-006-P1-K3-F12
Method	BLASTX
NCBI GI	g3894183
BLAST score	267
E value	3.0e-23
Match length	164
% identity	27
NCBI Description	(AC005662) calmodulin-like protein [Arabidopsis thaliana]

Seq. No.	221219
Seq. ID	LIB3165-006-P1-K3-F2
Method	BLASTX
NCBI GI	g3928089
BLAST score	358
E value	8.0e-34
Match length	116
% identity	65
NCBI Description	(AC005770) putative osr40 [Arabidopsis thaliana]

Seq. No.	221220
Seq. ID	LIB3165-006-P1-K3-F4
Method	BLASTX
NCBI GI	g1352821
BLAST score	848
E value	3.0e-91
Match length	162
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221221
Seq. ID	LIB3165-006-P1-K3-F5
Method	BLASTX
NCBI GI	g1771778
BLAST score	832
E value	2.0e-89
Match length	183
% identity	83
NCBI Description	(X99320) 23 kDa oxygen evolving protein of photosystem II [Solanum tuberosum]

Seq. No.	221222
Seq. ID	LIB3165-006-P1-K3-F9

Method	BLASTX
NCBI GI	g4193388
BLAST score	633
E value	5.0e-66
Match length	168
% identity	75
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	221223
Seq. ID	LIB3165-006-P1-K3-G1
Method	BLASTX
NCBI GI	g231610
BLAST score	160
E value	1.0e-19
Match length	129
% identity	52
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]

Seq. No.	221224
Seq. ID	LIB3165-006-P1-K3-G10
Method	BLASTX
NCBI GI	g1352821
BLAST score	724
E value	8.0e-77
Match length	149
% identity	92
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221225
Seq. ID	LIB3165-006-P1-K3-G3
Method	BLASTX
NCBI GI	g2828252
BLAST score	381
E value	8.0e-41
Match length	141
% identity	63
NCBI Description	(AJ003137) CYP1 [Lycopersicon esculentum]

Seq. No.	221226
Seq. ID	LIB3165-006-P1-K3-G4
Method	BLASTX
NCBI GI	g2511691
BLAST score	521
E value	3.0e-72
Match length	170
% identity	79
NCBI Description	(Z99953) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No.	221227
Seq. ID	LIB3165-006-P1-K3-G5
Method	BLASTX
NCBI GI	g421826
BLAST score	973
E value	1.0e-106
Match length	202
% identity	90
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	221228
Seq. ID	LIB3165-006-P1-K3-G6
Method	BLASTX
NCBI GI	g82080
BLAST score	916
E value	3.0e-99
Match length	224
% identity	78
NCBI Description	chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf__1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No.	221229
Seq. ID	LIB3165-006-P1-K3-G7
Method	BLASTX
NCBI GI	g4406530
BLAST score	705
E value	1.0e-74
Match length	171
% identity	83
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221230
Seq. ID	LIB3165-006-P1-K3-G8
Method	BLASTX
NCBI GI	g585322
BLAST score	398
E value	2.0e-38
Match length	147
% identity	53
NCBI Description	INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi_539751_pir__A45153 inorganic pyrophosphatase (EC 3.6.1.1) - bovine

Seq. No.	221231
Seq. ID	LIB3165-006-P1-K3-H1
Method	BLASTX
NCBI GI	g4512667
BLAST score	782
E value	1.0e-83
Match length	183
% identity	78
NCBI Description	(AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	221232

Seq. ID	LIB3165-006-P1-K3-H10
Method	BLASTX
NCBI GI	g231610
BLAST score	452
E value	6.0e-45
Match length	155
% identity	62
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]

Seq. No.	221233
Seq. ID	LIB3165-006-P1-K3-H11
Method	BLASTX
NCBI GI	g100200
BLAST score	715
E value	5.0e-79
Match length	185
% identity	82
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	221234
Seq. ID	LIB3165-006-P1-K3-H2
Method	BLASTX
NCBI GI	g2462746
BLAST score	313
E value	7.0e-29
Match length	106
% identity	59
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	221235
Seq. ID	LIB3165-006-P1-K3-H3
Method	BLASTX
NCBI GI	g3582333
BLAST score	730
E value	2.0e-77
Match length	175
% identity	78
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	221236
Seq. ID	LIB3165-006-P1-K3-H5
Method	BLASTX
NCBI GI	g1352821
BLAST score	870
E value	7.0e-94
Match length	168
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221237
Seq. ID	LIB3165-006-P1-K3-H6
Method	BLASTX
NCBI GI	g505482
BLAST score	745
E value	3.0e-79
Match length	177
% identity	84
NCBI Description	(X64349) 33 kDa polypeptide of water-oxidizing complex of photosystem II [Nicotiana tabacum]

Seq. No.	221238
Seq. ID	LIB3165-006-P1-K3-H7
Method	BLASTX
NCBI GI	g4103635
BLAST score	432
E value	2.0e-42
Match length	162
% identity	56
NCBI Description	(AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. No.	221239
Seq. ID	LIB3165-006-P1-K3-H8
Method	BLASTX
NCBI GI	g2244811
BLAST score	511
E value	8.0e-52
Match length	184
% identity	63
NCBI Description	(Z97336) unnamed protein product [Arabidopsis thaliana]

Seq. No.	221240
Seq. ID	LIB3165-006-P1-K3-H9
Method	BLASTX
NCBI GI	g2935300
BLAST score	348
E value	2.0e-41
Match length	145
% identity	54
NCBI Description	(AF038046) 3-hydroxy-3-methylglutaryl-coenzyme A reductase 2 [Gossypium hirsutum]

Seq. No.	221241
Seq. ID	LIB3165-006-P1-K4-A10
Method	BLASTX
NCBI GI	g1084372
BLAST score	931
E value	1.0e-101
Match length	208
% identity	87
NCBI Description	glyceraldehyde-3-phosphate dehydrogenase (NADP+) (EC 1.2.1.9) - garden pea

Seq. No.	221242
Seq. ID	LIB3165-006-P1-K4-A11
Method	BLASTX

NCBI GI g2239089
BLAST score 290
E value 5.0e-26
Match length 137
% identity 41
NCBI Description (Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] >gi_3288180_emb_CAB11466_ (Z98758) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]

Seq. No. 221243
Seq. ID LIB3165-006-P1-K4-A12
Method BLASTX
NCBI GI g100490
BLAST score 748
E value 1.0e-79
Match length 153
% identity 33
NCBI Description polyubiquitin - garden snapdragon (fragment) >gi_16071_emb_CAA48140_ (X67957) ubiquitin [Antirrhinum majus]

Seq. No. 221244
Seq. ID LIB3165-006-P1-K4-A2
Method BLASTX
NCBI GI g1353352
BLAST score 440
E value 2.0e-43
Match length 125
% identity 71
NCBI Description (U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No. 221245
Seq. ID LIB3165-006-P1-K4-A3
Method BLASTX
NCBI GI g1531672
BLAST score 644
E value 2.0e-67
Match length 131
% identity 93
NCBI Description (U68461) actin [Striga asiatica]

Seq. No. 221246
Seq. ID LIB3165-006-P1-K4-A6
Method BLASTX
NCBI GI g136707
BLAST score 720
E value 2.0e-76
Match length 181
% identity 75
NCBI Description CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_280397_pir__S26199 plastoquinol--plastocyanin reductase (EC 1.10.99.1) iron-sulfur protein precursor - garden pea >gi_20832_emb_CAA45151_ (X63605) chloroplast Rieske FeS protein [Pisum sativum]

Seq. No.	221247
Seq. ID	LIB3165-006-P1-K4-A8
Method	BLASTX
NCBI GI	g4206122
BLAST score	378
E value	4.0e-36
Match length	175
% identity	46
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No.	221248
Seq. ID	LIB3165-006-P1-K4-A9
Method	BLASTX
NCBI GI	g121353
BLAST score	827
E value	1.0e-88
Match length	201
% identity	76
NCBI Description	GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR (ISOZYME DELTA) (GLUTAMATE-AMMONIA LIGASE) >gi_68596_pir__AJFBQD glutamate--ammonia ligase (EC 6.3.1.2) delta precursor, chloroplast - kidney bean >gi_21005_emb_CAA31234_ (X12738) GS precursor protein [Phaseolus vulgaris]

Seq. No.	221249
Seq. ID	LIB3165-006-P1-K4-B1
Method	BLASTX
NCBI GI	g2559012
BLAST score	497
E value	3.0e-50
Match length	155
% identity	65
NCBI Description	(AF026293) chaperonin containing t-complex polypeptide 1, beta subunit; CCT-beta [Homo sapiens] >gi_4090929 (AF026166) chaperonin-containing TCP-1 beta subunit homolog [Homo sapiens]

Seq. No.	221250
Seq. ID	LIB3165-006-P1-K4-B10
Method	BLASTX
NCBI GI	g4406814
BLAST score	243
E value	4.0e-34
Match length	115
% identity	68
NCBI Description	(AC006201) putative peptidyl-prolyl isomerase [Arabidopsis thaliana]

Seq. No.	221251
Seq. ID	LIB3165-006-P1-K4-B11
Method	BLASTX
NCBI GI	g115765
BLAST score	803
E value	5.0e-86
Match length	174

% identity	83
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]
Seq. No.	221252
Seq. ID	LIB3165-006-P1-K4-B12
Method	BLASTX
NCBI GI	g3914605
BLAST score	593
E value	2.0e-61
Match length	175
% identity	67
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase - apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica]
Seq. No.	221253
Seq. ID	LIB3165-006-P1-K4-B4
Method	BLASTX
NCBI GI	g1928981
BLAST score	880
E value	5.0e-95
Match length	198
% identity	89
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]
Seq. No.	221254
Seq. ID	LIB3165-006-P1-K4-B6
Method	BLASTX
NCBI GI	g2529342
BLAST score	577
E value	1.0e-59
Match length	151
% identity	75
NCBI Description	(L76554) transketolase [Spinacia oleracea]
Seq. No.	221255
Seq. ID	LIB3165-006-P1-K4-B7
Method	BLASTX
NCBI GI	g1657617
BLAST score	593
E value	2.0e-61
Match length	152
% identity	74
NCBI Description	(U72503) G2p [Arabidopsis thaliana] >gi_3068707 (AF049236) putative nuclear DNA-binding protein G2p [Arabidopsis thaliana]

Seq. No.	221256
Seq. ID	LIB3165-006-P1-K4-B8
Method	BLASTX
NCBI GI	g3822036
BLAST score	357
E value	1.0e-33
Match length	185
% identity	43
NCBI Description	(AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]

Seq. No.	221257
Seq. ID	LIB3165-006-P1-K4-B9
Method	BLASTX
NCBI GI	g4406814
BLAST score	303
E value	1.0e-42
Match length	115
% identity	79
NCBI Description	(AC006201) putative peptidyl-prolyl isomerase [Arabidopsis thaliana]

Seq. No.	221258
Seq. ID	LIB3165-006-P1-K4-C10
Method	BLASTX
NCBI GI	g542100
BLAST score	723
E value	1.0e-76
Match length	165
% identity	84
NCBI Description	H-protein - Flaveria pringlei >gi_2147453_pir__S60195 H-protein precursor (clone HFC1) - Flaveria cronquistii >gi_437993_emb_CAA81073_ (Z25854) H-protein [Flaveria cronquistii] >gi_437999_emb_CAA81074_ (Z25855) H-protein [Flaveria pringlei] >gi_3688299_emb_CAB16912_ (Z99763) H-protein [Flaveria pringlei]

Seq. No.	221259
Seq. ID	LIB3165-006-P1-K4-C11
Method	BLASTX
NCBI GI	g115765
BLAST score	759
E value	7.0e-81
Match length	167
% identity	56
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	221260
Seq. ID	LIB3165-006-P1-K4-C7
Method	BLASTX

NCBI GI	g131397
BLAST score	498
E value	3.0e-50
Match length	186
% identity	58
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_81480_pir__S00008 photosystem II oxygen-evolving complex protein 3 precursor - spinach >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi_225597_prf__1307179B luminal protein 16kD [Spinacia oleracea]

Seq. No.	221261
Seq. ID	LIB3165-006-P1-K4-C8
Method	BLASTX
NCBI GI	g1352821
BLAST score	679
E value	1.0e-71
Match length	134
% identity	93
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221262
Seq. ID	LIB3165-006-P1-K4-C9
Method	BLASTX
NCBI GI	g2369714
BLAST score	859
E value	1.0e-92
Match length	181
% identity	89
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	221263
Seq. ID	LIB3165-006-P1-K4-D2
Method	BLASTX
NCBI GI	g115765
BLAST score	708
E value	5.0e-75
Match length	161
% identity	54
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	221264
Seq. ID	LIB3165-006-P1-K4-D3

Method	BLASTX
NCBI GI	g1172664
BLAST score	521
E value	5.0e-53
Match length	102
% identity	94
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_419791_pir__S31165 photosystem I chain III precursor - Flaveria trinervia >gi_298482_bbs_127083 photosystem I reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem I subunit III [Flaveria trinervia]

Seq. No.	221265
Seq. ID	LIB3165-006-P1-K4-D6
Method	BLASTX
NCBI GI	g3894183
BLAST score	342
E value	6.0e-32
Match length	184
% identity	31
NCBI Description	(AC005662) calmodulin-like protein [Arabidopsis thaliana]

Seq. No.	221266
Seq. ID	LIB3165-006-P1-K4-D7
Method	BLASTX
NCBI GI	g1709651
BLAST score	515
E value	3.0e-52
Match length	132
% identity	73
NCBI Description	PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209 plastocyanin a precursor - black poplar >gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus nigra]

Seq. No.	221267
Seq. ID	LIB3165-006-P1-K4-D8
Method	BLASTN
NCBI GI	g3869069
BLAST score	39
E value	2.0e-12
Match length	133
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	221268
Seq. ID	LIB3165-006-P1-K4-E10
Method	BLASTX
NCBI GI	g974782
BLAST score	1097
E value	1.0e-120
Match length	216
% identity	96
NCBI Description	(Z49150) cobalamine-independent methionine synthase

[Solenostemon scutellarioides]

Seq. No.	221269
Seq. ID	LIB3165-006-P1-K4-E11
Method	BLASTX
NCBI GI	g549063
BLAST score	598
E value	5.0e-62
Match length	161
% identity	72
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]

Seq. No.	221270
Seq. ID	LIB3165-006-P1-K4-E2
Method	BLASTX
NCBI GI	g2511691
BLAST score	756
E value	2.0e-80
Match length	194
% identity	73
NCBI Description	(Z99953) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No.	221271
Seq. ID	LIB3165-006-P1-K4-E3
Method	BLASTX
NCBI GI	g266893
BLAST score	836
E value	5.0e-90
Match length	163
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__S28172 ribulose-bisphosphate carboxylase activase - cucumber >gi_18284_emb_CAA47906_ (X67674) rubisco activase [Cucumis sativus]

Seq. No.	221272
Seq. ID	LIB3165-006-P1-K4-E4
Method	BLASTX
NCBI GI	g68200
BLAST score	580
E value	6.0e-60
Match length	142
% identity	83
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	221273
Seq. ID	LIB3165-006-P1-K4-E8
Method	BLASTX
NCBI GI	g3914136
BLAST score	268
E value	3.0e-23

Match length	116
% identity	46
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) >gi_2632171_emb_CAA05771_ (AJ002958) lipid transfer protein [Cicer arietinum]

Seq. No.	221274
Seq. ID	LIB3165-006-P1-K4-E9
Method	BLASTX
NCBI GI	g3747111
BLAST score	380
E value	2.0e-36
Match length	121
% identity	60
NCBI Description	(AF095641) MTN3 homolog [Arabidopsis thaliana]

Seq. No.	221275
Seq. ID	LIB3165-006-P1-K4-F1
Method	BLASTX
NCBI GI	g3928543
BLAST score	563
E value	7.0e-58
Match length	179
% identity	56
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	221276
Seq. ID	LIB3165-006-P1-K4-F10
Method	BLASTX
NCBI GI	g3894183
BLAST score	347
E value	2.0e-32
Match length	196
% identity	32
NCBI Description	(AC005662) calmodulin-like protein [Arabidopsis thaliana]

Seq. No.	221277
Seq. ID	LIB3165-006-P1-K4-F12
Method	BLASTX
NCBI GI	g1352821
BLAST score	819
E value	7.0e-88
Match length	166
% identity	93
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221278
Seq. ID	LIB3165-006-P1-K4-F2
Method	BLASTX
NCBI GI	g3928089
BLAST score	358
E value	8.0e-34

Match length	116
% identity	65
NCBI Description	(AC005770) putative osr40 [Arabidopsis thaliana]

Seq. No.	221279
Seq. ID	LIB3165-006-P1-K4-F4
Method	BLASTX
NCBI GI	g1352821
BLAST score	848
E value	3.0e-91
Match length	162
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221280
Seq. ID	LIB3165-006-P1-K4-F5
Method	BLASTX
NCBI GI	g1771778
BLAST score	824
E value	2.0e-88
Match length	183
% identity	83
NCBI Description	(X99320) 23 kDa oxygen evolving protein of photosystem II [Solanum tuberosum]

Seq. No.	221281
Seq. ID	LIB3165-006-P1-K4-F9
Method	BLASTX
NCBI GI	g4406530
BLAST score	605
E value	8.0e-63
Match length	154
% identity	79
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221282
Seq. ID	LIB3165-006-P1-K4-G1
Method	BLASTX
NCBI GI	g461550
BLAST score	142
E value	1.0e-08
Match length	48
% identity	67
NCBI Description	ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR >gi_81635_pir__B39732 H+-transporting ATP synthase (EC 3.6.1.34) gamma-1 chain precursor, chloroplast - Arabidopsis thaliana >gi_166632 (M61741) ATP synthase gamma-subunit [Arabidopsis thaliana]

Seq. No.	221283
Seq. ID	LIB3165-006-P1-K4-G11
Method	BLASTX
NCBI GI	g2935298

BLAST score	646
E value	1.0e-67
Match length	189
% identity	69
NCBI Description	(AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 [Gossypium hirsutum]

Seq. No.	221284
Seq. ID	LIB3165-006-P1-K4-G12
Method	BLASTX
NCBI GI	g231610
BLAST score	447
E value	2.0e-44
Match length	153
% identity	62
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]

Seq. No.	221285
Seq. ID	LIB3165-006-P1-K4-G3
Method	BLASTX
NCBI GI	g2511693
BLAST score	475
E value	1.0e-47
Match length	138
% identity	68
NCBI Description	(Z99954) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No.	221286
Seq. ID	LIB3165-006-P1-K4-G4
Method	BLASTX
NCBI GI	g2511691
BLAST score	521
E value	5.0e-73
Match length	174
% identity	79
NCBI Description	(Z99953) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No.	221287
Seq. ID	LIB3165-006-P1-K4-G5
Method	BLASTX
NCBI GI	g445116
BLAST score	771
E value	2.0e-82
Match length	159
% identity	91
NCBI Description	light-harvesting complex IIa protein; [Hordeum vulgare]

Seq. No.	221288
Seq. ID	LIB3165-006-P1-K4-G6
Method	BLASTX
NCBI GI	g82080
BLAST score	822
E value	2.0e-88

Match length	170
% identity	88
NCBI Description	chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf__1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No.	221289
Seq. ID	LIB3165-006-P1-K4-G7
Method	BLASTX
NCBI GI	g4406530
BLAST score	695
E value	2.0e-73
Match length	171
% identity	82
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221290
Seq. ID	LIB3165-006-P1-K4-G8
Method	BLASTX
NCBI GI	g585322
BLAST score	354
E value	2.0e-33
Match length	137
% identity	53
NCBI Description	INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi_539751_pir__A45153 inorganic pyrophosphatase (EC 3.6.1.1) - bovine

Seq. No.	221291
Seq. ID	LIB3165-006-P1-K4-H1
Method	BLASTX
NCBI GI	g4512667
BLAST score	763
E value	2.0e-81
Match length	178
% identity	79
NCBI Description	(AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	221292
Seq. ID	LIB3165-006-P1-K4-H10
Method	BLASTX
NCBI GI	g4426565
BLAST score	246
E value	1.0e-20
Match length	203
% identity	32
NCBI Description	(AF031483) unknown [Rattus norvegicus]

Seq. No.	221293
Seq. ID	LIB3165-006-P1-K4-H11
Method	BLASTX
NCBI GI	g3914605
BLAST score	702
E value	4.0e-74
Match length	193
% identity	71
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

	PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase - apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica]
Seq. No.	221294
Seq. ID	LIB3165-006-P1-K4-H2
Method	BLASTX
NCBI GI	g2462746
BLAST score	269
E value	4.0e-28
Match length	117
% identity	61
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]
Seq. No.	221295
Seq. ID	LIB3165-006-P1-K4-H3
Method	BLASTX
NCBI GI	g3582333
BLAST score	820
E value	5.0e-88
Match length	175
% identity	86
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]
Seq. No.	221296
Seq. ID	LIB3165-006-P1-K4-H5
Method	BLASTX
NCBI GI	g1352821
BLAST score	795
E value	4.0e-85
Match length	152
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	221297
Seq. ID	LIB3165-006-P1-K4-H6
Method	BLASTX
NCBI GI	g505482
BLAST score	795
E value	4.0e-85
Match length	192
% identity	83
NCBI Description	(X64349) 33 kDa polypeptide of water-oxidizing complex of photosystem II [Nicotiana tabacum]
Seq. No.	221298
Seq. ID	LIB3165-006-P1-K4-H7
Method	BLASTX
NCBI GI	g4103635
BLAST score	324

E value 6.0e-30
Match length 138
% identity 51
NCBI Description (AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. No. 221299
Seq. ID LIB3165-006-P1-K4-H8
Method BLASTX
NCBI GI g2244811
BLAST score 534
E value 2.0e-54
Match length 184
% identity 65
NCBI Description (Z97336) unnamed protein product [Arabidopsis thaliana]

Seq. No. 221300
Seq. ID LIB3165-006-P1-K4-H9
Method BLASTX
NCBI GI g100200
BLAST score 712
E value 2.0e-75
Match length 165
% identity 67
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato

Seq. No. 221301
Seq. ID LIB3165-007-P1-K1-A10
Method BLASTX
NCBI GI g1928981
BLAST score 257
E value 1.0e-22
Match length 57
% identity 88
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No. 221302
Seq. ID LIB3165-007-P1-K1-A12
Method BLASTX
NCBI GI g4406530
BLAST score 252
E value 9.0e-22
Match length 71
% identity 75
NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 221303
Seq. ID LIB3165-007-P1-K1-A2
Method BLASTX
NCBI GI g1172664
BLAST score 218
E value 1.0e-17
Match length 48
% identity 90
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_419791_pir__S31165 photosystem I chain III precursor -

Flaveria trinervia >gi_298482_bbs_127083 photosystem I reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem I subunit III [Flaveria trinervia]

Seq. No.	221304
Seq. ID	LIB3165-007-P1-K1-A6
Method	BLASTX
NCBI GI	g266893
BLAST score	648
E value	4.0e-68
Match length	127
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__S28172 ribulose-bisphosphate carboxylase activase - cucumber >gi_18284_emb_CAA47906_ (X67674) rubisco activase [Cucumis sativus]

Seq. No.	221305
Seq. ID	LIB3165-007-P1-K1-A8
Method	BLASTX
NCBI GI	g1352821
BLAST score	390
E value	7.0e-38
Match length	95
% identity	80
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221306
Seq. ID	LIB3165-007-P1-K1-B1
Method	BLASTX
NCBI GI	g1352821
BLAST score	494
E value	5.0e-50
Match length	96
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221307
Seq. ID	LIB3165-007-P1-K1-B11
Method	BLASTX
NCBI GI	g1168411
BLAST score	446
E value	2.0e-44
Match length	119
% identity	79
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	221308
Seq. ID	LIB3165-007-P1-K1-B2
Method	BLASTX
NCBI GI	g1931640
BLAST score	488
E value	2.0e-49
Match length	124
% identity	71
NCBI Description	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]

Seq. No.	221309
Seq. ID	LIB3165-007-P1-K1-B4
Method	BLASTN
NCBI GI	g450504
BLAST score	132
E value	4.0e-68
Match length	247
% identity	97
NCBI Description	G.hirsutum rbcS gene for ribulose-1,5-bisphosphate carboxylase, small subunit

Seq. No.	221310
Seq. ID	LIB3165-007-P1-K1-B5
Method	BLASTX
NCBI GI	g1352821
BLAST score	460
E value	4.0e-46
Match length	87
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221311
Seq. ID	LIB3165-007-P1-K1-B6
Method	BLASTX
NCBI GI	g4406530
BLAST score	349
E value	4.0e-33
Match length	93
% identity	76
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221312
Seq. ID	LIB3165-007-P1-K1-B7
Method	BLASTX
NCBI GI	g3021357
BLAST score	271
E value	5.0e-24
Match length	58
% identity	84
NCBI Description	(AJ005082) UDP-galactose 4-epimerase [Cyamopsis tetragonoloba]

Seq. No.	221313
Seq. ID	LIB3165-007-P1-K1-B9
Method	BLASTX
NCBI GI	g3036944
BLAST score	213
E value	3.0e-23
Match length	114
% identity	57
NCBI Description	(AB012637) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	221314
Seq. ID	LIB3165-007-P1-K1-C1
Method	BLASTX
NCBI GI	g3510256
BLAST score	179
E value	4.0e-13
Match length	98
% identity	43
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	221315
Seq. ID	LIB3165-007-P1-K1-C11
Method	BLASTX
NCBI GI	g68200
BLAST score	350
E value	3.0e-33
Match length	92
% identity	79
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	221316
Seq. ID	LIB3165-007-P1-K1-C12
Method	BLASTX
NCBI GI	g115813
BLAST score	395
E value	2.0e-38
Match length	96
% identity	77
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE III PRECURSOR (CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	221317
Seq. ID	LIB3165-007-P1-K1-C2
Method	BLASTN
NCBI GI	g169818
BLAST score	39
E value	1.0e-12
Match length	79
% identity	87
NCBI Description	Rice 25S ribosomal RNA gene

Seq. No.	221318
Seq. ID	LIB3165-007-P1-K1-C8

Method	BLASTX
NCBI GI	g2244797
BLAST score	144
E value	5.0e-09
Match length	52
% identity	58
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	221319
Seq. ID	LIB3165-007-P1-K1-C9
Method	BLASTX
NCBI GI	g231688
BLAST score	683
E value	3.0e-72
Match length	130
% identity	99
NCBI Description	CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC 1.11.1.6) - upland cotton >gi_18488_emb_CAA39998_ (X56675) subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No.	221320
Seq. ID	LIB3165-007-P1-K1-D10
Method	BLASTX
NCBI GI	g1545805
BLAST score	172
E value	7.0e-13
Match length	65
% identity	62
NCBI Description	(D64052) cytochrome P450 like_TBP [Nicotiana tabacum]

Seq. No.	221321
Seq. ID	LIB3165-007-P1-K1-D11
Method	BLASTX
NCBI GI	g115471
BLAST score	557
E value	2.0e-57
Match length	127
% identity	82
NCBI Description	CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) >gi_100078_pir__S10200 carbonate dehydratase (EC 4.2.1.1) precursor - garden pea >gi_20673_emb_CAA36792_ (X52558) precursor peptide (AA -104 to 224) [Pisum sativum]

Seq. No.	221322
Seq. ID	LIB3165-007-P1-K1-D12
Method	BLASTX
NCBI GI	g1354515
BLAST score	205
E value	3.0e-16
Match length	94
% identity	51
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	221323
Seq. ID	LIB3165-007-P1-K1-D2
Method	BLASTX

NCBI GI	g1346155
BLAST score	315
E value	5.0e-50
Match length	124
% identity	78
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_481942_pir__S40212 glycine hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei >gi_437995_emb_CAA81078_ (Z25859) glycine hydroxymethyltransferase [Flaveria pringlei]

Seq. No.	221324
Seq. ID	LIB3165-007-P1-K1-D3
Method	BLASTX
NCBI GI	g1352821
BLAST score	238
E value	2.0e-20
Match length	56
% identity	82
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221325
Seq. ID	LIB3165-007-P1-K1-D4
Method	BLASTX
NCBI GI	g1362086
BLAST score	558
E value	1.0e-57
Match length	117
% identity	89
NCBI Description	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir__S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]

Seq. No.	221326
Seq. ID	LIB3165-007-P1-K1-D5
Method	BLASTX
NCBI GI	g2583125
BLAST score	642
E value	2.0e-67
Match length	124
% identity	94
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	221327
Seq. ID	LIB3165-007-P1-K1-D6
Method	BLASTX
NCBI GI	g3334405

BLAST score	484
E value	7.0e-49
Match length	103
% identity	98
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) >gi_2267583 (AF009338) vacuolar H+-ATPase subunit E [Gossypium hirsutum]

Seq. No.	221328
Seq. ID	LIB3165-007-P1-K1-D9
Method	BLASTX
NCBI GI	g100203
BLAST score	370
E value	2.0e-35
Match length	94
% identity	77
NCBI Description	cysteine proteinase (EC 3.4.22.-) precursor - tomato >gi_19195_emb_CAA78403_ (Z14028) pre-pro-cysteine proteinase [Lycopersicon esculentum]

Seq. No.	221329
Seq. ID	LIB3165-007-P1-K1-E1
Method	BLASTX
NCBI GI	g430947
BLAST score	448
E value	1.0e-44
Match length	109
% identity	82
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	221330
Seq. ID	LIB3165-007-P1-K1-E11
Method	BLASTX
NCBI GI	g4406530
BLAST score	339
E value	7.0e-32
Match length	89
% identity	78
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221331
Seq. ID	LIB3165-007-P1-K1-E2
Method	BLASTX
NCBI GI	g2191136
BLAST score	310
E value	2.0e-28
Match length	110
% identity	60
NCBI Description	(AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290 [Arabidopsis thaliana]

Seq. No.	221332
Seq. ID	LIB3165-007-P1-K1-E3
Method	BLASTX

NCBI GI g2739375
BLAST score 219
E value 7.0e-18
Match length 83
% identity 55
NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

Seq. No. 221333
Seq. ID LIB3165-007-P1-K1-E7
Method BLASTX
NCBI GI g902584
BLAST score 425
E value 4.0e-42
Match length 94
% identity 15
NCBI Description (U29159) polyubiquitin containing 7 ubiquitin monomers [Zea mays]

Seq. No. 221334
Seq. ID LIB3165-007-P1-K1-F11
Method BLASTN
NCBI GI g4220633
BLAST score 39
E value 1.0e-12
Match length 203
% identity 80
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No. 221335
Seq. ID LIB3165-007-P1-K1-F3
Method BLASTX
NCBI GI g421826
BLAST score 309
E value 2.0e-28
Match length 61
% identity 87
NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No. 221336
Seq. ID LIB3165-007-P1-K1-F4
Method BLASTX
NCBI GI g547683
BLAST score 538
E value 3.0e-55
Match length 113
% identity 92
NCBI Description HEAT SHOCK COGNATE PROTEIN 80 >gi_170456 (M96549) heat shock cognate protein 80 [Solanum lycopersicum] >gi_445601_prf__1909348A heat shock protein hsp80 [Lycopersicon esculentum]

Seq. No. 221337
Seq. ID LIB3165-007-P1-K1-F5
Method BLASTX

NCBI GI	g115765
BLAST score	661
E value	1.0e-69
Match length	127
% identity	92
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	221338
Seq. ID	LIB3165-007-P1-K1-F7
Method	BLASTX
NCBI GI	g1709651
BLAST score	347
E value	8.0e-33
Match length	114
% identity	60
NCBI Description	PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209 plastocyanin a precursor - black poplar >gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus nigra]

Seq. No.	221339
Seq. ID	LIB3165-007-P1-K1-F8
Method	BLASTX
NCBI GI	g100616
BLAST score	189
E value	2.0e-14
Match length	47
% identity	81
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	221340
Seq. ID	LIB3165-007-P1-K1-G10
Method	BLASTX
NCBI GI	g1419090
BLAST score	317
E value	3.0e-29
Match length	92
% identity	68
NCBI Description	(X94968) 37kDa chloroplast inner envelope membrane polypeptide precursor [Nicotiana tabacum]

Seq. No.	221341
Seq. ID	LIB3165-007-P1-K1-G2
Method	BLASTN
NCBI GI	g4545261
BLAST score	355

E value	0.0e+00
Match length	391
% identity	98
NCBI Description	Gossypium hirsutum metallothionein-like protein mRNA, complete cds

Seq. No.	221342
Seq. ID	LIB3165-007-P1-K1-G3
Method	BLASTX
NCBI GI	g2662310
BLAST score	449
E value	7.0e-45
Match length	118
% identity	70
NCBI Description	(AB009307) bpw1 [Hordeum vulgare]

Seq. No.	221343
Seq. ID	LIB3165-007-P1-K1-G4
Method	BLASTX
NCBI GI	g441457
BLAST score	249
E value	2.0e-21
Match length	53
% identity	91
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]

Seq. No.	221344
Seq. ID	LIB3165-007-P1-K1-G8
Method	BLASTX
NCBI GI	g2493144
BLAST score	345
E value	1.0e-32
Match length	87
% identity	82
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	221345
Seq. ID	LIB3165-007-P1-K1-H1
Method	BLASTX
NCBI GI	g170354
BLAST score	545
E value	5.0e-56
Match length	113
% identity	21
NCBI Description	(M74156) pentameric polyubiquitin [Nicotiana sylvestris]

Seq. No.	221346
Seq. ID	LIB3165-007-P1-K1-H12
Method	BLASTX
NCBI GI	g231688
BLAST score	574

E value	2.0e-59
Match length	111
% identity	98
NCBI Description	CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC 1.11.1.6) - upland cotton >gi_18488_emb_CAA39998_ (X56675) subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No.	221347
Seq. ID	LIB3165-007-P1-K1-H2
Method	BLASTX
NCBI GI	g3687652
BLAST score	515
E value	1.0e-52
Match length	106
% identity	94
NCBI Description	(AF047352) rubisco activase precursor [Datisca glomerata]

Seq. No.	221348
Seq. ID	LIB3165-007-P1-K1-H3
Method	BLASTX
NCBI GI	g2245096
BLAST score	450
E value	6.0e-45
Match length	103
% identity	80
NCBI Description	(Z97343) inositol 2-dehydrogenase homolog [Arabidopsis thaliana]

Seq. No.	221349
Seq. ID	LIB3165-007-P1-K1-H4
Method	BLASTN
NCBI GI	g2687435
BLAST score	128
E value	6.0e-66
Match length	192
% identity	92
NCBI Description	Hamamelis virginiana large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	221350
Seq. ID	LIB3165-007-P1-K1-H6
Method	BLASTX
NCBI GI	g3738285
BLAST score	382
E value	5.0e-37
Match length	111
% identity	66
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	221351
Seq. ID	LIB3165-007-P1-K1-H7
Method	BLASTX
NCBI GI	g1246823
BLAST score	321
E value	1.0e-34
Match length	118
% identity	67

NCBI Description	(X89865) unknown [Phoenix dactylifera]

Seq. No.	221352
Seq. ID	LIB3165-007-P1-K1-H8
Method	BLASTX
NCBI GI	g1572819
BLAST score	191
E value	8.0e-15
Match length	79
% identity	51
NCBI Description	(U70855) similar to the RAS gene family [Caenorhabditis elegans]

Seq. No.	221353
Seq. ID	LIB3165-007-P1-K1-H9
Method	BLASTX
NCBI GI	g115813
BLAST score	306
E value	3.0e-28
Match length	96
% identity	65
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE III PRECURSOR (CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	221354
Seq. ID	LIB3165-008-P1-K1-A12
Method	BLASTX
NCBI GI	g1352821
BLAST score	510
E value	6.0e-52
Match length	98
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221355
Seq. ID	LIB3165-008-P1-K1-A3
Method	BLASTX
NCBI GI	g4406530
BLAST score	315
E value	5.0e-29
Match length	87
% identity	75
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221356
Seq. ID	LIB3165-008-P1-K1-A7
Method	BLASTX
NCBI GI	g3914472
BLAST score	376
E value	3.0e-36
Match length	90
% identity	81

NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10) >gi_322764_pir__S32021 photosystem II 10K protein - common tobacco >gi_22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana tabacum]
Seq. No.	221357
Seq. ID	LIB3165-008-P1-K1-A9
Method	BLASTX
NCBI GI	g4406530
BLAST score	262
E value	6.0e-23
Match length	96
% identity	60
NCBI Description	(AF126870) rubisco activase [Vigna radiata]
Seq. No.	221358
Seq. ID	LIB3165-008-P1-K1-B10
Method	BLASTX
NCBI GI	g1171577
BLAST score	549
E value	2.0e-56
Match length	129
% identity	80
NCBI Description	(X95343) hypersensitivity-related gene [Nicotiana tabacum]
Seq. No.	221359
Seq. ID	LIB3165-008-P1-K1-B12
Method	BLASTX
NCBI GI	g1352821
BLAST score	524
E value	1.0e-53
Match length	99
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	221360
Seq. ID	LIB3165-008-P1-K1-B2
Method	BLASTX
NCBI GI	g2738949
BLAST score	325
E value	2.0e-38
Match length	95
% identity	88
NCBI Description	(AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa]
Seq. No.	221361
Seq. ID	LIB3165-008-P1-K1-B3
Method	BLASTX
NCBI GI	g4008159
BLAST score	635
E value	1.0e-66
Match length	131

% identity	89
NCBI Description	(AB015601) DnaJ homolog [Salix gilgiana]

Seq. No.	221362
Seq. ID	LIB3165-008-P1-K1-B4
Method	BLASTX
NCBI GI	g430947
BLAST score	433
E value	6.0e-43
Match length	109
% identity	80
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	221363
Seq. ID	LIB3165-008-P1-K1-B6
Method	BLASTX
NCBI GI	g68200
BLAST score	417
E value	5.0e-41
Match length	105
% identity	81
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	221364
Seq. ID	LIB3165-008-P1-K1-B7
Method	BLASTX
NCBI GI	g586797
BLAST score	227
E value	9.0e-19
Match length	85
% identity	48
NCBI Description	HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III

Seq. No.	221365
Seq. ID	LIB3165-008-P1-K1-B9
Method	BLASTX
NCBI GI	g3869088
BLAST score	535
E value	7.0e-55
Match length	102
% identity	100
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No.	221366
Seq. ID	LIB3165-008-P1-K1-C1
Method	BLASTN
NCBI GI	g450504
BLAST score	83
E value	5.0e-39
Match length	118
% identity	93
NCBI Description	G.hirsutum rbcS gene for ribulose-1,5-bisphosphate carboxylase, small subunit

Seq. No.	221367
Seq. ID	LIB3165-008-P1-K1-C10
Method	BLASTX
NCBI GI	g3881507
BLAST score	367
E value	4.0e-35
Match length	129
% identity	52
NCBI Description	(Z47357) cDNA EST yk375c3.5 comes from this gene; cDNA EST yk375c3.3 comes from this gene [Caenorhabditis elegans]

Seq. No.	221368
Seq. ID	LIB3165-008-P1-K1-C12
Method	BLASTX
NCBI GI	g2832682
BLAST score	209
E value	1.0e-16
Match length	97
% identity	54
NCBI Description	(AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No.	221369
Seq. ID	LIB3165-008-P1-K1-C2
Method	BLASTX
NCBI GI	g119640
BLAST score	327
E value	2.0e-30
Match length	106
% identity	59
NCBI Description	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN E8) >gi_82109_pir__S01642 ripening protein E8 - tomato >gi_19199_emb_CAA31789_ (X13437) E8 protein [Lycopersicon esculentum]

Seq. No.	221370
Seq. ID	LIB3165-008-P1-K1-C3
Method	BLASTX
NCBI GI	g2213610
BLAST score	178
E value	5.0e-13
Match length	112
% identity	19
NCBI Description	(AC000103) F21J9.4 [Arabidopsis thaliana]

Seq. No.	221371
Seq. ID	LIB3165-008-P1-K1-C5
Method	BLASTX
NCBI GI	g1354515
BLAST score	223
E value	2.0e-18
Match length	94
% identity	54
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	221372
Seq. ID	LIB3165-008-P1-K1-D1

Method	BLASTX
NCBI GI	g289920
BLAST score	584
E value	1.0e-60
Match length	119
% identity	92
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221373
Seq. ID	LIB3165-008-P1-K1-D10
Method	BLASTX
NCBI GI	g400890
BLAST score	261
E value	1.0e-22
Match length	116
% identity	45
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_282837_pir__S26953 photosystem II 22K protein precursor - spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864) photosystem II 22 kda polypeptide [spinach, Peptide, 274 aa] [Spinacia oleracea]

Seq. No.	221374
Seq. ID	LIB3165-008-P1-K1-D11
Method	BLASTX
NCBI GI	g1168251
BLAST score	570
E value	6.0e-59
Match length	130
% identity	78
NCBI Description	PROBABLE CYSTEINE PROTEINASE A494 PRECURSOR >gi_1076384_pir__S46535 probable cysteine proteinase (EC 3.4.22.-) (clone A1494) - Arabidopsis thaliana (fragment) >gi_516865_emb_CAA52403_ (X74359) putative thiol protease [Arabidopsis thaliana]

Seq. No.	221375
Seq. ID	LIB3165-008-P1-K1-D12
Method	BLASTX
NCBI GI	g1352821
BLAST score	562
E value	5.0e-58
Match length	106
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221376
Seq. ID	LIB3165-008-P1-K1-D3
Method	BLASTX
NCBI GI	g100616
BLAST score	614

E value	4.0e-64
Match length	130
% identity	85
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	221377
Seq. ID	LIB3165-008-P1-K1-D4
Method	BLASTX
NCBI GI	g4406530
BLAST score	330
E value	8.0e-31
Match length	87
% identity	78
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221378
Seq. ID	LIB3165-008-P1-K1-D5
Method	BLASTX
NCBI GI	g602292
BLAST score	453
E value	3.0e-45
Match length	108
% identity	81
NCBI Description	(U17987) RCH2 protein [Brassica napus]

Seq. No.	221379
Seq. ID	LIB3165-008-P1-K1-D6
Method	BLASTX
NCBI GI	g1346156
BLAST score	621
E value	5.0e-65
Match length	131
% identity	92
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 2 PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_481943_pir__S40213 glycine hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei >gi_437997_emb_CAA81079_ (Z25860) glycine hydroxymethyltransferase [Flaveria pringlei]

Seq. No.	221380
Seq. ID	LIB3165-008-P1-K1-D7
Method	BLASTX
NCBI GI	g131385
BLAST score	497
E value	2.0e-50
Match length	122
% identity	84
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN)

Seq. No.	221381

Seq. ID	LIB3165-008-P1-K1-D9
Method	BLASTX
NCBI GI	g1354517
BLAST score	294
E value	1.0e-26
Match length	129
% identity	54
NCBI Description	(U55838) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	221382
Seq. ID	LIB3165-008-P1-K1-E12
Method	BLASTX
NCBI GI	g2129538
BLAST score	319
E value	2.0e-29
Match length	67
% identity	88
NCBI Description	AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232) AT103 [Arabidopsis thaliana]

Seq. No.	221383
Seq. ID	LIB3165-008-P1-K1-E3
Method	BLASTN
NCBI GI	g2687430
BLAST score	63
E value	1.0e-27
Match length	67
% identity	99
NCBI Description	Acorus gramineus large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	221384
Seq. ID	LIB3165-008-P1-K1-E4
Method	BLASTX
NCBI GI	g166834
BLAST score	602
E value	1.0e-62
Match length	124
% identity	92
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	221385
Seq. ID	LIB3165-008-P1-K1-E5
Method	BLASTX
NCBI GI	g3738261
BLAST score	179
E value	4.0e-13
Match length	45
% identity	87
NCBI Description	(AB018412) chloroplast phosphoglycerate kinase [Populus nigra]

Seq. No.	221386
Seq. ID	LIB3165-008-P1-K1-E6

Method	BLASTX
NCBI GI	g3334245
BLAST score	325
E-value	3.0e-30
Match length	74
% identity	84
NCBI Description	LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi_2909424_emb_CAA12028_ (AJ224520) Glyoxalase I [Cicer arietinum]

Seq. No.	221387
Seq. ID	LIB3165-008-P1-K1-E8
Method	BLASTX
NCBI GI	g417154
BLAST score	628
E value	9.0e-66
Match length	123
% identity	98
NCBI Description	HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

Seq. No.	221388
Seq. ID	LIB3165-008-P1-K1-F1
Method	BLASTX
NCBI GI	g3659907
BLAST score	388
E value	1.0e-37
Match length	105
% identity	74
NCBI Description	(AF091857) protein translation factor SUI1 homolog [Pimpinella brachycarpa]

Seq. No.	221389
Seq. ID	LIB3165-008-P1-K1-F10
Method	BLASTX
NCBI GI	g1352821
BLAST score	584
E value	1.0e-60
Match length	119
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221390
Seq. ID	LIB3165-008-P1-K1-F11
Method	BLASTX
NCBI GI	g3335350
BLAST score	393
E value	3.0e-38
Match length	126

% identity	55
NCBI Description	(AC004512) Similar to gb_Z84386 anthranilate N-hydroxycinnamoyl/benzoyltransferase from Dianthus caryophyllus. [Arabidopsis thaliana]

Seq. No.	221391
Seq. ID	LIB3165-008-P1-K1-F12
Method	BLASTN
NCBI GI	g18511
BLAST score	96
E value	1.0e-46
Match length	160
% identity	90
NCBI Description	G.hirsutum light regulated unknown reading frame DNA

Seq. No.	221392
Seq. ID	LIB3165-008-P1-K1-F2
Method	BLASTX
NCBI GI	g2494076
BLAST score	492
E value	9.0e-50
Match length	104
% identity	88
NCBI Description	NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi_1842115 (U87848) non-phosphorylating glyceraldehyde dehydrogenase [Nicotiana plumbaginifolia]

Seq. No.	221393
Seq. ID	LIB3165-008-P1-K1-F5
Method	BLASTX
NCBI GI	g393707
BLAST score	561
E value	6.0e-58
Match length	129
% identity	86
NCBI Description	(X67696) acetyl-CoA acyltransferase [Cucumis sativus]

Seq. No.	221394
Seq. ID	LIB3165-008-P1-K1-F6
Method	BLASTX
NCBI GI	g2443886
BLAST score	262
E value	7.0e-23
Match length	68
% identity	79
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No.	221395
Seq. ID	LIB3165-008-P1-K1-F7
Method	BLASTX
NCBI GI	g1694976
BLAST score	275
E value	2.0e-24
Match length	106

% identity	52
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis thaliana]

Seq. No.	221396
Seq. ID	LIB3165-008-P1-K1-G10
Method	BLASTX
NCBI GI	g2501356
BLAST score	437
E value	2.0e-43
Match length	85
% identity	93
NCBI Description	TRANSKETOLASE, CHLOROPLAST PRECURSOR (TK) >gi_1658322_emb_CAA90427_ (Z50099) transketolase precursor [Solanum tuberosum]

Seq. No.	221397
Seq. ID	LIB3165-008-P1-K1-G11
Method	BLASTX
NCBI GI	g131397
BLAST score	291
E value	3.0e-26
Match length	128
% identity	54
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_81480_pir__S00008 photosystem II oxygen-evolving complex protein 3 precursor - spinach >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi_225597_prf__1307179B luminal protein 16kD [Spinacia oleracea]

Seq. No.	221398
Seq. ID	LIB3165-008-P1-K1-G3
Method	BLASTX
NCBI GI	g2864617
BLAST score	221
E value	5.0e-18
Match length	111
% identity	43
NCBI Description	(AL021811) H+-transporting ATP synthase chain9 - like protein [Arabidopsis thaliana]

Seq. No.	221399
Seq. ID	LIB3165-008-P1-K1-G4
Method	BLASTX
NCBI GI	g1352683
BLAST score	219
E value	8.0e-18
Match length	60
% identity	73
NCBI Description	PROTEIN PHOSPHATASE 2C PPH1 (PP2C) >gi_995839 (U34803) protein phosphatase homolog [Arabidopsis thaliana]

Seq. No.	221400

Seq. ID	LIB3165-008-P1-K1-G5
Method	BLASTX
NCBI GI	g4538913
BLAST score	415
E value	8.0e-41
Match length	100
% identity	79
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

Seq. No.	221401
Seq. ID	LIB3165-008-P1-K1-G7
Method	BLASTX
NCBI GI	g3914603
BLAST score	489
E value	2.0e-49
Match length	115
% identity	78
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No.	221402
Seq. ID	LIB3165-008-P1-K1-G8
Method	BLASTX
NCBI GI	g2970051
BLAST score	373
E value	7.0e-36
Match length	100
% identity	70
NCBI Description	(AB012110) ARG10 [Vigna radiata]

Seq. No.	221403
Seq. ID	LIB3165-008-P1-K1-G9
Method	BLASTX
NCBI GI	g122106
BLAST score	375
E value	4.0e-36
Match length	76
% identity	100
NCBI Description	HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana >gi_2119028_pir__S60475 histone H4 - garden pea >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_225838_prf__1314298A histone H4 [Arabidopsis thaliana]

Seq. No.	221404

Seq. ID	LIB3165-008-P1-K1-H2
Method	BLASTX
NCBI GI	g2894599
BLAST score	414
E value	1.0e-40
Match length	108
% identity	67
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	221405
Seq. ID	LIB3165-008-P1-K1-H5
Method	BLASTX
NCBI GI	g119194
BLAST score	182
E value	8.0e-14
Match length	69
% identity	64
NCBI Description	ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >gi_81607_pir__S09152 translation elongation factor Tu precursor, chloroplast - Arabidopsis thaliana >gi_22565_emb_CAA36498_ (X52256) elongation factor Tu precursor [Arabidopsis thaliana] >gi_226817_prf__1607332A elongation factor Tu [Arabidopsis thaliana]

Seq. No.	221406
Seq. ID	LIB3165-008-P1-K1-H6
Method	BLASTX
NCBI GI	g4056506
BLAST score	369
E value	2.0e-35
Match length	111
% identity	61
NCBI Description	(AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	221407
Seq. ID	LIB3165-008-P1-K1-H7
Method	BLASTX
NCBI GI	g1565225
BLAST score	227
E value	9.0e-19
Match length	49
% identity	86
NCBI Description	(X95572) salt-tolerance protein [Arabidopsis thaliana]

Seq. No.	221408
Seq. ID	LIB3165-008-P1-K1-H9
Method	BLASTX
NCBI GI	g2465773
BLAST score	147
E value	6.0e-12
Match length	92
% identity	33
NCBI Description	(AF022186) homologous to orf238 in Porphyra purpurea [Cyanidium caldarium]

Seq. No.	221409
Seq. ID	LIB3165-009-P1-K1-A1

Method	BLASTX
NCBI GI	g3880432
BLAST score	165
E value	2.0e-11
Match length	114
% identity	37
NCBI Description	(Z66521) similar to kinensin-like protein; cDNA EST yk198e10.3 comes from this gene; cDNA EST yk198e10.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	221410
Seq. ID	LIB3165-009-P1-K1-A10
Method	BLASTX
NCBI GI	g4337025
BLAST score	443
E value	4.0e-44
Match length	114
% identity	75
NCBI Description	(AF123253) AIM1 protein [Arabidopsis thaliana]

Seq. No.	221411
Seq. ID	LIB3165-009-P1-K1-A11
Method	BLASTX
NCBI GI	g1168408
BLAST score	533
E value	1.0e-54
Match length	121
% identity	88
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1 >gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828) fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No.	221412
Seq. ID	LIB3165-009-P1-K1-A12
Method	BLASTX
NCBI GI	g3158474
BLAST score	327
E value	2.0e-30
Match length	90
% identity	73
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]

Seq. No.	221413
Seq. ID	LIB3165-009-P1-K1-A3
Method	BLASTX
NCBI GI	g128194
BLAST score	464
E value	1.0e-46
Match length	110
% identity	77
NCBI Description	NITRATE REDUCTASE (NR) >gi_81572_pir__A41667 nitrate reductase (NADH) (EC 1.6.6.1) - winter squash >gi_167499 (M33154) nitrate reductase [Cucurbita maxima]

Seq. No.	221414
Seq. ID	LIB3165-009-P1-K1-A7

Method	BLASTX
NCBI GI	g3880432
BLAST score	171
E value	3.0e-12
Match length	60
% identity	50
NCBI Description	(Z66521) similar to kinensin-like protein; cDNA EST yk198e10.3 comes from this gene; cDNA EST yk198e10.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	221415
Seq. ID	LIB3165-009-P1-K1-B11
Method	BLASTX
NCBI GI	g3914605
BLAST score	530
E value	3.0e-54
Match length	124
% identity	81
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase - apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica]

Seq. No.	221416
Seq. ID	LIB3165-009-P1-K1-B12
Method	BLASTX
NCBI GI	g289920
BLAST score	587
E value	5.0e-61
Match length	108
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221417
Seq. ID	LIB3165-009-P1-K1-B3
Method	BLASTX
NCBI GI	g551428
BLAST score	92
E value	1.0e-08
Match length	89
% identity	43
NCBI Description	(X78996) tetrafunctional protein [Cucumis sativus]

Seq. No.	221418
Seq. ID	LIB3165-009-P1-K1-B4
Method	BLASTX
NCBI GI	g4091806
BLAST score	364
E value	8.0e-35
Match length	115
% identity	64
NCBI Description	(AF052585) CONSTANS-like protein 2 [Malus domestica]

Seq. No.	221419

Seq. ID	LIB3165-009-P1-K1-B5
Method	BLASTX
NCBI GI	g4337025
BLAST score	186
E value	5.0e-14
Match length	92
% identity	48
NCBI Description	(AF123253) AIM1 protein [Arabidopsis thaliana]

Seq. No.	221420
Seq. ID	LIB3165-009-P1-K1-B6
Method	BLASTX
NCBI GI	g2661021
BLAST score	559
E value	1.0e-57
Match length	107
% identity	96
NCBI Description	(AF035255) catalase [Glycine max]

Seq. No.	221421
Seq. ID	LIB3165-009-P1-K1-B9
Method	BLASTX
NCBI GI	g4204267
BLAST score	461
E value	3.0e-46
Match length	114
% identity	77
NCBI Description	(AC005223) 55585 [Arabidopsis thaliana]

Seq. No.	221422
Seq. ID	LIB3165-009-P1-K1-C1
Method	BLASTX
NCBI GI	g551428
BLAST score	188
E value	3.0e-14
Match length	108
% identity	40
NCBI Description	(X78996) tetrafunctional protein [Cucumis sativus]

Seq. No.	221423
Seq. ID	LIB3165-009-P1-K1-C4
Method	BLASTX
NCBI GI	g115705
BLAST score	479
E value	2.0e-48
Match length	105
% identity	87
NCBI Description	CATALASE >gi_279448_pir__CSPM catalase (EC 1.11.1.6) - garden pea >gi_20677_emb_CAA42736_ (X60169) catalase [Pisum sativum]

Seq. No.	221424
Seq. ID	LIB3165-009-P1-K1-C7
Method	BLASTX
NCBI GI	g4406530
BLAST score	293
E value	2.0e-26

Match length 104
% identity 62
NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 221425
Seq. ID LIB3165-009-P1-K1-C8
Method BLASTX
NCBI GI g2306917
BLAST score 301
E value 1.0e-27
Match length 71
% identity 86
NCBI Description (AF003728) plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No. 221426
Seq. ID LIB3165-009-P1-K1-D10
Method BLASTX
NCBI GI g4406530
BLAST score 302
E value 1.0e-27
Match length 107
% identity 62
NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 221427
Seq. ID LIB3165-009-P1-K1-D11
Method BLASTX
NCBI GI g4115357
BLAST score 190
E value 2.0e-14
Match length 90
% identity 44
NCBI Description (AC005957) hypothetical protein [Arabidopsis thaliana]

Seq. No. 221428
Seq. ID LIB3165-009-P1-K1-D12
Method BLASTX
NCBI GI g3928760
BLAST score 223
E value 3.0e-18
Match length 108
% identity 48
NCBI Description (AB011797) homolog to plastid-lipid-associated protein [Citrus unshiu]

Seq. No. 221429
Seq. ID LIB3165-009-P1-K1-D4
Method BLASTX
NCBI GI g2661021
BLAST score 566
E value 2.0e-58
Match length 110
% identity 96
NCBI Description (AF035255) catalase [Glycine max]

Seq. No. 221430

Seq. ID	LIB3165-009-P1-K1-D5
Method	BLASTX
NCBI GI	g1352821
BLAST score	486
E value	4.0e-49
Match length	94
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221431
Seq. ID	LIB3165-009-P1-K1-D6
Method	BLASTX
NCBI GI	g4455208
BLAST score	309
E value	2.0e-28
Match length	117
% identity	59
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	221432
Seq. ID	LIB3165-009-P1-K1-D7
Method	BLASTX
NCBI GI	g1709690
BLAST score	318
E value	2.0e-29
Match length	87
% identity	70
NCBI Description	PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PEPTIDE MET(O) REDUCTASE) >gi_1076454_pir__S55365 probable peptide methionine sulfoxide reductase - rape >gi_853739_emb_CAA88538_ (Z48619) peptide methionine sulfoxide reductase [Brassica napus] >gi_1143406_emb_CAA63919_ (X94225) methionine sulfoxide reductase [Brassica napus]

Seq. No.	221433
Seq. ID	LIB3165-009-P1-K1-D8
Method	BLASTX
NCBI GI	g3298548
BLAST score	434
E value	5.0e-43
Match length	115
% identity	71
NCBI Description	(AC004681) putative spliceosomal protein [Arabidopsis thaliana]

Seq. No.	221434
Seq. ID	LIB3165-009-P1-K1-D9
Method	BLASTN
NCBI GI	g18058
BLAST score	293
E value	1.0e-164
Match length	357

% identity	96
NCBI Description	Citrus limon cistron for 26S ribosomal RNA

Seq. No.	221435
Seq. ID	LIB3165-009-P1-K1-E3
Method	BLASTX
NCBI GI	g132794
BLAST score	437
E value	2.0e-43
Match length	112
% identity	75
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L22 >gi_71288_pir__R5NT22 ribosomal protein L22 - common tobacco chloroplast >gi_11866_emb_CAA77382_ (Z00044) ribosomal protein L22 [Nicotiana tabacum] >gi_225236_prf__1211235BU ribosomal protein L22 [Nicotiana tabacum]

Seq. No.	221436
Seq. ID	LIB3165-009-P1-K1-E6
Method	BLASTX
NCBI GI	g81548
BLAST score	433
E value	6.0e-43
Match length	110
% identity	77
NCBI Description	catalase (EC 1.11.1.6) chain 1 - upland cotton

Seq. No.	221437
Seq. ID	LIB3165-009-P1-K1-E7
Method	BLASTX
NCBI GI	g166834
BLAST score	631
E value	4.0e-66
Match length	128
% identity	95
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	221438
Seq. ID	LIB3165-009-P1-K1-E8
Method	BLASTX
NCBI GI	g1352821
BLAST score	546
E value	3.0e-56
Match length	114
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221439
Seq. ID	LIB3165-009-P1-K1-E9
Method	BLASTX
NCBI GI	g3550519

BLAST score 367
E value 3.0e-35
Match length 106
% identity 63
NCBI Description (AJ007630) oxygenase [Nicotiana tabacum]

Seq. No. 221440
Seq. ID LIB3165-009-P1-K1-F10
Method BLASTX
NCBI GI g1352821
BLAST score 574
E value 2.0e-59
Match length 112
% identity 99
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221441
Seq. ID LIB3165-009-P1-K1-F11
Method BLASTX
NCBI GI g2661021
BLAST score 525
E value 1.0e-53
Match length 109
% identity 92
NCBI Description (AF035255) catalase [Glycine max]

Seq. No. 221442
Seq. ID LIB3165-009-P1-K1-F3
Method BLASTX
NCBI GI g4415992
BLAST score 607
E value 2.0e-63
Match length 121
% identity 96
NCBI Description (AF059288) beta-tubulin 2 [Eleusine indica]

Seq. No. 221443
Seq. ID LIB3165-009-P1-K1-F8
Method BLASTX
NCBI GI g4454458
BLAST score 276
E value 2.0e-24
Match length 104
% identity 60
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 221444
Seq. ID LIB3165-009-P1-K1-G10
Method BLASTX
NCBI GI g1354515
BLAST score 220
E value 6.0e-18
Match length 101

% identity	50
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	221445
Seq. ID	LIB3165-009-P1-K1-G3
Method	BLASTX
NCBI GI	g131384
BLAST score	311
E value	1.0e-28
Match length	75
% identity	80
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_81934_pir__S04132 photosystem II oxygen-evolving complex protein 1 precursor - garden pea >gi_20621_emb_CAA33408_ (X15350) precursor (AA -81 to 248) [Pisum sativum] >gi_344004_dbj_BAA02554_ (D13297) precursor for 33-kDa protein of photosystem II [Pisum sativum] >gi_226937_prf__1611461A O2 evolving complex 33kD protein [Arachis hypogaea]

Seq. No.	221446
Seq. ID	LIB3165-009-P1-K1-G5
Method	BLASTX
NCBI GI	g1352821
BLAST score	479
E value	4.0e-50
Match length	108
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221447
Seq. ID	LIB3165-009-P1-K1-G7
Method	BLASTX
NCBI GI	g1256595
BLAST score	369
E value	2.0e-35
Match length	106
% identity	65
NCBI Description	(U38915) LytB [Synechocystis PCC6803]

Seq. No.	221448
Seq. ID	LIB3165-009-P1-K1-G8
Method	BLASTX
NCBI GI	g20729
BLAST score	462
E value	2.0e-46
Match length	125
% identity	75
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	221449

Seq. ID	LIB3165-009-P1-K1-H10
Method	BLASTX
NCBI GI	g3860323
BLAST score	377
E value	2.0e-36
Match length	78
% identity	88
NCBI Description	(AJ012688) hypothetical protein [Cicer arietinum]

Seq. No.	221450
Seq. ID	LIB3165-009-P1-K1-H11
Method	BLASTX
NCBI GI	g131167
BLAST score	311
E value	1.0e-28
Match length	120
% identity	62
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_100292_pir__S18348 photosystem I chain II precursor - wood tobacco >gi_19748_emb_CAA42623_ (X60008) PSI-D2 [Nicotiana sylvestris]

Seq. No.	221451
Seq. ID	LIB3165-009-P1-K1-H3
Method	BLASTN
NCBI GI	g18058
BLAST score	76
E value	1.0e-34
Match length	260
% identity	83
NCBI Description	Citrus limon cistron for 26S ribosomal RNA

Seq. No.	221452
Seq. ID	LIB3165-009-P1-K1-H5
Method	BLASTX
NCBI GI	g3096949
BLAST score	397
E value	1.0e-38
Match length	121
% identity	60
NCBI Description	(Y16328) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic nucleotide-gated cation channel [Arabidopsis thaliana]

Seq. No.	221453
Seq. ID	LIB3165-009-P1-K1-H7
Method	BLASTX
NCBI GI	g3914940
BLAST score	389
E value	9.0e-38
Match length	128
% identity	65
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_2529376 (L76556) sedoheptulose-1,7-bisphosphatase [Spinacia oleracea]

Seq. No.	221454
Seq. ID	LIB3165-009-P1-K1-H9
Method	BLASTX
NCBI GI	g2245066
BLAST score	348
E value	6.0e-33
Match length	117
% identity	53
NCBI Description	(Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No.	221455
Seq. ID	LIB3165-011-P1-K1-A11
Method	BLASTX
NCBI GI	g169199
BLAST score	143
E value	3.0e-09
Match length	48
% identity	33
NCBI Description	(K00973) Major Cab protein [Petunia sp.]

Seq. No.	221456
Seq. ID	LIB3165-011-P1-K1-A2
Method	BLASTX
NCBI GI	g3023752
BLAST score	280
E value	6.0e-25
Match length	103
% identity	58
NCBI Description	FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520) ferredoxin-I [Lycopersicon esculentum]

Seq. No.	221457
Seq. ID	LIB3165-011-P1-K1-A3
Method	BLASTX
NCBI GI	g4406530
BLAST score	349
E value	5.0e-33
Match length	118
% identity	63
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221458
Seq. ID	LIB3165-011-P1-K1-A4
Method	BLASTN
NCBI GI	g2687430
BLAST score	42
E value	6.0e-15
Match length	86
% identity	87
NCBI Description	Acorus gramineus large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	221459
Seq. ID	LIB3165-011-P1-K1-A7
Method	BLASTX
NCBI GI	g1352821

BLAST score	554
E value	5.0e-57
Match length	108
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221460
Seq. ID	LIB3165-011-P1-K1-A8
Method	BLASTX
NCBI GI	g541979
BLAST score	313
E value	9.0e-29
Match length	79
% identity	80
NCBI Description	guanine nucleotide regulatory protein - fava bean >gi_303744_dbj_BAA02113_ (D12545) GTP-binding protein [Pisum sativum] >gi_452361_emb_CAA82709_ (Z29592) guanine nucleotide regulatory protein [Vicia faba] >gi_738937_prf__2001457E GTP-binding protein [Pisum sativum] >gi_1098295_prf__2115367C small GTP-binding protein [Vicia faba]

Seq. No.	221461
Seq. ID	LIB3165-011-P1-K1-A9
Method	BLASTX
NCBI GI	g289920
BLAST score	678
E value	1.0e-71
Match length	128
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221462
Seq. ID	LIB3165-011-P1-K1-B1
Method	BLASTX
NCBI GI	g1346155
BLAST score	639
E value	5.0e-67
Match length	138
% identity	89
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_481942_pir__S40212 glycine hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei >gi_437995_emb_CAA81078_ (Z25859) glycine hydroxymethyltransferase [Flaveria pringlei]

Seq. No.	221463
Seq. ID	LIB3165-011-P1-K1-B11
Method	BLASTX
NCBI GI	g2677828
BLAST score	460

E value	5.0e-46
Match length	131
% identity	66
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	221464
Seq. ID	LIB3165-011-P1-K1-B2
Method	BLASTX
NCBI GI	g2911085
BLAST score	341
E value	5.0e-32
Match length	134
% identity	57
NCBI Description	(AL021960) photosystem II oxygen-evolving complex protein 3 - like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_ (AL031187) photosystem II oxygen-evolving complex protein 3 - like [Arabidopsis thaliana]

Seq. No.	221465
Seq. ID	LIB3165-011-P1-K1-B4
Method	BLASTX
NCBI GI	g231688
BLAST score	237
E value	4.0e-21
Match length	99
% identity	63
NCBI Description	CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC 1.11.1.6) - upland cotton >gi_18488_emb_CAA39998_ (X56675) subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No.	221466
Seq. ID	LIB3165-011-P1-K1-B6
Method	BLASTX
NCBI GI	g100615
BLAST score	261
E value	8.0e-23
Match length	115
% identity	48
NCBI Description	ribulose-bisphosphate carboxylase activase A short form precursor - barley >gi_167091 (M55447) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	221467
Seq. ID	LIB3165-011-P1-K1-B7
Method	BLASTX
NCBI GI	g4115726
BLAST score	152
E value	6.0e-10
Match length	115
% identity	32
NCBI Description	(AB015947) aquaporin-4 [Bos taurus]

Seq. No.	221468
Seq. ID	LIB3165-011-P1-K1-B8
Method	BLASTX
NCBI GI	g1053216
BLAST score	486

E value	4.0e-49
Match length	92
% identity	98
NCBI Description	(U39475) chlorophyll a/b-binding protein [Glycine max]

Seq. No.	221469
Seq. ID	LIB3165-011-P1-K1-C12
Method	BLASTX
NCBI GI	g289920
BLAST score	450
E value	6.0e-45
Match length	112
% identity	79
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221470
Seq. ID	LIB3165-011-P1-K1-C2
Method	BLASTX
NCBI GI	g1352821
BLAST score	604
E value	7.0e-63
Match length	112
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221471
Seq. ID	LIB3165-011-P1-K1-C3
Method	BLASTX
NCBI GI	g505482
BLAST score	524
E value	2.0e-53
Match length	139
% identity	78
NCBI Description	(X64349) 33 kDa polypeptide of water-oxidizing complex of photosystem II [Nicotiana tabacum]

Seq. No.	221472
Seq. ID	LIB3165-011-P1-K1-C6
Method	BLASTX
NCBI GI	g4539335
BLAST score	262
E value	8.0e-23
Match length	132
% identity	44
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	221473
Seq. ID	LIB3165-011-P1-K1-C8
Method	BLASTX
NCBI GI	g166835
BLAST score	729
E value	1.0e-77

Match length	141
% identity	97
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642170 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	221474
Seq. ID	LIB3165-011-P1-K1-D1
Method	BLASTX
NCBI GI	g3128177
BLAST score	529
E value	4.0e-54
Match length	125
% identity	82
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	221475
Seq. ID	LIB3165-011-P1-K1-D10
Method	BLASTX
NCBI GI	g417103
BLAST score	654
E value	9.0e-69
Match length	131
% identity	100
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	221476
Seq. ID	LIB3165-011-P1-K1-D11
Method	BLASTX
NCBI GI	g2462931
BLAST score	512
E value	3.0e-52
Match length	102
% identity	90
NCBI Description	(Z83833) UDP-glucose:sterol glucosyltransferase [Arabidopsis thaliana]

Seq. No.	221477
Seq. ID	LIB3165-011-P1-K1-D2

Method	BLASTX
NCBI GI	g3122232
BLAST score	278
E value	1.0e-24
Match length	105
% identity	58
NCBI Description	MITOCHONDRIAL HEAT SHOCK 22 KD PROTEIN PRECURSOR >gi_1669866 (U72958) AtHSP23.6-mito [Arabidopsis thaliana] >gi_4454008_emb_CAA23061_ (AL035396) Arabidopsis mitochondrion-localized small heat shock protein (AtHSP23.6-mito) [Arabidopsis thaliana]

Seq. No.	221478
Seq. ID	LIB3165-011-P1-K1-D6
Method	BLASTX
NCBI GI	g1935914
BLAST score	184
E value	1.0e-13
Match length	63
% identity	56
NCBI Description	(U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana]

Seq. No.	221479
Seq. ID	LIB3165-011-P1-K1-D8
Method	BLASTX
NCBI GI	g289920
BLAST score	699
E value	4.0e-74
Match length	130
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221480
Seq. ID	LIB3165-011-P1-K1-D9
Method	BLASTX
NCBI GI	g2970051
BLAST score	421
E value	2.0e-41
Match length	113
% identity	71
NCBI Description	(AB012110) ARG10 [Vigna radiata]

Seq. No.	221481
Seq. ID	LIB3165-011-P1-K1-E10
Method	BLASTX
NCBI GI	g2501578
BLAST score	619
E value	1.0e-64
Match length	132
% identity	95
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No.	221482

Seq. ID	LIB3165-011-P1-K1-E12
Method	BLASTX
NCBI GI	g1168411
BLAST score	529
E value	4.0e-54
Match length	128
% identity	84
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	221483
Seq. ID	LIB3165-011-P1-K1-E3
Method	BLASTX
NCBI GI	g3023281
BLAST score	429
E value	2.0e-42
Match length	131
% identity	63
NCBI Description	HIGH AFFINITY AMMONIUM TRANSPORTER >gi_2065194_emb_CAA64475_ (X95098) ammonium transporter [Lycopersicon esculentum]

Seq. No.	221484
Seq. ID	LIB3165-011-P1-K1-E5
Method	BLASTX
NCBI GI	g3702332
BLAST score	235
E value	1.0e-19
Match length	80
% identity	54
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	221485
Seq. ID	LIB3165-011-P1-K1-E6
Method	BLASTX
NCBI GI	g4467158
BLAST score	281
E value	5.0e-25
Match length	125
% identity	57
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	221486
Seq. ID	LIB3165-011-P1-K1-E8
Method	BLASTX
NCBI GI	g20729
BLAST score	508
E value	1.0e-51
Match length	134
% identity	78
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	221487
Seq. ID	LIB3165-011-P1-K1-E9
Method	BLASTX
NCBI GI	g1332579
BLAST score	578
E value	7.0e-60

Match length	116
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	221488
Seq. ID	LIB3165-011-P1-K1-F1
Method	BLASTX
NCBI GI	g1708313
BLAST score	475
E value	8.0e-48
Match length	100
% identity	95
NCBI Description	HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi_999396_bbs_163637 (S77849) heat-shock Protein=HSP81-3 [Arabidopsis thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis thaliana]

Seq. No.	221489
Seq. ID	LIB3165-011-P1-K1-F12
Method	BLASTX
NCBI GI	g2501568
BLAST score	177
E value	8.0e-13
Match length	55
% identity	55
NCBI Description	HYPOTHETICAL 28.8 KD PROTEIN SLL0506 >gi_1001342_dbj_BAA10829_ (D64006) hypothetical protein [Synechocystis sp.]

Seq. No.	221490
Seq. ID	LIB3165-011-P1-K1-F2
Method	BLASTX
NCBI GI	g1352821
BLAST score	742
E value	4.0e-79
Match length	141
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221491
Seq. ID	LIB3165-011-P1-K1-F4
Method	BLASTX
NCBI GI	g266893
BLAST score	564
E value	3.0e-58
Match length	122
% identity	91
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__S28172 ribulose-bisphosphate carboxylase activase - cucumber >gi_18284_emb_CAA47906_ (X67674) rubisco activase [Cucumis sativus]

Seq. No.	221492
Seq. ID	LIB3165-011-P1-K1-F5
Method	BLASTX
NCBI GI	g1352821
BLAST score	600
E value	2.0e-62
Match length	114
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221493
Seq. ID	LIB3165-011-P1-K1-F7
Method	BLASTX
NCBI GI	g3212852
BLAST score	259
E value	2.0e-22
Match length	98
% identity	53
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	221494
Seq. ID	LIB3165-011-P1-K1-F8
Method	BLASTX
NCBI GI	g1168411
BLAST score	545
E value	5.0e-56
Match length	135
% identity	82
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	221495
Seq. ID	LIB3165-011-P1-K1-G1
Method	BLASTX
NCBI GI	g68200
BLAST score	379
E value	2.0e-36
Match length	99
% identity	80
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	221496
Seq. ID	LIB3165-011-P1-K1-G10
Method	BLASTX
NCBI GI	g1483218
BLAST score	182
E value	2.0e-13
Match length	102
% identity	41
NCBI Description	(X99793) induced upon wounding stress [Arabidopsis thaliana]

Seq. No.	221497
Seq. ID	LIB3165-011-P1-K1-G11
Method	BLASTX
NCBI GI	g1352821
BLAST score	594
E value	1.0e-61
Match length	111
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221498
Seq. ID	LIB3165-011-P1-K1-G12
Method	BLASTX
NCBI GI	g20729
BLAST score	405
E value	1.0e-39
Match length	108
% identity	75
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	221499
Seq. ID	LIB3165-011-P1-K1-G2
Method	BLASTX
NCBI GI	g1703129
BLAST score	553
E value	6.0e-57
Match length	103
% identity	98
NCBI Description	ACTIN 11 >gi_2129522_pir__S68109 actin 11 - Arabidopsis thaliana >gi_1002533 (U27981) actin-11 [Arabidopsis thaliana]

Seq. No.	221500
Seq. ID	LIB3165-011-P1-K1-G4
Method	BLASTX
NCBI GI	g231610
BLAST score	395
E value	2.0e-38
Match length	128
% identity	66
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]

Seq. No.	221501
Seq. ID	LIB3165-011-P1-K1-G5
Method	BLASTX
NCBI GI	g131384
BLAST score	534
E value	8.0e-55
Match length	115

% identity	91
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_81934_pir__S04132 photosystem II oxygen-evolving complex protein 1 precursor - garden pea >gi_20621_emb_CAA33408_ (X15350) precursor (AA -81 to 248) [Pisum sativum] >gi_344004_dbj_BAA02554_ (D13297) precursor for 33-kDa protein of photosystem II [Pisum sativum] >gi_226937_prf__1611461A O2 evolving complex 33kD protein [Arachis hypogaea]
Seq. No.	221502
Seq. ID	LIB3165-011-P1-K1-G6
Method	BLASTX
NCBI GI	g1781348
BLAST score	645
E value	1.0e-67
Match length	140
% identity	89
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]
Seq. No.	221503
Seq. ID	LIB3165-011-P1-K1-H1
Method	BLASTX
NCBI GI	g4105798
BLAST score	229
E value	6.0e-19
Match length	61
% identity	61
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]
Seq. No.	221504
Seq. ID	LIB3165-011-P1-K1-H10
Method	BLASTX
NCBI GI	g1351630
BLAST score	254
E value	7.0e-22
Match length	104
% identity	48
NCBI Description	PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE) >gi_2130253_pir__S62537 hypothetical protein SPAC12G12.06c - fission yeast (Schizosaccharomyces pombe) >gi_1052524_emb_CAA91501_ (Z66568) SPAC12G12.06c, unknown, len: 363 [Schizosaccharomyces pombe]
Seq. No.	221505
Seq. ID	LIB3165-011-P1-K1-H11
Method	BLASTX
NCBI GI	g3738261
BLAST score	212
E value	5.0e-17
Match length	54
% identity	83
NCBI Description	(AB018412) chloroplast phosphoglycerate kinase [Populus nigra]

Seq. No.	221506
Seq. ID	LIB3165-011-P1-K1-H4
Method	BLASTX
NCBI GI	g4490728
BLAST score	324
E value	4.0e-30
Match length	99
% identity	64
NCBI Description	(AL035709) putative protein [Arabidopsis thaliana]

Seq. No.	221507
Seq. ID	LIB3165-011-P1-K1-H9
Method	BLASTN
NCBI GI	g16472
BLAST score	41
E value	9.0e-14
Match length	228
% identity	79
NCBI Description	A.thaliana rRNA repeat unit, most frequent IGR type

Seq. No.	221508
Seq. ID	LIB3165-012-P1-K1-A10
Method	BLASTX
NCBI GI	g2864617
BLAST score	266
E value	3.0e-23
Match length	124
% identity	52
NCBI Description	(AL021811) H+-transporting ATP synthase chain9 - like protein [Arabidopsis thaliana]

Seq. No.	221509
Seq. ID	LIB3165-012-P1-K1-A2
Method	BLASTX
NCBI GI	g4406530
BLAST score	355
E value	1.0e-33
Match length	98
% identity	74
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221510
Seq. ID	LIB3165-012-P1-K1-A3
Method	BLASTX
NCBI GI	g115470
BLAST score	259
E value	9.0e-23
Match length	91
% identity	60
NCBI Description	CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) >gi_320554_pir__S28412 carbonate dehydratase (EC 4.2.1.1) precursor - Arabidopsis thaliana >gi_14343_emb_CAA46508_ (X65541) carbonic anhydrase [Arabidopsis thaliana]

Seq. No.	221511

Seq. ID	LIB3165-012-P1-K1-A6
Method	BLASTX
NCBI GI	g1168411
BLAST score	537
E value	4.0e-55
Match length	127
% identity	87
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	221512
Seq. ID	LIB3165-012-P1-K1-A9
Method	BLASTX
NCBI GI	g1352821
BLAST score	539
E value	3.0e-55
Match length	102
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221513
Seq. ID	LIB3165-012-P1-K1-B10
Method	BLASTX
NCBI GI	g1709651
BLAST score	391
E value	6.0e-38
Match length	119
% identity	65
NCBI Description	PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209 plastocyanin a precursor - black poplar >gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus nigra]

Seq. No.	221514
Seq. ID	LIB3165-012-P1-K1-B2
Method	BLASTX
NCBI GI	g20729
BLAST score	383
E value	4.0e-37
Match length	106
% identity	74
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	221515
Seq. ID	LIB3165-012-P1-K1-B4
Method	BLASTX
NCBI GI	g4406530
BLAST score	247
E value	2.0e-28
Match length	92
% identity	68
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221516

Seq. ID	LIB3165-012-P1-K1-B5
Method	BLASTX
NCBI GI	g1199772
BLAST score	284
E value	2.0e-25
Match length	120
% identity	56
NCBI Description	(D83226) extensin like protein [Populus nigra] >gi_1199774_dbj_BAA11855_ (D83227) extensin like protein [Populus nigra]

Seq. No.	221517
Seq. ID	LIB3165-012-P1-K1-B8
Method	BLASTX
NCBI GI	g3335341
BLAST score	149
E value	1.0e-09
Match length	109
% identity	42
NCBI Description	(AC004512) T8F5.10 [Arabidopsis thaliana]

Seq. No.	221518
Seq. ID	LIB3165-012-P1-K1-C12
Method	BLASTX
NCBI GI	g4454466
BLAST score	197
E value	3.0e-15
Match length	52
% identity	69
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	221519
Seq. ID	LIB3165-012-P1-K1-C3
Method	BLASTX
NCBI GI	g68200
BLAST score	381
E value	6.0e-37
Match length	102
% identity	79
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	221520
Seq. ID	LIB3165-012-P1-K1-C5
Method	BLASTX
NCBI GI	g131385
BLAST score	525
E value	1.0e-53
Match length	127
% identity	84
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN)

Seq. No.	221521
Seq. ID	LIB3165-012-P1-K1-C6

Method	BLASTX
NCBI GI	g1172664
BLAST score	175
E value	1.0e-12
Match length	37
% identity	92
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_419791_pir__S31165 photosystem I chain III precursor - Flaveria trinervia >gi_298482_bbs_127083 photosystem I reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem I subunit III [Flaveria trinervia]

Seq. No.	221522
Seq. ID	LIB3165-012-P1-K1-C7
Method	BLASTX
NCBI GI	g1168728
BLAST score	339
E value	8.0e-32
Match length	116
% identity	53
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_598071 (L37883) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	221523
Seq. ID	LIB3165-012-P1-K1-C8
Method	BLASTX
NCBI GI	g487046
BLAST score	264
E value	4.0e-23
Match length	109
% identity	49
NCBI Description	photosystem I chain II precursor - wood tobacco >gi_407769_dbj_BAA02871_ (D13718) PSI-D1 precursor [Nicotiana sylvestris]

Seq. No.	221524
Seq. ID	LIB3165-012-P1-K1-D1
Method	BLASTX
NCBI GI	g4481934
BLAST score	143
E value	7.0e-09
Match length	101
% identity	15
NCBI Description	(AL035640) CDA peptide synthetase I [Streptomyces coelicolor]

Seq. No.	221525
Seq. ID	LIB3165-012-P1-K1-D10
Method	BLASTX
NCBI GI	g4545262
BLAST score	165
E value	2.0e-11
Match length	44
% identity	66
NCBI Description	(AF118230) metallothionein-like protein [Gossypium

hirsutum]

Seq. No.	221526
Seq. ID	LIB3165-012-P1-K1-D11
Method	BLASTX
NCBI GI	g3123271
BLAST score	497
E value	2.0e-50
Match length	114
% identity	84
NCBI Description	40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No.	221527
Seq. ID	LIB3165-012-P1-K1-D12
Method	BLASTX
NCBI GI	g1617206
BLAST score	344
E value	2.0e-32
Match length	78
% identity	78
NCBI Description	(Z72489) CP12 [Pisum sativum]

Seq. No.	221528
Seq. ID	LIB3165-012-P1-K1-D2
Method	BLASTX
NCBI GI	g542020
BLAST score	348
E value	4.0e-45
Match length	121
% identity	77
NCBI Description	sucrose transport protein - castor bean >gi_468562_emb_CAA83436_ (Z31561) sucrose carrier [Ricinus communis]

Seq. No.	221529
Seq. ID	LIB3165-012-P1-K1-D5
Method	BLASTX
NCBI GI	g282833
BLAST score	296
E value	8.0e-27
Match length	73
% identity	84
NCBI Description	phosphoglycerate kinase (EC 2.7.2.3) - spinach (fragment)

Seq. No.	221530
Seq. ID	LIB3165-012-P1-K1-D6
Method	BLASTX
NCBI GI	g693916
BLAST score	171
E value	3.0e-12
Match length	66
% identity	59
NCBI Description	(U21111) chlorophyll a/b binding protein [Solanum tuberosum]

Seq. No. 221531

Seq. ID	LIB3165-012-P1-K1-D7
Method	BLASTX
NCBI GI	g3831458
BLAST score	133
E value	3.0e-16
Match length	114
% identity	36
NCBI Description	(AC005700) hypothetical protein [Arabidopsis thaliana]

Seq. No.	221532
Seq. ID	LIB3165-012-P1-K1-E10
Method	BLASTX
NCBI GI	g3193326
BLAST score	171
E value	3.0e-12
Match length	83
% identity	52
NCBI Description	(AF069299) contains similarity to transcriptional activators such as Ra-like and myc-like regulatory R proteins [Arabidopsis thaliana]

Seq. No.	221533
Seq. ID	LIB3165-012-P1-K1-E11
Method	BLASTX
NCBI GI	g1352683
BLAST score	163
E value	3.0e-11
Match length	46
% identity	72
NCBI Description	PROTEIN PHOSPHATASE 2C PPH1 (PP2C) >gi_995839 (U34803) protein phosphatase homolog [Arabidopsis thaliana]

Seq. No.	221534
Seq. ID	LIB3165-012-P1-K1-E12
Method	BLASTX
NCBI GI	g3377812
BLAST score	194
E value	7.0e-15
Match length	62
% identity	68
NCBI Description	(AF076275) contains similarity to heavy-metal-associated domain containing proteins (Pfam: HMA.hm, score: 12.02) [Arabidopsis thaliana]

Seq. No.	221535
Seq. ID	LIB3165-012-P1-K1-E2
Method	BLASTX
NCBI GI	g1408471
BLAST score	535
E value	7.0e-55
Match length	120
% identity	82
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	221536

Seq. ID	LIB3165-012-P1-K1-E3
Method	BLASTX
NCBI GI	g131187
BLAST score	301
E value	2.0e-27
Match length	132
% identity	55
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_72681_pir__F1SP3 photosystem I chain III precursor - spinach >gi_21303_emb_CAA31523_ (X13133) PSI subunit IV preprotein (AA -77 to 154) [Spinacia oleracea] >gi_226166_prf__1413236A photosystem I reaction center IV [Spinacia oleracea]

Seq. No.	221537
Seq. ID	LIB3165-012-P1-K1-E5
Method	BLASTX
NCBI GI	g4510373
BLAST score	266
E value	3.0e-23
Match length	72
% identity	71
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]

Seq. No.	221538
Seq. ID	LIB3165-012-P1-K1-E6
Method	BLASTX
NCBI GI	g1130682
BLAST score	323
E value	5.0e-30
Match length	62
% identity	100
NCBI Description	(Z46959) acetohydroxyacid synthase [Gossypium hirsutum]

Seq. No.	221539
Seq. ID	LIB3165-012-P1-K1-E7
Method	BLASTX
NCBI GI	g2209332
BLAST score	610
E value	1.0e-63
Match length	133
% identity	86
NCBI Description	(U89272) chloroplast membrane protein ALBINO3 [Arabidopsis thaliana] >gi_3927828 (AC005727) chloroplast membrane protein ALBINO3 [Arabidopsis thaliana]

Seq. No.	221540
Seq. ID	LIB3165-012-P1-K1-E8
Method	BLASTN
NCBI GI	g2687434
BLAST score	307
E value	1.0e-172
Match length	367
% identity	96
NCBI Description	Eucryphia lucida large subunit 26S ribosomal RNA gene,

partial sequence

Seq. No.	221541
Seq. ID	LIB3165-012-P1-K1-E9
Method	BLASTX
NCBI GI	g4406530
BLAST score	329
E value	1.0e-30
Match length	92
% identity	74
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221542
Seq. ID	LIB3165-012-P1-K1-F10
Method	BLASTX
NCBI GI	g1706107
BLAST score	632
E value	3.0e-66
Match length	130
% identity	95
NCBI Description	CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT) >gi_1143709 (U13630) chloroplast phosphate/triose-phosphate translocator precursor [Brassica oleracea]

Seq. No.	221543
Seq. ID	LIB3165-012-P1-K1-F11
Method	BLASTX
NCBI GI	g421826
BLAST score	291
E value	2.0e-26
Match length	57
% identity	88
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	221544
Seq. ID	LIB3165-012-P1-K1-F3
Method	BLASTX
NCBI GI	g1168408
BLAST score	574
E value	2.0e-59
Match length	128
% identity	89
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1 >gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828) fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No.	221545
Seq. ID	LIB3165-012-P1-K1-F6
Method	BLASTX
NCBI GI	g1352821
BLAST score	671
E value	8.0e-71
Match length	126
% identity	95

NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221546
Seq. ID	LIB3165-012-P1-K1-F7
Method	BLASTX
NCBI GI	g4105794
BLAST score	200
E value	2.0e-15
Match length	45
% identity	62
NCBI Description	(AF049928) PGP224 [Petunia x hybrida]

Seq. No.	221547
Seq. ID	LIB3165-012-P1-K1-F9
Method	BLASTX
NCBI GI	g4008159
BLAST score	269
E value	8.0e-24
Match length	84
% identity	64
NCBI Description	(AB015601) DnaJ homolog [Salix gilgiana]

Seq. No.	221548
Seq. ID	LIB3165-012-P1-K1-G3
Method	BLASTX
NCBI GI	g462195
BLAST score	432
E value	9.0e-43
Match length	93
% identity	91
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir__S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No.	221549
Seq. ID	LIB3165-012-P1-K1-G5
Method	BLASTX
NCBI GI	g1653089
BLAST score	305
E value	7.0e-28
Match length	89
% identity	63
NCBI Description	(D90911) hypothetical protein [Synechocystis sp.]

Seq. No.	221550
Seq. ID	LIB3165-012-P1-K1-G6
Method	BLASTX
NCBI GI	g1170711
BLAST score	394
E value	2.0e-38
Match length	92

% identity	86
NCBI Description	SHAGGY RELATED PROTEIN KINASE ASK-ALPHA >gi_541901_pir__S41596 protein kinase ASK-alpha (EC 2.7.1.-) - Arabidopsis thaliana >gi_460832_emb_CAA53181_ (X75432) shaggy related kinase [Arabidopsis thaliana] >gi_1769889_emb_CAA48538_ (X68525) serine /threonine protein kinase [Arabidopsis thaliana]
Seq. No.	221551
Seq. ID	LIB3165-012-P1-K1-G7
Method	BLASTX
NCBI GI	g3288821
BLAST score	557
E value	2.0e-57
Match length	133
% identity	78
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana]
Seq. No.	221552
Seq. ID	LIB3165-012-P1-K1-G8
Method	BLASTX
NCBI GI	g4468979
BLAST score	278
E value	6.0e-25
Match length	54
% identity	94
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]
Seq. No.	221553
Seq. ID	LIB3165-012-P1-K1-H10
Method	BLASTX
NCBI GI	g4406530
BLAST score	296
E value	2.0e-27
Match length	59
% identity	95
NCBI Description	(AF126870) rubisco activase [Vigna radiata]
Seq. No.	221554
Seq. ID	LIB3165-012-P1-K1-H11
Method	BLASTN
NCBI GI	g2687435
BLAST score	262
E value	1.0e-145
Match length	350
% identity	95
NCBI Description	Hamamelis virginiana large subunit 26S ribosomal RNA gene; partial sequence
Seq. No.	221555
Seq. ID	LIB3165-012-P1-K1-H5
Method	BLASTX
NCBI GI	g2662343
BLAST score	587
E value	6.0e-61
Match length	116

% identity	97
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	221556
Seq. ID	LIB3165-012-P1-K1-H7
Method	BLASTX
NCBI GI	g3202032
BLAST score	263
E value	4.0e-23
Match length	96
% identity	41
NCBI Description	(AF069319) leaf catalase [Mesembryanthemum crystallinum]

Seq. No.	221557
Seq. ID	LIB3165-012-P1-K1-H8
Method	BLASTX
NCBI GI	g1791309
BLAST score	203
E value	5.0e-16
Match length	106
% identity	50
NCBI Description	(U83500) cystathionine gamma-synthase [Arabidopsis thaliana] >gi_2852454_dbj_BAA24699_ (AB010888) cystathionine gamma-synthase [Arabidopsis thaliana]

Seq. No.	221558
Seq. ID	LIB3165-012-P1-K1-H9
Method	BLASTX
NCBI GI	g1684857
BLAST score	596
E value	5.0e-62
Match length	120
% identity	40
NCBI Description	(U77940) polyubiquitin [Phaseolus vulgaris]

Seq. No.	221559
Seq. ID	LIB3165-013-P1-K1-A2
Method	BLASTX
NCBI GI	g115765
BLAST score	734
E value	4.0e-78
Match length	143
% identity	65
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	221560
Seq. ID	LIB3165-013-P1-K1-A6
Method	BLASTX
NCBI GI	g4406530
BLAST score	627

E value	1.0e-65
Match length	132
% identity	88
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221561
Seq. ID	LIB3165-013-P1-K1-A7
Method	BLASTX
NCBI GI	g1172664
BLAST score	207
E value	2.0e-16
Match length	45
% identity	91
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_419791_pir__S31165 photosystem I chain III precursor - Flaveria trinervia >gi_298482_bbs_127083 photosystem I reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem I subunit III [Flaveria trinervia]

Seq. No.	221562
Seq. ID	LIB3165-013-P1-K1-B1
Method	BLASTX
NCBI GI	g2956717
BLAST score	268
E value	2.0e-23
Match length	117
% identity	55
NCBI Description	(Y09722) beta-carotene hydroxylase 2 [Capsicum annuum]

Seq. No.	221563
Seq. ID	LIB3165-013-P1-K1-B11
Method	BLASTX
NCBI GI	g2738756
BLAST score	549
E value	3.0e-63
Match length	130
% identity	94
NCBI Description	(AF016282) 5'-adenylylsulfate reductase [Arabidopsis thaliana]

Seq. No.	221564
Seq. ID	LIB3165-013-P1-K1-B12
Method	BLASTX
NCBI GI	g4406530
BLAST score	361
E value	2.0e-34
Match length	98
% identity	76
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221565
Seq. ID	LIB3165-013-P1-K1-B2
Method	BLASTX
NCBI GI	g487046
BLAST score	426

E value	5.0e-42
Match length	141
% identity	60
NCBI Description	photosystem I chain II precursor - wood tobacco >gi_407769_dbj_BAA02871_ (D13718) PSI-D1 precursor [Nicotiana sylvestris]

Seq. No.	221566
Seq. ID	LIB3165-013-P1-K1-B4
Method	BLASTN
NCBI GI	g4519194
BLAST score	34
E value	1.0e-09
Match length	194
% identity	80
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence

Seq. No.	221567
Seq. ID	LIB3165-013-P1-K1-B5
Method	BLASTX
NCBI GI	g3184098
BLAST score	276
E value	2.0e-24
Match length	134
% identity	46
NCBI Description	(AL023777) coenzyme a synthetase [Schizosaccharomyces pombe]

Seq. No.	221568
Seq. ID	LIB3165-013-P1-K1-B6
Method	BLASTX
NCBI GI	g1174162
BLAST score	580
E value	4.0e-60
Match length	109
% identity	92
NCBI Description	(U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi_3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No.	221569
Seq. ID	LIB3165-013-P1-K1-B7
Method	BLASTX
NCBI GI	g1217601
BLAST score	266
E value	2.0e-23
Match length	56
% identity	88
NCBI Description	(D42070) PSI-E subunit of photosystem I [Nicotiana sylvestris]

Seq. No.	221570
Seq. ID	LIB3165-013-P1-K1-B8
Method	BLASTX
NCBI GI	g3033400
BLAST score	562

E value	5.0e-58
Match length	128
% identity	84
NCBI Description	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	221571
Seq. ID	LIB3165-013-P1-K1-C11
Method	BLASTX
NCBI GI	g1352821
BLAST score	574
E value	2.0e-59
Match length	108
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221572
Seq. ID	LIB3165-013-P1-K1-C2
Method	BLASTX
NCBI GI	g68200
BLAST score	528
E value	5.0e-54
Match length	134
% identity	81
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	221573
Seq. ID	LIB3165-013-P1-K1-C3
Method	BLASTX
NCBI GI	g2664210
BLAST score	368
E value	2.0e-40
Match length	139
% identity	57
NCBI Description	(AJ222644) asparaginyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	221574
Seq. ID	LIB3165-013-P1-K1-C4
Method	BLASTX
NCBI GI	g2244806
BLAST score	257
E value	3.0e-22
Match length	138
% identity	46
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	221575
Seq. ID	LIB3165-013-P1-K1-C6
Method	BLASTX
NCBI GI	g2894565

BLAST score	151
E value	8.0e-10
Match length	70
% identity	67
NCBI Description	(AL021890) heat shock protein - like [Arabidopsis thaliana]

Seq. No.	221576
Seq. ID	LIB3165-013-P1-K1-C7
Method	BLASTX
NCBI GI	g115471
BLAST score	625
E value	2.0e-65
Match length	140
% identity	82
NCBI Description	CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) >gi_100078_pir__S10200 carbonate dehydratase (EC 4.2.1.1) precursor - garden pea >gi_20673_emb_CAA36792_ (X52558) precursor peptide (AA -104 to 224) [Pisum sativum]

Seq. No.	221577
Seq. ID	LIB3165-013-P1-K1-C8
Method	BLASTX
NCBI GI	g231610
BLAST score	279
E value	7.0e-27
Match length	113
% identity	63
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]

Seq. No.	221578
Seq. ID	LIB3165-013-P1-K1-D10
Method	BLASTX
NCBI GI	g100616
BLAST score	387
E value	2.0e-37
Match length	100
% identity	76
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	221579
Seq. ID	LIB3165-013-P1-K1-D12
Method	BLASTX
NCBI GI	g1710112
BLAST score	423
E value	7.0e-42
Match length	101
% identity	82
NCBI Description	(U53864) PRH19 [Arabidopsis thaliana]

Seq. No.	221580
Seq. ID	LIB3165-013-P1-K1-D4
Method	BLASTX
NCBI GI	g2244954
BLAST score	105
E value	2.0e-09
Match length	44
% identity	60
NCBI Description	(Z97340) strong similarity to ATsEH (EC 3.3.2.3) - Arabidopsis thaliana [Arabidopsis thaliana]

Seq. No.	221581
Seq. ID	LIB3165-013-P1-K1-D8
Method	BLASTX
NCBI GI	g1946367
BLAST score	164
E value	3.0e-11
Match length	57
% identity	51
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	221582
Seq. ID	LIB3165-013-P1-K1-D9
Method	BLASTX
NCBI GI	g266893
BLAST score	715
E value	6.0e-76
Match length	139
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__S28172 ribulose-bisphosphate carboxylase activase - cucumber >gi_18284_emb_CAA47906_ (X67674) rubisco activase [Cucumis sativus]

Seq. No.	221583
Seq. ID	LIB3165-013-P1-K1-E1
Method	BLASTX
NCBI GI	g1181599
BLAST score	492
E value	8.0e-50
Match length	127
% identity	76
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.	221584
Seq. ID	LIB3165-013-P1-K1-E10
Method	BLASTX
NCBI GI	g131385
BLAST score	562
E value	5.0e-58
Match length	136
% identity	85
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN)

Seq. No.	221585
Seq. ID	LIB3165-013-P1-K1-E11
Method	BLASTX
NCBI GI	g166834
BLAST score	705
E value	9.0e-75
Match length	137
% identity	97
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	221586
Seq. ID	LIB3165-013-P1-K1-E3
Method	BLASTX
NCBI GI	g2829903
BLAST score	360
E value	3.0e-34
Match length	75
% identity	89
NCBI Description	(AC002311) unknown protein [Arabidopsis thaliana]

Seq. No.	221587
Seq. ID	LIB3165-013-P1-K1-E4
Method	BLASTN
NCBI GI	g3985958
BLAST score	33
E value	6.0e-09
Match length	97
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	221588
Seq. ID	LIB3165-013-P1-K1-E5
Method	BLASTX
NCBI GI	g4406530
BLAST score	359
E value	3.0e-34
Match length	118
% identity	64
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221589
Seq. ID	LIB3165-013-P1-K1-E6
Method	BLASTX
NCBI GI	g3914435
BLAST score	399
E value	7.0e-39
Match length	109
% identity	67
NCBI Description	PROFILIN 1 >gi_3021375_emb_CAA11756_ (AJ223982) profilin [Glycine max]

Seq. No.	221590
Seq. ID	LIB3165-013-P1-K1-F1
Method	BLASTX

NCBI GI	g445116
BLAST score	142
E value	6.0e-15
Match length	73
% identity	57
NCBI Description	light-harvesting complex IIa protein; [Hordeum vulgare]

Seq. No.	221591
Seq. ID	LIB3165-013-P1-K1-F10
Method	BLASTX
NCBI GI	g1352821
BLAST score	713
E value	1.0e-75
Match length	135
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221592
Seq. ID	LIB3165-013-P1-K1-F11
Method	BLASTX
NCBI GI	g3282092
BLAST score	163
E value	3.0e-11
Match length	106
% identity	38
NCBI Description	(AJ007446) hypothetical protein [Thermotoga neapolitana]

Seq. No.	221593
Seq. ID	LIB3165-013-P1-K1-F3
Method	BLASTX
NCBI GI	g1352821
BLAST score	469
E value	5.0e-47
Match length	124
% identity	79
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221594
Seq. ID	LIB3165-013-P1-K1-F4
Method	BLASTX
NCBI GI	g1439609
BLAST score	592
E value	2.0e-61
Match length	119
% identity	55
NCBI Description	(U62778) delta-tonoplast intrinsic protein [Gossypium hirsutum]

Seq. No.	221595

Seq. ID	LIB3165-013-P1-K1-F5
Method	BLASTX
NCBI GI	g100196
BLAST score	473
E value	1.0e-47
Match length	105
% identity	82
NCBI Description	chlorophyll a/b-binding protein (cab-11) - tomato

Seq. No.	221596
Seq. ID	LIB3165-013-P1-K1-F9
Method	BLASTX
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	37
% identity	61
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	221597
Seq. ID	LIB3165-013-P1-K1-G1
Method	BLASTX
NCBI GI	g479406
BLAST score	525
E value	1.0e-53
Match length	103
% identity	65
NCBI Description	chlorophyll a/b-binding protein - garden pea >gi_20871_emb_CAA49149_ (X69215) chlorophyll a/b-binding protein [Pisum sativum]

Seq. No.	221598
Seq. ID	LIB3165-013-P1-K1-G11
Method	BLASTX
NCBI GI	g120663
BLAST score	546
E value	4.0e-56
Match length	135
% identity	77
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR, CHLOROPLAST >gi_66027_pir__DEPMNB glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast - garden pea >gi_309671 (M55147) glyceraldehyde-3-phosphate dehydrogenase B subunit [Pisum sativum]

Seq. No.	221599
Seq. ID	LIB3165-013-P1-K1-G3
Method	BLASTX
NCBI GI	g1350680
BLAST score	521
E value	3.0e-53
Match length	120
% identity	80
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	221600

Seq. ID	LIB3165-013-P1-K1-G6
Method	BLASTX
NCBI GI	g3080390
BLAST score	494
E value	5.0e-50
Match length	119
% identity	78
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana]

Seq. No.	221601
Seq. ID	LIB3165-013-P1-K1-G7
Method	BLASTX
NCBI GI	g1352821
BLAST score	640
E value	4.0e-67
Match length	122
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221602
Seq. ID	LIB3165-013-P1-K1-G9
Method	BLASTX
NCBI GI	g2088662
BLAST score	227
E value	1.0e-18
Match length	116
% identity	47
NCBI Description	(AF002109) unknown protein [Arabidopsis thaliana]

Seq. No.	221603
Seq. ID	LIB3165-013-P1-K1-H1
Method	BLASTX
NCBI GI	g120662
BLAST score	579
E value	5.0e-60
Match length	119
% identity	89
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR, CHLOROPLAST >gi_81621_pir__JQ1286 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast - Arabidopsis thaliana >gi_336390 (M64115) glyceraldehyde 3-phosphate dehydrogenase B subunit [Arabidopsis thaliana]

Seq. No.	221604
Seq. ID	LIB3165-013-P1-K1-H10
Method	BLASTN
NCBI GI	g18058
BLAST score	187
E value	1.0e-101
Match length	311
% identity	91
NCBI Description	Citrus limon cistron for 26S ribosomal RNA

Seq. No.	221605
Seq. ID	LIB3165-013-P1-K1-H12
Method	BLASTX
NCBI GI	g2832643
BLAST score	200
E value	1.0e-15
Match length	57
% identity	74
NCBI Description	(AL021710) hypothetical protein [Arabidopsis thaliana]

Seq. No.	221606
Seq. ID	LIB3165-013-P1-K1-H2
Method	BLASTX
NCBI GI	g625547
BLAST score	495
E value	4.0e-50
Match length	128
% identity	77
NCBI Description	chlorophyll a/b-binding protein type I - common tobacco >gi_493723_emb_CAA45523_ (X64198) photosystem I light-harvesting chlorophyll a/b-binding protein [Nicotiana tabacum]

Seq. No.	221607
Seq. ID	LIB3165-013-P1-K1-H3
Method	BLASTX
NCBI GI	g1352821
BLAST score	567
E value	2.0e-58
Match length	111
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221608
Seq. ID	LIB3165-013-P1-K1-H4
Method	BLASTX
NCBI GI	g1856971
BLAST score	412
E value	2.0e-40
Match length	91
% identity	89
NCBI Description	(D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	221609
Seq. ID	LIB3165-013-P1-K1-H5
Method	BLASTX
NCBI GI	g1352821
BLAST score	555
E value	4.0e-57
Match length	106

% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	221610
Seq. ID	LIB3165-013-P1-K1-H6
Method	BLASTX
NCBI GI	g1071913
BLAST score	256
E value	4.0e-22
Match length	110
% identity	56
NCBI Description	cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial - spinach >gi_1066153_dbj_BAA07177_ (D37963) cysteine synthase [Spinacia oleracea]
Seq. No.	221611
Seq. ID	LIB3165-013-P1-K1-H7
Method	BLASTX
NCBI GI	g3687652
BLAST score	606
E value	3.0e-63
Match length	128
% identity	92
NCBI Description	(AF047352) rubisco activase precursor [Datisca glomerata]
Seq. No.	221612
Seq. ID	LIB3165-014-P1-K1-A11
Method	BLASTX
NCBI GI	g1352821
BLAST score	572
E value	4.0e-59
Match length	110
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	221613
Seq. ID	LIB3165-014-P1-K1-A12
Method	BLASTX
NCBI GI	g3913651
BLAST score	161
E value	6.0e-11
Match length	47
% identity	70
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR (FNR) >gi_2225993_emb_CAA74359_ (Y14032) ferredoxin--NADP(+) reductase [Nicotiana tabacum]
Seq. No.	221614
Seq. ID	LIB3165-014-P1-K1-A2

Method	BLASTX
NCBI GI	g2854153
BLAST score	196
E value	4.0e-15
Match length	91
% identity	46
NCBI Description	(AF045640) No definition line found [Caenorhabditis elegans]

Seq. No.	221615
Seq. ID	LIB3165-014-P1-K1-A5
Method	BLASTX
NCBI GI	g3928760
BLAST score	268
E value	2.0e-23
Match length	115
% identity	52
NCBI Description	(AB011797) homolog to plastid-lipid-associated protein [Citrus unshiu]

Seq. No.	221616
Seq. ID	LIB3165-014-P1-K1-A6
Method	BLASTX
NCBI GI	g1168411
BLAST score	537
E value	5.0e-55
Match length	132
% identity	83
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	221617
Seq. ID	LIB3165-014-P1-K1-A7
Method	BLASTX
NCBI GI	g2244905
BLAST score	245
E value	9.0e-22
Match length	115
% identity	50
NCBI Description	(Z97339) indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	221618
Seq. ID	LIB3165-014-P1-K1-B10
Method	BLASTX
NCBI GI	g1353352
BLAST score	325
E value	3.0e-30
Match length	91
% identity	73
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	221619
Seq. ID	LIB3165-014-P1-K1-B11
Method	BLASTX
NCBI GI	g1781348
BLAST score	620

E value	8.0e-65
Match length	135
% identity	88
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No.	221620
Seq. ID	LIB3165-014-P1-K1-B12
Method	BLASTX
NCBI GI	g2342674
BLAST score	294
E value	1.0e-26
Match length	118
% identity	56
NCBI Description	(AC000106) Similar to ATP-dependent Clp protease (gb_D90915). EST gb_N65461 comes from this gene. [Arabidopsis thaliana]

Seq. No.	221621
Seq. ID	LIB3165-014-P1-K1-B3
Method	BLASTX
NCBI GI	g1168411
BLAST score	379
E value	1.0e-36
Match length	99
% identity	80
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	221622
Seq. ID	LIB3165-014-P1-K1-B4
Method	BLASTX
NCBI GI	g1771780
BLAST score	391
E value	6.0e-38
Match length	108
% identity	78
NCBI Description	(Y10024) ubiquitin extension protein [Solanum tuberosum]

Seq. No.	221623
Seq. ID	LIB3165-014-P1-K1-B5
Method	BLASTX
NCBI GI	g1346809
BLAST score	363
E value	1.0e-34
Match length	108
% identity	64
NCBI Description	PATHOGEN-RELATED PROTEIN >gi_499074_emb_CAA34641_ (X16648) pathogenesis related protein [Hordeum vulgare]

Seq. No.	221624
Seq. ID	LIB3165-014-P1-K1-B6
Method	BLASTX
NCBI GI	g228403
BLAST score	247
E value	2.0e-39
Match length	130
% identity	72

NCBI Description	glycolate oxidase [Lens culinaris]
Seq. No.	221625
Seq. ID	LIB3165-014-P1-K1-B7
Method	BLASTN
NCBI GI	g2687434
BLAST score	233
E value	1.0e-128
Match length	285
% identity	95
NCBI Description	Eucryphia lucida large subunit 26S ribosomal RNA gene, partial sequence
Seq. No.	221626
Seq. ID	LIB3165-014-P1-K1-B9
Method	BLASTX
NCBI GI	g2815246
BLAST score	225
E value	2.0e-18
Match length	55
% identity	73
NCBI Description	(X95709) class I type 2 metallothionein [Cicer arietinum]
Seq. No.	221627
Seq. ID	LIB3165-014-P1-K1-C2
Method	BLASTX
NCBI GI	g20729
BLAST score	505
E value	2.0e-51
Match length	122
% identity	81
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]
Seq. No.	221628
Seq. ID	LIB3165-014-P1-K1-C9
Method	BLASTX
NCBI GI	g100616
BLAST score	286
E value	1.0e-25
Match length	64
% identity	86
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]
Seq. No.	221629
Seq. ID	LIB3165-014-P1-K1-D1
Method	BLASTX
NCBI GI	g417103
BLAST score	524
E value	1.0e-53
Match length	112
% identity	94
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana

>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	221630
Seq. ID	LIB3165-014-P1-K1-D11
Method	BLASTX
NCBI GI	g1352821
BLAST score	527
E value	7.0e-54
Match length	102
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221631
Seq. ID	LIB3165-014-P1-K1-D12
Method	BLASTX
NCBI GI	g2618686
BLAST score	142
E value	9.0e-09
Match length	88
% identity	40
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No.	221632
Seq. ID	LIB3165-014-P1-K1-D3
Method	BLASTX
NCBI GI	g20733
BLAST score	515
E value	2.0e-52
Match length	118
% identity	83
NCBI Description	(X15188) precursor C-terminal fragment (A -80 to 367) [Pisum sativum]

Seq. No.	221633
Seq. ID	LIB3165-014-P1-K1-D4
Method	BLASTX
NCBI GI	g2956717

BLAST score	169
E value	7.0e-12
Match length	106
% identity	43
NCBI Description	(Y09722) beta-carotene hydroxylase 2 [Capsicum annuum]

Seq. No.	221634
Seq. ID	LIB3165-014-P1-K1-D6
Method	BLASTX
NCBI GI	g131385
BLAST score	570
E value	6.0e-59
Match length	136
% identity	85
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN)

Seq. No.	221635
Seq. ID	LIB3165-014-P1-K1-D7
Method	BLASTX
NCBI GI	g3834306
BLAST score	244
E value	7.0e-21
Match length	84
% identity	57
NCBI Description	(AC005679) EST gb_R65024 comes from this gene. [Arabidopsis thaliana]

Seq. No.	221636
Seq. ID	LIB3165-014-P1-K1-D9
Method	BLASTX
NCBI GI	g1169494
BLAST score	237
E value	7.0e-20
Match length	70
% identity	71
NCBI Description	ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >gi_2119915_pir__S60659 EF-Tu protein precursor - soybean >gi_949873_emb_CAA61444_ (X89058) EF-Tu protein [Glycine max]

Seq. No.	221637
Seq. ID	LIB3165-014-P1-K1-E1
Method	BLASTX
NCBI GI	g2119927
BLAST score	612
E value	7.0e-64
Match length	134
% identity	90
NCBI Description	translation elongation factor G, chloroplast - soybean

Seq. No.	221638
Seq. ID	LIB3165-014-P1-K1-E11
Method	BLASTX
NCBI GI	g289920
BLAST score	704

E value	1.0e-74
Match length	131
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221639
Seq. ID	LIB3165-014-P1-K1-E12
Method	BLASTX
NCBI GI	g585118
BLAST score	636
E value	1.0e-66
Match length	133
% identity	91
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_289367 (L15303) fructose-1,6-bisphosphate [Brassica napus]

Seq. No.	221640
Seq. ID	LIB3165-014-P1-K1-E6
Method	BLASTX
NCBI GI	g2505876
BLAST score	329
E value	1.0e-30
Match length	70
% identity	89
NCBI Description	(Y12776) MYB-related protein [Arabidopsis thaliana]

Seq. No.	221641
Seq. ID	LIB3165-014-P1-K1-E7
Method	BLASTX
NCBI GI	g170354
BLAST score	533
E value	1.0e-54
Match length	108
% identity	21
NCBI Description	(M74156) pentameric polyubiquitin [Nicotiana sylvestris]

Seq. No.	221642
Seq. ID	LIB3165-014-P1-K1-E8
Method	BLASTX
NCBI GI	g2621154
BLAST score	144
E value	5.0e-09
Match length	124
% identity	30
NCBI Description	(AE000801) unknown [Methanobacterium thermoautotrophicum]

Seq. No.	221643
Seq. ID	LIB3165-014-P1-K1-F10
Method	BLASTX
NCBI GI	g1928981
BLAST score	544
E value	7.0e-56
Match length	116
% identity	93

NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	221644
Seq. ID	LIB3165-014-P1-K1-F2
Method	BLASTX
NCBI GI	g3885511
BLAST score	381
E value	9.0e-37
Match length	95
% identity	79
NCBI Description	(AF084200) similar to PSI-K subunit of photosystem I from barley [Medicago sativa]

Seq. No.	221645
Seq. ID	LIB3165-014-P1-K1-F3
Method	BLASTX
NCBI GI	g2995384
BLAST score	153
E value	3.0e-10
Match length	41
% identity	73
NCBI Description	(AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No.	221646
Seq. ID	LIB3165-014-P1-K1-F4
Method	BLASTX
NCBI GI	g2894599
BLAST score	496
E value	3.0e-50
Match length	104
% identity	83
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	221647
Seq. ID	LIB3165-014-P1-K1-F5
Method	BLASTX
NCBI GI	g3063396
BLAST score	492
E value	9.0e-50
Match length	119
% identity	79
NCBI Description	(AB012947) vcCyP [Vicia faba]

Seq. No.	221648
Seq. ID	LIB3165-014-P1-K1-F6
Method	BLASTX
NCBI GI	g119748
BLAST score	542
E value	1.0e-55
Match length	121
% identity	88
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_67241_pir__PASPY fructose-bisphosphatase (EC 3.1.3.11), cytosolic - spinach >gi_21245_emb_CAA43860_ (X61690) fructose-bisphosphatase [Spinacia oleracea]

Seq. No.	221649
Seq. ID	LIB3165-014-P1-K1-G1
Method	BLASTX
NCBI GI	g3290020
BLAST score	442
E value	6.0e-44
Match length	96
% identity	91
NCBI Description	(AF044172) cysteine synthase; CS-A; O-acetylserine (thiol) lyase; cytosolic isoform [Solanum tuberosum]

Seq. No.	221650
Seq. ID	LIB3165-014-P1-K1-G11
Method	BLASTX
NCBI GI	g4406530
BLAST score	364
E value	9.0e-35
Match length	98
% identity	76
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221651
Seq. ID	LIB3165-014-P1-K1-G2
Method	BLASTX
NCBI GI	g1703129
BLAST score	557
E value	2.0e-57
Match length	103
% identity	99
NCBI Description	ACTIN 11 >gi_2129522_pir__S68109 actin 11 - Arabidopsis thaliana >gi_1002533 (U27981) actin-11 [Arabidopsis thaliana]

Seq. No.	221652
Seq. ID	LIB3165-014-P1-K1-G5
Method	BLASTN
NCBI GI	g18058
BLAST score	57
E value	1.0e-23
Match length	144
% identity	88
NCBI Description	Citrus limon cistron for 26S ribosomal RNA

Seq. No.	221653
Seq. ID	LIB3165-014-P1-K1-G8
Method	BLASTX
NCBI GI	g1346155
BLAST score	611
E value	9.0e-64
Match length	133
% identity	89
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_481942_pir__S40212 glycine hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei >gi_437995_emb_CAA81078_ (Z25859) glycine

hydroxymethyltransferase [Flaveria pringlei]

Seq. No.	221654
Seq. ID	LIB3165-014-P1-K1-G9
Method	BLASTX
NCBI GI	g994736
BLAST score	148
E value	5.0e-10
Match length	52
% identity	60
NCBI Description	(M18327) LacOPZ-alpha peptide from pUC9; putative [cloning vectors] >gi_994738 (M18328) LacOPZ-alpha peptide from pUC9; putative [cloning vectors] >gi_994740 (M18329) LacOPZ-alpha peptide from pUC9; putative [cloning vectors]

Seq. No.	221655
Seq. ID	LIB3165-014-P1-K1-H10
Method	BLASTX
NCBI GI	g1353352
BLAST score	286
E value	1.0e-25
Match length	74
% identity	76
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	221656
Seq. ID	LIB3165-014-P1-K1-H2
Method	BLASTX
NCBI GI	g1168411
BLAST score	517
E value	1.0e-52
Match length	127
% identity	83
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	221657
Seq. ID	LIB3165-014-P1-K1-H3
Method	BLASTX
NCBI GI	g100203
BLAST score	241
E value	1.0e-20
Match length	66
% identity	71
NCBI Description	cysteine proteinase (EC 3.4.22.-) precursor - tomato >gi_19195_emb_CAA78403_ (Z14028) pre-pro-cysteine proteinase [Lycopersicon esculentum]

Seq. No.	221658
Seq. ID	LIB3165-014-P1-K1-H6
Method	BLASTX
NCBI GI	g82437
BLAST score	453
E value	3.0e-45
Match length	83
% identity	100
NCBI Description	plastoquinol--plastocyanin reductase (EC 1.10.99.1) 17K

protein short form - barley chloroplast (fragment) >gi_1617032_emb_CAA32269_ (X14107) petD [Hordeum vulgare]

Seq. No.	221659
Seq. ID	LIB3165-014-P1-K1-H7
Method	BLASTX
NCBI GI	g4115931
BLAST score	317
E value	3.0e-29
Match length	119
% identity	60
NCBI Description	(AF118223) contains similarity to Guillardia theta ABC transporter (GB:AF041468) [Arabidopsis thaliana]

Seq. No.	221660
Seq. ID	LIB3165-016-P1-K1-A1
Method	BLASTN
NCBI GI	g3128142
BLAST score	34
E value	1.0e-09
Match length	62
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	221661
Seq. ID	LIB3165-016-P1-K1-A12
Method	BLASTX
NCBI GI	g3450842
BLAST score	190
E value	5.0e-20
Match length	90
% identity	58
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	221662
Seq. ID	LIB3165-016-P1-K1-A4
Method	BLASTX
NCBI GI	g120661
BLAST score	472
E value	8.0e-66
Match length	140
% identity	91
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_170237 (M14417) glyceraldehyde-3-phosphate dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No.	221663
Seq. ID	LIB3165-016-P1-K1-A6
Method	BLASTX
NCBI GI	g2498629
BLAST score	181
E value	2.0e-13
Match length	99
% identity	9
NCBI Description	TRANSCRIPTIONAL REPRESSOR NF-X1 >gi_2135825_pir__I38869

NFX1 - human >gi_563217 (U15306) NFX1 [Homo sapiens] >gi_4505387_ref_NP_002495.1_pNFX1_ nuclear transcription factor, X-box binding

Seq. No.	221664
Seq. ID	LIB3165-016-P1-K1-A9
Method	BLASTX
NCBI GI	g927601
BLAST score	252
E value	8.0e-22
Match length	56
% identity	84
NCBI Description	[2Fe-2S] ferredoxin [Datura arborea, Peptide, 97 aa] >gi_1097873_prf__2114375A ferredoxin [Datura arborea]

Seq. No.	221665
Seq. ID	LIB3165-016-P1-K1-B1
Method	BLASTX
NCBI GI	g266892
BLAST score	258
E value	2.0e-35
Match length	99
% identity	70
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_82028_pir__S16272 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - Para rubber tree >gi_168217 (M60274) ribulose-1,5-bisphosphate carboxylase small subunit [Hevea brasiliensis]

Seq. No.	221666
Seq. ID	LIB3165-016-P1-K1-B4
Method	BLASTX
NCBI GI	g100362
BLAST score	235
E value	2.0e-37
Match length	122
% identity	70
NCBI Description	photosystem II oxygen-evolving complex protein 2 precursor (clone T23-5B) - common tobacco (fragment) >gi_1345550_emb_CAA44292_ (X62426) 23-kDa ploypeptide of photosystem II oxygen-evolving complex [Nicotiana tabacum]

Seq. No.	221667
Seq. ID	LIB3165-016-P1-K1-B7
Method	BLASTX
NCBI GI	g3298439
BLAST score	547
E value	3.0e-56
Match length	134
% identity	81
NCBI Description	(AB010878) chloroplast ribosomal protein L4 [Nicotiana tabacum]

Seq. No.	221668
Seq. ID	LIB3165-016-P1-K1-B8
Method	BLASTX

NCBI GI	g1708191
BLAST score	325
E value	2.0e-44
Match length	111
% identity	84
NCBI Description	HEXOSE CARRIER PROTEIN HEX6 >gi_467319 (L08188) hexose carrier protein [Ricinus communis]

Seq. No.	221669
Seq. ID	LIB3165-016-P1-K1-B9
Method	BLASTX
NCBI GI	g132091
BLAST score	308
E value	2.0e-35
Match length	87
% identity	86
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN F1 PRECURSOR (RUBISCO SMALL SUBUNIT F1) >gi_68065_pir__RKRPF1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (gene rbcSF1) - rape >gi_17852_emb_CAA39402_ (X55937) ribulose bisphosphate carboxylase /oxygenase small subunit [Brassica napus]

Seq. No.	221670
Seq. ID	LIB3165-016-P1-K1-C1
Method	BLASTX
NCBI GI	g1527191
BLAST score	233
E value	1.0e-22
Match length	77
% identity	64
NCBI Description	(U67861) 1-aminocyclopropane-1-carboxylate oxidase [Pelargonium x hortorum]

Seq. No.	221671
Seq. ID	LIB3165-016-P1-K1-C6
Method	BLASTX
NCBI GI	g118564
BLAST score	475
E value	1.0e-55
Match length	139
% identity	81
NCBI Description	GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE REDUCTASE) (HPR) (GDH) >gi_65955_pir__DEKVG glycerate dehydrogenase (EC 1.1.1.29) - cucumber >gi_18264_emb_CAA41434_ (X58542) NADH-dependent hydroxypyruvate reductase [Cucumis sativus] >gi_18275_emb_CAA32764_ (X14609) NAPH-dependent hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

Seq. No.	221672
Seq. ID	LIB3165-016-P1-K1-C7
Method	BLASTX
NCBI GI	g462187
BLAST score	429
E value	1.0e-62
Match length	126

% identity	92
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_282928_pir__A42906 serine hydroxymethyltransferase - garden pea >gi_169158 (M87649) serine hydroxymethyltransferase [Pisum sativum]
Seq. No.	221673
Seq. ID	LIB3165-016-P1-K1-C8
Method	BLASTX
NCBI GI	g2894599
BLAST score	429
E value	3.0e-61
Match length	135
% identity	84
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]
Seq. No.	221674
Seq. ID	LIB3165-016-P1-K1-D1
Method	BLASTX
NCBI GI	g136707
BLAST score	289
E value	7.0e-45
Match length	123
% identity	77
NCBI Description	CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_280397_pir__S26199 plastoquinol--plastocyanin reductase (EC 1.10.99.1) iron-sulfur protein precursor - garden pea >gi_20832_emb_CAA45151_ (X63605) chloroplast Rieske FeS protein [Pisum sativum]
Seq. No.	221675
Seq. ID	LIB3165-016-P1-K1-D11
Method	BLASTX
NCBI GI	g2129825
BLAST score	215
E value	7.0e-37
Match length	96
% identity	79
NCBI Description	dynamin-like protein phragmoplastin 12 - soybean >gi_1217994 (U25547) SDL [Glycine max]
Seq. No.	221676
Seq. ID	LIB3165-016-P1-K1-D7
Method	BLASTX
NCBI GI	g3789940
BLAST score	405
E value	9.0e-58
Match length	124
% identity	22
NCBI Description	(AF093504) tetra-ubiquitin [Saccharum hybrid cultivar H32-8560]
Seq. No.	221677
Seq. ID	LIB3165-016-P1-K1-D8
Method	BLASTX

NCBI GI	g1168411
BLAST score	203
E value	4.0e-29
Match length	92
% identity	76
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	221678
Seq. ID	LIB3165-016-P1-K1-E10
Method	BLASTX
NCBI GI	g3192881
BLAST score	234
E value	1.0e-19
Match length	94
% identity	59
NCBI Description	(AF068834) starch synthase [Ipomoea batatas]

Seq. No.	221679
Seq. ID	LIB3165-016-P1-K1-E11
Method	BLASTX
NCBI GI	g115765
BLAST score	285
E value	3.0e-44
Match length	112
% identity	74
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	221680
Seq. ID	LIB3165-016-P1-K1-E2
Method	BLASTX
NCBI GI	g3288821
BLAST score	270
E value	2.0e-42
Match length	107
% identity	85
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana]

Seq. No.	221681
Seq. ID	LIB3165-016-P1-K1-E3
Method	BLASTX
NCBI GI	g1168411
BLAST score	208
E value	1.0e-35
Match length	105
% identity	82
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	221682
Seq. ID	LIB3165-016-P1-K1-E5

Method	BLASTX
NCBI GI	g421826
BLAST score	464
E value	9.0e-66
Match length	141
% identity	86
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	221683
Seq. ID	LIB3165-016-P1-K1-E6
Method	BLASTX
NCBI GI	g4544427
BLAST score	213
E value	9.0e-28
Match length	86
% identity	77
NCBI Description	(AC006955) putative ferredoxin-thioredoxin reductase [Arabidopsis thaliana]

Seq. No.	221684
Seq. ID	LIB3165-016-P1-K1-E7
Method	BLASTX
NCBI GI	g2501578
BLAST score	397
E value	2.0e-39
Match length	116
% identity	80
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No.	221685
Seq. ID	LIB3165-016-P1-K1-E9
Method	BLASTN
NCBI GI	g18058
BLAST score	309
E value	1.0e-173
Match length	380
% identity	96
NCBI Description	Citrus limon cistron for 26S ribosomal RNA

Seq. No.	221686
Seq. ID	LIB3165-016-P1-K1-F10
Method	BLASTX
NCBI GI	g2494299
BLAST score	194
E value	3.0e-29
Match length	134
% identity	58
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT (EIF-2-BETA) >gi_1732361 (U80269) translation initiation factor 2 beta [Malus domestica]

Seq. No.	221687

Seq. ID	LIB3165-016-P1-K1-F11
Method	BLASTX
NCBI GI	g117290
BLAST score	196
E value	6.0e-26
Match length	111
% identity	59
NCBI Description	CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT) (P36) (E30) >gi_100071_pir__S23774 triose phosphate/3-phosphoglycerate/phosphate translocator precursor - garden pea >gi_20691_emb_CAA38451_ (X54639) chloroplast import receptor p36 [Pisum sativum] >gi_20853_emb_CAA48210_ (X68077) phosphate translocator [Pisum sativum] >gi_228551_prf__1805409A phosphate translocator [Pisum sativum]

Seq. No.	221688
Seq. ID	LIB3165-016-P1-K1-F12
Method	BLASTX
NCBI GI	g100200
BLAST score	239
E value	1.0e-38
Match length	113
% identity	69
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	221689
Seq. ID	LIB3165-016-P1-K1-F2
Method	BLASTX
NCBI GI	g508304
BLAST score	171
E value	1.0e-24
Match length	74
% identity	76
NCBI Description	(L22305) corC [Medicago sativa]

Seq. No.	221690
Seq. ID	LIB3165-016-P1-K1-F3
Method	BLASTX
NCBI GI	g4263712
BLAST score	234
E value	6.0e-31
Match length	91
% identity	76
NCBI Description	(AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]

Seq. No.	221691
Seq. ID	LIB3165-016-P1-K1-F5
Method	BLASTX
NCBI GI	g3831467
BLAST score	143
E value	1.0e-16
Match length	119
% identity	41
NCBI Description	(AC005700) putative beta-amylase [Arabidopsis thaliana]

Seq. No.	221692
Seq. ID	LIB3165-016-P1-K1-F7
Method	BLASTX
NCBI GI	g289920
BLAST score	418
E value	3.0e-57
Match length	111
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221693
Seq. ID	LIB3165-016-P1-K1-G1
Method	BLASTX
NCBI GI	g82537
BLAST score	107
E value	6.0e-11
Match length	58
% identity	61
NCBI Description	hypothetical 8K protein (rps12-trnN intergenic region) - rice chloroplast >gi_12039_emb_CAA33943_ (X15901) ORF72 [Oryza sativa] >gi_12063_emb_CAA33917_ (X15901) ORF72 [Oryza sativa] >gi_226659_prf__1603356CK ORF 71 [Oryza sativa]

Seq. No.	221694
Seq. ID	LIB3165-016-P1-K1-G10
Method	BLASTX
NCBI GI	g289920
BLAST score	487
E value	2.0e-69
Match length	133
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221695
Seq. ID	LIB3165-016-P1-K1-G2
Method	BLASTN
NCBI GI	g4545261
BLAST score	33
E value	5.0e-09
Match length	57
% identity	89
NCBI Description	Gossypium hirsutum metallothionein-like protein mRNA, complete cds

Seq. No.	221696
Seq. ID	LIB3165-016-P1-K1-G7
Method	BLASTX
NCBI GI	g2739365
BLAST score	330
E value	5.0e-44
Match length	129
% identity	64
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	221697
Seq. ID	LIB3165-016-P1-K1-G8
Method	BLASTX
NCBI GI	g1352821
BLAST score	393
E value	4.0e-51
Match length	109
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221698
Seq. ID	LIB3165-016-P1-K1-G9
Method	BLASTN
NCBI GI	g18058
BLAST score	311
E value	1.0e-175
Match length	414
% identity	94
NCBI Description	Citrus limon cistron for 26S ribosomal RNA

Seq. No.	221699
Seq. ID	LIB3165-016-P1-K1-H1
Method	BLASTX
NCBI GI	g4455208
BLAST score	226
E value	1.0e-18
Match length	124
% identity	36
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	221700
Seq. ID	LIB3165-016-P1-K1-H11
Method	BLASTX
NCBI GI	g1354515
BLAST score	216
E value	1.0e-17
Match length	100
% identity	53
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	221701
Seq. ID	LIB3165-016-P1-K1-H12
Method	BLASTX
NCBI GI	g3885334
BLAST score	250
E value	2.0e-21
Match length	55
% identity	84
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	221702

Seq. ID	LIB3165-016-P1-K1-H2
Method	BLASTX
NCBI GI	g1063400
BLAST score	311
E value	1.0e-28
Match length	85
% identity	88
NCBI Description	(X92888) glycolate oxidase [Lycopersicon esculentum]

Seq. No.	221703
Seq. ID	LIB3165-016-P1-K1-H5
Method	BLASTX
NCBI GI	g1168411
BLAST score	246
E value	9.0e-41
Match length	124
% identity	80
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	221704
Seq. ID	LIB3165-016-P1-K1-H6
Method	BLASTX
NCBI GI	g430947
BLAST score	312
E value	1.0e-46
Match length	127
% identity	74
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	221705
Seq. ID	LIB3165-016-P1-K1-H7
Method	BLASTX
NCBI GI	g3914605
BLAST score	484
E value	3.0e-63
Match length	138
% identity	90
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase - apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica]

Seq. No.	221706
Seq. ID	LIB3165-016-P1-K1-H8
Method	BLASTX
NCBI GI	g4325345
BLAST score	155
E value	3.0e-10
Match length	74
% identity	34
NCBI Description	(AF128393) similar to thioredoxin-like proteins (Pfam: PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42, N=1) [Arabidopsis thaliana]

Seq. No.	221707
Seq. ID	LIB3165-017-P1-K1-A10
Method	BLASTX
NCBI GI	gl168411
BLAST score	487
E value	3.0e-49
Match length	122
% identity	81
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	221708
Seq. ID	LIB3165-017-P1-K1-A11
Method	BLASTX
NCBI GI	g1352821
BLAST score	638
E value	6.0e-67
Match length	127
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221709
Seq. ID	LIB3165-017-P1-K1-A12
Method	BLASTX
NCBI GI	g553107
BLAST score	388
E value	1.0e-37
Match length	113
% identity	68
NCBI Description	(L04967) triosephosphate isomerase [Oryza sativa]

Seq. No.	221710
Seq. ID	LIB3165-017-P1-K1-A2
Method	BLASTX
NCBI GI	g2213629
BLAST score	403
E value	2.0e-39
Match length	99
% identity	71
NCBI Description	(AC000103) F21J9.21 [Arabidopsis thaliana]

Seq. No.	221711
Seq. ID	LIB3165-017-P1-K1-A5
Method	BLASTX
NCBI GI	g20733
BLAST score	567
E value	1.0e-58
Match length	118
% identity	89
NCBI Description	(X15188) precursor C-terminal fragment (AA -80 to 367) [Pisum sativum]

Seq. No.	221712

Seq. ID	LIB3165-017-P1-K1-A6
Method	BLASTX
NCBI GI	g2582822
BLAST score	353
E value	2.0e-33
Match length	102
% identity	37
NCBI Description	(Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]

Seq. No.	221713
Seq. ID	LIB3165-017-P1-K1-A7
Method	BLASTX
NCBI GI	g3402487
BLAST score	374
E value	3.0e-36
Match length	87
% identity	83
NCBI Description	(AB015138) Vacuolar proton pyrophosphatase [Arabidopsis thaliana]

Seq. No.	221714
Seq. ID	LIB3165-017-P1-K1-A9
Method	BLASTX
NCBI GI	g3914658
BLAST score	404
E value	1.0e-39
Match length	108
% identity	74
NCBI Description	50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR >gi_1694974_emb_CAA70851_ (Y09635) plastid ribosomal protein [Arabidopsis thaliana]

Seq. No.	221715
Seq. ID	LIB3165-017-P1-K1-B1
Method	BLASTX
NCBI GI	g2501568
BLAST score	146
E value	3.0e-09
Match length	44
% identity	57
NCBI Description	HYPOTHETICAL 28.8 KD PROTEIN SLL0506 >gi_1001342_dbj_BAA10829_ (D64006) hypothetical protein [Synechocystis sp.]

Seq. No.	221716
Seq. ID	LIB3165-017-P1-K1-B12
Method	BLASTX
NCBI GI	g2511693
BLAST score	389
E value	8.0e-38
Match length	110
% identity	71
NCBI Description	(Z99954) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No.	221717
Seq. ID	LIB3165-017-P1-K1-B3

Method	BLASTX
NCBI GI	g119937
BLAST score	393
E value	3.0e-38
Match length	109
% identity	68
NCBI Description	FERREDOXIN I PRECURSOR >gi_65741_pir__FESP1 ferredoxin [2Fe-2S] I precursor - spinach >gi_170109 (M35660) ferredoxin I precursor [Spinacia oleracea] >gi_227453_prf__1704156A ferredoxin I [Spinacia oleracea]

Seq. No.	221718
Seq. ID	LIB3165-017-P1-K1-B6
Method	BLASTX
NCBI GI	g2546954
BLAST score	437
E value	2.0e-48
Match length	113
% identity	88
NCBI Description	(Y15108) translation elongation factor-TU [Glycine max]

Seq. No.	221719
Seq. ID	LIB3165-017-P1-K1-B7
Method	BLASTX
NCBI GI	g3786001
BLAST score	424
E value	8.0e-42
Match length	93
% identity	82
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	221720
Seq. ID	LIB3165-017-P1-K1-B8
Method	BLASTX
NCBI GI	g115765
BLAST score	469
E value	4.0e-47
Match length	106
% identity	47
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	221721
Seq. ID	LIB3165-017-P1-K1-C10
Method	BLASTX
NCBI GI	g2558962
BLAST score	280
E value	6.0e-25
Match length	60
% identity	97
NCBI Description	(AF025667) histone H2B1 [Gossypium hirsutum]

Seq. No.	221722
Seq. ID	LIB3165-017-P1-K1-C11
Method	BLASTX
NCBI GI	g3702327
BLAST score	257
E value	3.0e-22
Match length	126
% identity	50
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	221723
Seq. ID	LIB3165-017-P1-K1-C12
Method	BLASTX
NCBI GI	g3913018
BLAST score	646
E value	7.0e-68
Match length	135
% identity	90
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No.	221724
Seq. ID	LIB3165-017-P1-K1-C2
Method	BLASTX
NCBI GI	g3850111
BLAST score	150
E value	1.0e-09
Match length	115
% identity	37
NCBI Description	(AL033388) hypothetical integral membrane protein, putative involvement in lipid metabolism [Schizosaccharomyces pombe]

Seq. No.	221725
Seq. ID	LIB3165-017-P1-K1-C3
Method	BLASTX
NCBI GI	g20729
BLAST score	595
E value	7.0e-62
Match length	137
% identity	86
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	221726
Seq. ID	LIB3165-017-P1-K1-C6
Method	BLASTX
NCBI GI	g2582822
BLAST score	203
E value	6.0e-16
Match length	115
% identity	47
NCBI Description	(Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]

Seq. No.	221727
Seq. ID	LIB3165-017-P1-K1-C8

Method	BLASTX
NCBI GI	g4056456
BLAST score	225
E value	2.0e-18
Match length	52
% identity	81
NCBI Description	(AC005990) Strong similarity to gb_U20808 auxin-induced protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF_00107. ESTs gb_T43674, gb_H77006 and gb_AA395179 come from this gene. [Arabidopsis thaliana]

Seq. No.	221728
Seq. ID	LIB3165-017-P1-K1-C9
Method	BLASTX
NCBI GI	g1732511
BLAST score	396
E value	2.0e-38
Match length	91
% identity	82
NCBI Description	(U62742) Ran binding protein 1 homolog [Arabidopsis thaliana]

Seq. No.	221729
Seq. ID	LIB3165-017-P1-K1-D1
Method	BLASTX
NCBI GI	g1495366
BLAST score	338
E value	7.0e-32
Match length	102
% identity	59
NCBI Description	(Z69370) nitrite transporter [Cucumis sativus]

Seq. No.	221730
Seq. ID	LIB3165-017-P1-K1-D11
Method	BLASTX
NCBI GI	g3184258
BLAST score	153
E value	5.0e-10
Match length	59
% identity	44
NCBI Description	(U82130) tumor susceptibility protein [Homo sapiens]

Seq. No.	221731
Seq. ID	LIB3165-017-P1-K1-D12
Method	BLASTX
NCBI GI	g3451068
BLAST score	413
E value	2.0e-40
Match length	120
% identity	73
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	221732
Seq. ID	LIB3165-017-P1-K1-D2
Method	BLASTX
NCBI GI	g4220480
BLAST score	265

E value 4.0e-23
Match length 102
% identity 53
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 221733
Seq. ID LIB3165-017-P1-K1-D3
Method BLASTX
NCBI GI g1352821
BLAST score 591
E value 2.0e-61
Match length 119
% identity 97
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221734
Seq. ID LIB3165-017-P1-K1-D5
Method BLASTX
NCBI GI g3548806
BLAST score 310
E value 2.0e-28
Match length 129
% identity 43
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

Seq. No. 221735
Seq. ID LIB3165-017-P1-K1-D6
Method BLASTX
NCBI GI g166834
BLAST score 627
E value 1.0e-65
Match length 134
% identity 87
NCBI Description (M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No. 221736
Seq. ID LIB3165-017-P1-K1-D7
Method BLASTX
NCBI GI g3334197
BLAST score 470
E value 3.0e-47
Match length 117
% identity 76
NCBI Description AMINOMETHYLTRANSFERASE PRECURSOR (GLYCINE CLEAVAGE SYSTEM T PROTEIN) >gi_2894400_emb_CAA94902_ (Z71184) T-protein [Flaveria anomala]

Seq. No. 221737
Seq. ID LIB3165-017-P1-K1-D8
Method BLASTX
NCBI GI g2565436

BLAST score	270
E value	9.0e-24
Match length	115
% identity	56
NCBI Description	(AF028842) DegP protease precursor [Arabidopsis thaliana]

Seq. No.	221738
Seq. ID	LIB3165-017-P1-K1-D9
Method	BLASTX
NCBI GI	g1168411
BLAST score	387
E value	2.0e-37
Match length	101
% identity	80
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	221739
Seq. ID	LIB3165-017-P1-K1-E1
Method	BLASTX
NCBI GI	g131399
BLAST score	502
E value	6.0e-51
Match length	112
% identity	84
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi_82277_pir__S00411 photosystem II 10K protein precursor - potato >gi_21489_emb_CAA28450_ (X04753) ST-LS1 protein [Solanum tuberosum]

Seq. No.	221740
Seq. ID	LIB3165-017-P1-K1-E11
Method	BLASTX
NCBI GI	g2129921
BLAST score	194
E value	8.0e-15
Match length	51
% identity	75
NCBI Description	hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]

Seq. No.	221741
Seq. ID	LIB3165-017-P1-K1-E2
Method	BLASTN
NCBI GI	g12292
BLAST score	193
E value	1.0e-104
Match length	365
% identity	88
NCBI Description	Spinach chloroplast DNA homologous to ARS and ARC elements upstream of rDNA operon

Seq. No.	221742
Seq. ID	LIB3165-017-P1-K1-E3
Method	BLASTX
NCBI GI	g3510256
BLAST score	172

E value	3.0e-12
Match length	95
% identity	42
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	221743
Seq. ID	LIB3165-017-P1-K1-E4
Method	BLASTX
NCBI GI	g419781
BLAST score	186
E value	3.0e-14
Match length	54
% identity	70
NCBI Description	probable cysteine proteinase precursor (clone CYP-7) - common tobacco >gi_19849_emb_CAA78361_ (Z13959) tobacco pre-pro-cysteine proteinase [Nicotiana tabacum]

Seq. No.	221744
Seq. ID	LIB3165-017-P1-K1-E6
Method	BLASTX
NCBI GI	g3510256
BLAST score	166
E value	1.0e-11
Match length	105
% identity	37
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	221745
Seq. ID	LIB3165-017-P1-K1-E7
Method	BLASTX
NCBI GI	g115765
BLAST score	518
E value	7.0e-53
Match length	123
% identity	77
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	221746
Seq. ID	LIB3165-017-P1-K1-E8
Method	BLASTX
NCBI GI	g1709651
BLAST score	315
E value	4.0e-29
Match length	112
% identity	56
NCBI Description	PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209 plastocyanin a precursor - black poplar >gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus nigra]

Seq. No.	221747
Seq. ID	LIB3165-017-P1-K1-F1
Method	BLASTX
NCBI GI	g2864610
BLAST score	387
E value	2.0e-37
Match length	134
% identity	44
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana] >gi_4049336_emb_CAA22561_ (AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	221748
Seq. ID	LIB3165-017-P1-K1-F11
Method	BLASTX
NCBI GI	g1076678
BLAST score	172
E value	7.0e-13
Match length	45
% identity	78
NCBI Description	ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No.	221749
Seq. ID	LIB3165-017-P1-K1-F12
Method	BLASTX
NCBI GI	g4104929
BLAST score	190
E value	2.0e-14
Match length	118
% identity	42
NCBI Description	(AF042195) auxin response factor 7 [Arabidopsis thaliana]

Seq. No.	221750
Seq. ID	LIB3165-017-P1-K1-F5
Method	BLASTX
NCBI GI	g2494415
BLAST score	333
E value	4.0e-31
Match length	103
% identity	74
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_515747 (L34841) fructose-1,6-bisphosphatase [Glycine max]

Seq. No.	221751
Seq. ID	LIB3165-017-P1-K1-F6
Method	BLASTX
NCBI GI	g1771778
BLAST score	491
E value	9.0e-50
Match length	115
% identity	77
NCBI Description	(X99320) 23 kDa oxygen evolving protein of photosystem II [Solanum tuberosum]

Seq. No.	221752

Seq. ID	LIB3165-017-P1-K1-F7
Method	BLASTX
NCBI GI	g1351408
BLAST score	397
E value	1.0e-38
Match length	94
% identity	79
NCBI Description	VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) >gi_1076563_pir__S51117 cystein proteinase - sweet orange >gi_633185_emb_CAA87720_ (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi_1588548_prf__2208463A vascular processing protease [Citrus sinensis]

Seq. No.	221753
Seq. ID	LIB3165-017-P1-K1-F9
Method	BLASTX
NCBI GI	g625509
BLAST score	579
E value	5.0e-60
Match length	117
% identity	25
NCBI Description	ubiquitin precursor - Arabidopsis thaliana (fragment)

Seq. No.	221754
Seq. ID	LIB3165-017-P1-K1-G12
Method	BLASTX
NCBI GI	g1709846
BLAST score	293
E value	2.0e-26
Match length	126
% identity	45
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_706853 (U04336) 22 kDa component of photosystem II [Lycopersicon esculentum]

Seq. No.	221755
Seq. ID	LIB3165-017-P1-K1-G6
Method	BLASTX
NCBI GI	g433970
BLAST score	653
E value	1.0e-68
Match length	140
% identity	18
NCBI Description	(Z28649) polyubiquitin [Acetabularia cliftonii]

Seq. No.	221756
Seq. ID	LIB3165-017-P1-K1-G7
Method	BLASTX
NCBI GI	g1172664
BLAST score	308
E value	3.0e-28
Match length	132
% identity	59
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_419791_pir__S31165 photosystem I chain III precursor - Flaveria trinervia >gi_298482_bbs_127083 photosystem I

reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem I subunit III [Flaveria trinervia]

Seq. No.	221757
Seq. ID	LIB3165-017-P1-K1-H1
Method	BLASTX
NCBI GI	g3288821
BLAST score	406
E value	1.0e-39
Match length	99
% identity	79
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana]

Seq. No.	221758
Seq. ID	LIB3165-017-P1-K1-H10
Method	BLASTX
NCBI GI	g2493144
BLAST score	431
E value	1.0e-42
Match length	121
% identity	53
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	221759
Seq. ID	LIB3165-017-P1-K1-H11
Method	BLASTX
NCBI GI	g3063392
BLAST score	431
E value	1.0e-42
Match length	115
% identity	76
NCBI Description	(AB012932) Ca2+/H+ exchanger [Vigna radiata]

Seq. No.	221760
Seq. ID	LIB3165-017-P1-K1-H2
Method	BLASTX
NCBI GI	g68200
BLAST score	524
E value	2.0e-53
Match length	129
% identity	82
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	221761
Seq. ID	LIB3165-017-P1-K1-H3
Method	BLASTX
NCBI GI	g121080
BLAST score	454

E value	2.0e-45
Match length	105
% identity	86
NCBI Description	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_1070638_pir__GCPMH glycine cleavage system protein H precursor - garden pea >gi_20737_emb_CAA45978_ (X64726) H protein [Pisum sativum] >gi_169093 (J05164) H-protein of glycine decarboxylase precursor (EC 2.1.2.10) [Pisum sativum] >gi_287815_emb_CAA37704_ (X53656) H-protein [Pisum sativum]

Seq. No.	221762
Seq. ID	LIB3165-017-P1-K1-H5
Method	BLASTX
NCBI GI	g289920
BLAST score	667
E value	3.0e-70
Match length	124
% identity	100
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221763
Seq. ID	LIB3165-017-P1-K1-H6
Method	BLASTX
NCBI GI	g2765081
BLAST score	494
E value	5.0e-50
Match length	132
% identity	74
NCBI Description	(Y10557) g5bf [Arabidopsis thaliana]

Seq. No.	221764
Seq. ID	LIB3165-017-P1-K1-H7
Method	BLASTX
NCBI GI	g4406530
BLAST score	359
E value	3.0e-34
Match length	97
% identity	76
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221765
Seq. ID	LIB3165-017-P1-K1-H8
Method	BLASTX
NCBI GI	g68200
BLAST score	381
E value	9.0e-37
Match length	98
% identity	82
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	221766
Seq. ID	LIB3165-017-P1-K1-H9
Method	BLASTX

NCBI GI	g1352821
BLAST score	559
E value	1.0e-57
Match length	108
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221767
Seq. ID	LIB3165-018-P1-K1-A1
Method	BLASTX
NCBI GI	g115765
BLAST score	445
E value	2.0e-44
Match length	105
% identity	77
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	221768
Seq. ID	LIB3165-018-P1-K1-A10
Method	BLASTX
NCBI GI	g1352821
BLAST score	625
E value	2.0e-65
Match length	123
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221769
Seq. ID	LIB3165-018-P1-K1-A11
Method	BLASTX
NCBI GI	g231610
BLAST score	356
E value	8.0e-34
Match length	118
% identity	65
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]

Seq. No.	221770

Seq. ID	LIB3165-018-P1-K1-A12
Method	BLASTX
NCBI GI	g4164576
BLAST score	341
E value	4.0e-32
Match length	94
% identity	76
NCBI Description	(AF098946) CTF2A [Arabidopsis thaliana]

Seq. No.	221771
Seq. ID	LIB3165-018-P1-K1-A2
Method	BLASTX
NCBI GI	g2494415
BLAST score	295
E value	1.0e-26
Match length	97
% identity	71
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_515747 (L34841) fructose-1,6-bisphosphatase [Glycine max]

Seq. No.	221772
Seq. ID	LIB3165-018-P1-K1-A5
Method	BLASTN
NCBI GI	g468770
BLAST score	36
E value	1.0e-10
Match length	72
% identity	34
NCBI Description	A.thaliana genes for chloroplast ribosomal protein L12 and tRNA-Pro

Seq. No.	221773
Seq. ID	LIB3165-018-P1-K1-A6
Method	BLASTX
NCBI GI	g4097547
BLAST score	311
E value	2.0e-28
Match length	123
% identity	33
NCBI Description	(U64906) ATFP3 [Arabidopsis thaliana]

Seq. No.	221774
Seq. ID	LIB3165-018-P1-K1-A7
Method	BLASTX
NCBI GI	g20729
BLAST score	404
E value	2.0e-39
Match length	112
% identity	74
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	221775
Seq. ID	LIB3165-018-P1-K1-A9
Method	BLASTX
NCBI GI	g2505865

BLAST score	269
E value	1.0e-23
Match length	124
% identity	19
NCBI Description	(Y12227) putative topoisomerase [Arabidopsis thaliana]

Seq. No.	221776
Seq. ID	LIB3165-018-P1-K1-B1
Method	BLASTX
NCBI GI	g1352821
BLAST score	592
E value	2.0e-61
Match length	122
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221777
Seq. ID	LIB3165-018-P1-K1-B10
Method	BLASTX
NCBI GI	g1703478
BLAST score	613
E value	5.0e-64
Match length	125
% identity	90
NCBI Description	(U40566) ubiquitin activating enzyme 2 [Arabidopsis thaliana]

Seq. No.	221778
Seq. ID	LIB3165-018-P1-K1-B11
Method	BLASTX
NCBI GI	g1352821
BLAST score	566
E value	2.0e-58
Match length	107
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221779
Seq. ID	LIB3165-018-P1-K1-B4
Method	BLASTX
NCBI GI	g2501578
BLAST score	524
E value	2.0e-53
Match length	113
% identity	95
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No.	221780
Seq. ID	LIB3165-018-P1-K1-B5
Method	BLASTX
NCBI GI	g2435511
BLAST score	149
E value	1.0e-10
Match length	80
% identity	49
NCBI Description	(AF024504) contains similarity to prolyl 4-hydroxylase alpha subunit [Arabidopsis thaliana]

Seq. No.	221781
Seq. ID	LIB3165-018-P1-K1-B6
Method	BLASTX
NCBI GI	g4510363
BLAST score	545
E value	5.0e-56
Match length	113
% identity	89
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	221782
Seq. ID	LIB3165-018-P1-K1-B7
Method	BLASTX
NCBI GI	g3080428
BLAST score	372
E value	1.0e-35
Match length	98
% identity	69
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	221783
Seq. ID	LIB3165-018-P1-K1-B8
Method	BLASTX
NCBI GI	g100616
BLAST score	589
E value	3.0e-61
Match length	117
% identity	94
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	221784
Seq. ID	LIB3165-018-P1-K1-B9
Method	BLASTX
NCBI GI	g1352821
BLAST score	345
E value	1.0e-32
Match length	70
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

	ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	221785
Seq. ID	LIB3165-018-P1-K1-C10
Method	BLASTX
NCBI GI	g430947
BLAST score	496
E value	3.0e-50
Match length	120
% identity	82
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]
Seq. No.	221786
Seq. ID	LIB3165-018-P1-K1-C12
Method	BLASTX
NCBI GI	g2275219
BLAST score	497
E value	2.0e-50
Match length	133
% identity	70
NCBI Description	(AC002337) unknown protein [Arabidopsis thaliana]
Seq. No.	221787
Seq. ID	LIB3165-018-P1-K1-C2
Method	BLASTX
NCBI GI	g2435406
BLAST score	233
E value	2.0e-19
Match length	135
% identity	44
NCBI Description	(U83490) thaumatin-like protein [Arabidopsis thaliana]
Seq. No.	221788
Seq. ID	LIB3165-018-P1-K1-C5
Method	BLASTX
NCBI GI	g3915022
BLAST score	307
E value	3.0e-30
Match length	135
% identity	53
NCBI Description	SUCROSE-PHOSPHATE SYNTHASE 2 (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 2) >gi_2190350_emb_CAA72491_ (Y11795) sucrose-phosphate synthase [Craterostigma plantagineum]
Seq. No.	221789
Seq. ID	LIB3165-018-P1-K1-C6
Method	BLASTX
NCBI GI	g400890
BLAST score	162
E value	1.0e-20
Match length	117
% identity	43
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR

	>gi_282837_pir__S26953 photosystem II 22K protein precursor - spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864) photosystem II 22 kda polypeptide [spinach, Peptide, 274 aa] [Spinacia oleracea]
Seq. No.	221790
Seq. ID	LIB3165-018-P1-K1-C8
Method	BLASTX
NCBI GI	g1063400
BLAST score	488
E value	2.0e-49
Match length	112
% identity	88
NCBI Description	(X92888) glycolate oxidase [Lycopersicon esculentum]
Seq. No.	221791
Seq. ID	LIB3165-018-P1-K1-C9
Method	BLASTX
NCBI GI	g3885511
BLAST score	391
E value	5.0e-38
Match length	99
% identity	79
NCBI Description	(AF084200) similar to PSI-K subunit of photosystem I from barley [Medicago sativa]
Seq. No.	221792
Seq. ID	LIB3165-018-P1-K1-D1
Method	BLASTX
NCBI GI	g461501
BLAST score	599
E value	9.0e-67
Match length	140
% identity	92
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE 2, CHLOROPLAST >gi_418803_pir__S29048 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea (fragment)
Seq. No.	221793
Seq. ID	LIB3165-018-P1-K1-D10
Method	BLASTX
NCBI GI	g1351279
BLAST score	308
E value	4.0e-32
Match length	110
% identity	68
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_602590_emb_CAA58230_ (X83227) triosephosphate isomerase [Petunia x hybrida]
Seq. No.	221794
Seq. ID	LIB3165-018-P1-K1-D12
Method	BLASTX
NCBI GI	g115765
BLAST score	442
E value	6.0e-44

Match length	122
% identity	66
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]
Seq. No.	221795
Seq. ID	LIB3165-018-P1-K1-D2
Method	BLASTX
NCBI GI	g886100
BLAST score	325
E value	2.0e-50
Match length	132
% identity	79
NCBI Description	(U27347) putative water channel protein; plasmalemma intrinsic protein; similar to Arabidopsis Pip2a gene product, PIR Accession Number S44084 [Glycine max]
Seq. No.	221796
Seq. ID	LIB3165-018-P1-K1-D3
Method	BLASTX
NCBI GI	g2511693
BLAST score	389
E value	1.0e-37
Match length	107
% identity	71
NCBI Description	(Z99954) cysteine proteinase precursor [Phaseolus vulgaris]
Seq. No.	221797
Seq. ID	LIB3165-018-P1-K1-D4
Method	BLASTX
NCBI GI	g118564
BLAST score	473
E value	1.0e-47
Match length	101
% identity	89
NCBI Description	GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE REDUCTASE) (HPR) (GDH) >gi_65955_pir__DEKVG glycerate dehydrogenase (EC 1.1.1.29) - cucumber >gi_18264_emb_CAA41434_ (X58542) NADH-dependent hydroxypyruvate reductase [Cucumis sativus] >gi_18275_emb_CAA32764_ (X14609) NAPH-dependent hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]
Seq. No.	221798
Seq. ID	LIB3165-018-P1-K1-D5
Method	BLASTX
NCBI GI	g2246625
BLAST score	220
E value	7.0e-18
Match length	121
% identity	40

NCBI Description (AF004947) protein kinase [Oryza sativa]

Seq. No. 221799
Seq. ID LIB3165-018-P1-K1-D6
Method BLASTX
NCBI GI g1352821
BLAST score 594
E value 1.0e-61
Match length 111
% identity 97
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221800
Seq. ID LIB3165-018-P1-K1-D7
Method BLASTX
NCBI GI g2582822
BLAST score 239
E value 4.0e-20
Match length 126
% identity 51
NCBI Description (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]

Seq. No. 221801
Seq. ID LIB3165-018-P1-K1-D9
Method BLASTX
NCBI GI g2129538
BLAST score 504
E value 3.0e-51
Match length 105
% identity 91
NCBI Description AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232) AT103 [Arabidopsis thaliana]

Seq. No. 221802
Seq. ID LIB3165-018-P1-K1-E10
Method BLASTX
NCBI GI g131194
BLAST score 368
E value 3.0e-35
Match length 115
% identity 69
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi_72686_pir__F1SP5 photosystem I chain V precursor - spinach >gi_21299_emb_CAA31524_ (X13134) PSI subunit V preprotein (AA -69 to 98) [Spinacia oleracea] >gi_226167_prf__1413236B photosystem I reaction center V [Spinacia oleracea]

Seq. No. 221803
Seq. ID LIB3165-018-P1-K1-E11
Method BLASTX
NCBI GI g4406530

BLAST score	375
E value	5.0e-36
Match length	126
% identity	64
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221804
Seq. ID	LIB3165-018-P1-K1-E2
Method	BLASTX
NCBI GI	g3202042
BLAST score	488
E value	2.0e-49
Match length	114
% identity	82
NCBI Description	(AF069324) 26S proteasome regulatory subunit S5A [Mesembryanthemum crystallinum]

Seq. No.	221805
Seq. ID	LIB3165-018-P1-K1-E5
Method	BLASTX
NCBI GI	g3914603
BLAST score	532
E value	2.0e-54
Match length	130
% identity	76
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No.	221806
Seq. ID	LIB3165-018-P1-K1-E6
Method	BLASTX
NCBI GI	g132808
BLAST score	440
E value	1.0e-43
Match length	93
% identity	91
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L23 >gi_71299_pir__R5NT23 ribosomal protein L23 - common tobacco chloroplast >gi_11868_emb_CAA77385_ (Z00044) ribosomal protein L23 [Nicotiana tabacum] >gi_1223690_emb_CAA77408_ (Z00044) ribosomal protein L23 [Nicotiana tabacum] >gi_225239_prf__1211235BX ribosomal protein L23 [Nicotiana tabacum] >gi_227679_prf__1709206A ribosomal protein CL23 [Nicotiana tabacum]

Seq. No.	221807
Seq. ID	LIB3165-018-P1-K1-E7
Method	BLASTX
NCBI GI	g3158476
BLAST score	417
E value	4.0e-41
Match length	94
% identity	83
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	221808
Seq. ID	LIB3165-018-P1-K1-E8
Method	BLASTX
NCBI GI	g586004
BLAST score	618
E value	1.0e-64
Match length	128
% identity	88
NCBI Description	SUPEROXIDE DISMUTASE [CU-ZN] >gi_421962_pir__S34267 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato >gi_542090_pir__S40404 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato >gi_311971_emb_CAA51654_ (X73139) superoxide dismutase [Ipomoea batatas]

Seq. No.	221809
Seq. ID	LIB3165-018-P1-K1-E9
Method	BLASTX
NCBI GI	g131399
BLAST score	363
E value	8.0e-35
Match length	97
% identity	70
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi_82277_pir__S00411 photosystem II 10K protein precursor - potato >gi_21489_emb_CAA28450_ (X04753) ST-LS1 protein [Solanum tuberosum]

Seq. No.	221810
Seq. ID	LIB3165-018-P1-K1-F1
Method	BLASTX
NCBI GI	g730850
BLAST score	143
E value	7.0e-09
Match length	123
% identity	28
NCBI Description	SUR2 PROTEIN (SYRINGOMYCIN RESPONSE PROTEIN 2) >gi_626942_pir__S48533 SUR2 protein - yeast (Saccharomyces cerevisiae) >gi_458718 (U07171) Sur2p [Saccharomyces cerevisiae] >gi_849215 (U28374) Sur2p: syringomycin response protein 2 [Saccharomyces cerevisiae] >gi_1786173 (U10427) Syr2p [Saccharomyces cerevisiae]

Seq. No.	221811
Seq. ID	LIB3165-018-P1-K1-F10
Method	BLASTX
NCBI GI	g1673344
BLAST score	166
E value	1.0e-11
Match length	53
% identity	55
NCBI Description	(D64002) hypothetical protein [Synechocystis sp.]

Seq. No.	221812
Seq. ID	LIB3165-018-P1-K1-F12
Method	BLASTX
NCBI GI	g3935184

BLAST score	304
E value	9.0e-28
Match length	77
% identity	71
NCBI Description	(AC004557) F17L21.27 [Arabidopsis thaliana]

Seq. No.	221813
Seq. ID	LIB3165-018-P1-K1-F2
Method	BLASTX
NCBI GI	g2924262
BLAST score	576
E value	1.0e-59
Match length	139
% identity	77
NCBI Description	(Z00044) PSII 44kd protein [Nicotiana tabacum]

Seq. No.	221814
Seq. ID	LIB3165-018-P1-K1-F3
Method	BLASTX
NCBI GI	g3150412
BLAST score	327
E value	2.0e-30
Match length	101
% identity	64
NCBI Description	(AC004165) putative Fe(II) transport protein [Arabidopsis thaliana] >gi_3420044 (AC004680) putative Fe(II) transport protein [Arabidopsis thaliana]

Seq. No.	221815
Seq. ID	LIB3165-018-P1-K1-F4
Method	BLASTX
NCBI GI	g3808101
BLAST score	278
E value	1.0e-24
Match length	97
% identity	59
NCBI Description	(AJ012165) chloroplast protease [Capsicum annuum]

Seq. No.	221816
Seq. ID	LIB3165-018-P1-K1-F6
Method	BLASTX
NCBI GI	g131276
BLAST score	485
E value	5.0e-49
Match length	91
% identity	96
NCBI Description	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi_72704_pir__QJNT6A photosystem II chlorophyll a-binding protein psbB - common tobacco chloroplast >gi_11856_emb_CAA77373_ (Z00044) PSII 47kD protein [Nicotiana tabacum] >gi_225224_prf__1211235BF photosystem II P680 apoprotein [Nicotiana tabacum]

Seq. No.	221817
Seq. ID	LIB3165-018-P1-K1-F7
Method	BLASTX
NCBI GI	g1352821

BLAST score	641
E value	3.0e-67
Match length	121
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221818
Seq. ID	LIB3165-018-P1-K1-F8
Method	BLASTX
NCBI GI	g3176076
BLAST score	260
E value	1.0e-22
Match length	60
% identity	82
NCBI Description	(AJ002487) protein phosphatase 1 catalitic subunit [Medicago sativa]

Seq. No.	221819
Seq. ID	LIB3165-018-P1-K1-G10
Method	BLASTX
NCBI GI	g1170567
BLAST score	691
E value	4.0e-73
Match length	143
% identity	93
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1085960_pir__S52648 INO1 protein - Citrus paradisi >gi_602565_emb_CAA83565_ (Z32632) INO1 [Citrus x paradisi]

Seq. No.	221820
Seq. ID	LIB3165-018-P1-K1-G12
Method	BLASTX
NCBI GI	g3282092
BLAST score	170
E value	5.0e-12
Match length	116
% identity	36
NCBI Description	(AJ007446) hypothetical protein [Thermotoga neapolitana]

Seq. No.	221821
Seq. ID	LIB3165-018-P1-K1-G2
Method	BLASTX
NCBI GI	g1449179
BLAST score	153
E value	1.0e-14
Match length	78
% identity	60
NCBI Description	(D86506) N-ethylmaleimide sensitive fusion protein [Nicotiana tabacum]

Seq. No.	221822
Seq. ID	LIB3165-018-P1-K1-G3
Method	BLASTX

NCBI GI	g2262116
BLAST score	252
E value	2.0e-28
Match length	110
% identity	62
NCBI Description	(AC002343) cellulose synthase isolog [Arabidopsis thaliana]

Seq. No.	221823
Seq. ID	LIB3165-018-P1-K1-G4
Method	BLASTX
NCBI GI	g68200
BLAST score	519
E value	6.0e-53
Match length	128
% identity	83
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	221824
Seq. ID	LIB3165-018-P1-K1-G5
Method	BLASTX
NCBI GI	g3914605
BLAST score	665
E value	5.0e-70
Match length	140
% identity	89
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase - apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica]

Seq. No.	221825
Seq. ID	LIB3165-018-P1-K1-G7
Method	BLASTN
NCBI GI	g2687432
BLAST score	42
E value	1.0e-14
Match length	102
% identity	85
NCBI Description	Plumbago auriculata large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	221826
Seq. ID	LIB3165-018-P1-K1-G9
Method	BLASTX
NCBI GI	g2493694
BLAST score	257
E value	3.0e-22
Match length	112
% identity	54
NCBI Description	PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII 6.1 KD PROTEIN) >gi_1076268_pir__S53025 photosystem II protein - spinach >gi_728716_emb_CAA59409_ (X85038) protein of photosystem II [Spinacia oleracea]

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Seq. No.	221827
Seq. ID	LIB3165-018-P1-K1-H1
Method	BLASTX
NCBI GI	g68200
BLAST score	438
E value	1.0e-43
Match length	109
% identity	82
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	221828
Seq. ID	LIB3165-018-P1-K1-H10
Method	BLASTX
NCBI GI	g1709825
BLAST score	398
E value	9.0e-39
Match length	120
% identity	68
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No.	221829
Seq. ID	LIB3165-018-P1-K1-H11
Method	BLASTX
NCBI GI	g1353352
BLAST score	440
E value	1.0e-43
Match length	135
% identity	57
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	221830
Seq. ID	LIB3165-018-P1-K1-H12
Method	BLASTX
NCBI GI	g1354517
BLAST score	292
E value	3.0e-26
Match length	133
% identity	53
NCBI Description	(U55838) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	221831
Seq. ID	LIB3165-018-P1-K1-H2
Method	BLASTX
NCBI GI	g1181599
BLAST score	324
E value	4.0e-30
Match length	131
% identity	42
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.	221832

Seq. ID	LIB3165-018-P1-K1-H3
Method	BLASTX
NCBI GI	g1172664
BLAST score	223
E value	3.0e-18
Match length	48
% identity	92
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_419791_pir__S31165 photosystem I chain III precursor - Flaveria trinervia >gi_298482_bbs_127083 photosystem I reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem I subunit III [Flaveria trinervia]

Seq. No.	221833
Seq. ID	LIB3165-018-P1-K1-H5
Method	BLASTX
NCBI GI	g4545262
BLAST score	160
E value	7.0e-11
Match length	44
% identity	64
NCBI Description	(AF118230) metallothionein-like protein [Gossypium hirsutum]

Seq. No.	221834
Seq. ID	LIB3165-018-P1-K1-H7
Method	BLASTX
NCBI GI	g4325041
BLAST score	246
E value	7.0e-35
Match length	118
% identity	69
NCBI Description	(AF117339) FtsH-like protein Pftf precursor [Nicotiana tabacum]

Seq. No.	221835
Seq. ID	LIB3165-019-P1-K1-A2
Method	BLASTX
NCBI GI	g421826
BLAST score	148
E value	2.0e-17
Match length	69
% identity	66
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	221836
Seq. ID	LIB3165-019-P1-K1-A5
Method	BLASTX
NCBI GI	g3212610
BLAST score	287
E value	1.0e-25
Match length	108
% identity	54

NCBI Description	Chain A, Sulfite Oxidase From Chicken Liver >gi_3212611_pdb_1SOX_B Chain B, Sulfite Oxidase From Chicken Liver
Seq. No.	221837
Seq. ID	LIB3165-019-P1-K1-A6
Method	BLASTX
NCBI GI	g1351411
BLAST score	323
E value	3.0e-30
Match length	77
% identity	75
NCBI Description	VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) (PROTEINASE B) >gi_1076553_pir__S49175 cysteine proteinase precursor - spring vetch >gi_2129906_pir__S68984 cysteine proteinase precursor - spring vetch >gi_510358_emb_CAA84383_ (Z34899) cysteine proteinase [Vicia sativa]
Seq. No.	221838
Seq. ID	LIB3165-019-P1-K1-A7
Method	BLASTX
NCBI GI	g1644427
BLAST score	313
E value	9.0e-29
Match length	77
% identity	79
NCBI Description	(U74610) glyoxalase II [Arabidopsis thaliana]
Seq. No.	221839
Seq. ID	LIB3165-019-P1-K1-A8
Method	BLASTX
NCBI GI	g418854
BLAST score	617
E value	2.0e-64
Match length	124
% identity	18
NCBI Description	ubiquitin precursor - parsley >gi_288112_emb_CAA45621_ (X64344) polyubiquitin [Petroselinum crispum] >gi_288114_emb_CAA45622_ (X64345) polyubiquitin [Petroselinum crispum]
Seq. No.	221840
Seq. ID	LIB3165-019-P1-K1-B11
Method	BLASTX
NCBI GI	g3912953
BLAST score	197
E value	4.0e-15
Match length	77
% identity	51
NCBI Description	PUTATIVE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE DEAMINASE (ACC DEAMINASE)
Seq. No.	221841
Seq. ID	LIB3165-019-P1-K1-B3
Method	BLASTX
NCBI GI	g4263711
BLAST score	293

E value	2.0e-26
Match length	108
% identity	56
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	221842
Seq. ID	LIB3165-019-P1-K1-B5
Method	BLASTX
NCBI GI	g2104951
BLAST score	311
E value	1.0e-28
Match length	129
% identity	57
NCBI Description	(U96717) MAP kinase-like protein [Selaginella lepidophylla]

Seq. No.	221843
Seq. ID	LIB3165-019-P1-K1-B8
Method	BLASTX
NCBI GI	g3292814
BLAST score	158
E value	1.0e-10
Match length	96
% identity	44
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	221844
Seq. ID	LIB3165-019-P1-K1-B9
Method	BLASTX
NCBI GI	g20739
BLAST score	348
E value	6.0e-33
Match length	69
% identity	90
NCBI Description	(X54377) P-protein subunit of glycine decarboxylase enzyme complex [Pisum sativum]

Seq. No.	221845
Seq. ID	LIB3165-019-P1-K1-C10
Method	BLASTX
NCBI GI	g1172437
BLAST score	528
E value	5.0e-54
Match length	99
% identity	100
NCBI Description	CYTOCHROME B6-F COMPLEX SUBUNIT 4 (17 KD POLYPEPTIDE) >gi_1363524_pir__S58582 plastoquinol--plastocyanin reductase (EC 1.10.99.1) 17K protein - maize chloroplast >gi_902252_emb_CAA60316_ (X86563) cytochrome b/f [Zea mays]

Seq. No.	221846
Seq. ID	LIB3165-019-P1-K1-C12
Method	BLASTX
NCBI GI	g266893
BLAST score	645
E value	1.0e-67
Match length	125

% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__S28172 ribulose-bisphosphate carboxylase activase - cucumber >gi_18284_emb_CAA47906_ (X67674) rubisco activase [Cucumis sativus]
Seq. No.	221847
Seq. ID	LIB3165-019-P1-K1-C2
Method	BLASTX
NCBI GI	g289920
BLAST score	673
E value	5.0e-71
Match length	127
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]
Seq. No.	221848
Seq. ID	LIB3165-019-P1-K1-C7
Method	BLASTX
NCBI GI	g1707008
BLAST score	209
E value	1.0e-16
Match length	86
% identity	51
NCBI Description	(U78721) 30S ribosomal protein S5 isolog [Arabidopsis thaliana]
Seq. No.	221849
Seq. ID	LIB3165-019-P1-K1-C8
Method	BLASTX
NCBI GI	g3914603
BLAST score	592
E value	1.0e-61
Match length	128
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]
Seq. No.	221850
Seq. ID	LIB3165-019-P1-K1-D12
Method	BLASTX
NCBI GI	g3643608
BLAST score	266
E value	3.0e-23
Match length	101
% identity	52
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]
Seq. No.	221851
Seq. ID	LIB3165-019-P1-K1-D2
Method	BLASTX
NCBI GI	g2262170
BLAST score	204

E value	5.0e-16
Match length	114
% identity	44
NCBI Description	(AC002329) predicted glycosyl hydrolase [Arabidopsis thaliana]

Seq. No.	221852
Seq. ID	LIB3165-019-P1-K1-D3
Method	BLASTX
NCBI GI	g1352821
BLAST score	546
E value	4.0e-56
Match length	104
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221853
Seq. ID	LIB3165-019-P1-K1-D6
Method	BLASTX
NCBI GI	g2827548
BLAST score	258
E value	3.0e-22
Match length	85
% identity	56
NCBI Description	(AL021635) cytochrome P450 - like protein [Arabidopsis thaliana]

Seq. No.	221854
Seq. ID	LIB3165-019-P1-K1-D9
Method	BLASTX
NCBI GI	g1168411
BLAST score	332
E value	5.0e-31
Match length	88
% identity	80
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	221855
Seq. ID	LIB3165-019-P1-K1-E10
Method	BLASTX
NCBI GI	g3914603
BLAST score	546
E value	4.0e-56
Match length	131
% identity	79
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No.	221856
Seq. ID	LIB3165-019-P1-K1-E12
Method	BLASTX

NCBI GI	g289920
BLAST score	723
E value	7.0e-77
Match length	136
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221857
Seq. ID	LIB3165-019-P1-K1-E4
Method	BLASTX
NCBI GI	g480082
BLAST score	169
E value	7.0e-12
Match length	139
% identity	33
NCBI Description	catechol O-methyltransferase (EC 2.1.1.6) - common tobacco >gi_396589_emb_CAA52461_ (X74452) catechol O-methyltransferase [Nicotiana tabacum]

Seq. No.	221858
Seq. ID	LIB3165-019-P1-K1-E5
Method	BLASTX
NCBI GI	g3687652
BLAST score	180
E value	4.0e-13
Match length	96
% identity	48
NCBI Description	(AF047352) rubisco activase precursor [Datisca glomerata]

Seq. No.	221859
Seq. ID	LIB3165-019-P1-K1-E7
Method	BLASTX
NCBI GI	g1352821
BLAST score	593
E value	1.0e-61
Match length	111
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221860
Seq. ID	LIB3165-019-P1-K1-E8
Method	BLASTX
NCBI GI	g100203
BLAST score	141
E value	8.0e-09
Match length	104
% identity	40
NCBI Description	cysteine proteinase (EC 3.4.22.-) precursor - tomato >gi_19195_emb_CAA78403_ (Z14028) pre-pro-cysteine proteinase [Lycopersicon esculentum]

Seq. No.	221861

Seq. ID	LIB3165-019-P1-K1-E9
Method	BLASTX
NCBI GI	g2853087
BLAST score	401
E value	4.0e-39
Match length	126
% identity	41
NCBI Description	(AL021768) putative protein [Arabidopsis thaliana]

Seq. No.	221862
Seq. ID	LIB3165-019-P1-K1-F1
Method	BLASTX
NCBI GI	g1181599
BLAST score	381
E value	5.0e-37
Match length	105
% identity	72
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.	221863
Seq. ID	LIB3165-019-P1-K1-F10
Method	BLASTX
NCBI GI	g4574320
BLAST score	208
E value	2.0e-16
Match length	61
% identity	67
NCBI Description	(AF117224) wound-induced protein WI12 [Mesembryanthemum crystallinum]

Seq. No.	221864
Seq. ID	LIB3165-019-P1-K1-F11
Method	BLASTX
NCBI GI	g1174162
BLAST score	528
E value	4.0e-54
Match length	101
% identity	91
NCBI Description	(U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi_3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No.	221865
Seq. ID	LIB3165-019-P1-K1-F12
Method	BLASTX
NCBI GI	g3913018
BLAST score	518
E value	5.0e-53
Match length	108
% identity	91
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No.	221866
Seq. ID	LIB3165-019-P1-K1-F2
Method	BLASTX

NCBI GI	g4406530
BLAST score	206
E value	2.0e-16
Match length	63
% identity	71
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221867
Seq. ID	LIB3165-019-P1-K1-F6
Method	BLASTN
NCBI GI	g2477521
BLAST score	49
E value	2.0e-18
Match length	65
% identity	94
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	221868
Seq. ID	LIB3165-019-P1-K1-F7
Method	BLASTX
NCBI GI	g3334320
BLAST score	448
E value	9.0e-45
Match length	99
% identity	92
NCBI Description	40S RIBOSOMAL PROTEIN SA (P40) >gi_2444420 (AF020553) ribosome-associated protein p40 [Glycine max]

Seq. No.	221869
Seq. ID	LIB3165-019-P1-K1-F8
Method	BLASTX
NCBI GI	g1439609
BLAST score	556
E value	2.0e-57
Match length	112
% identity	53
NCBI Description	(U62778) delta-tonoplast intrinsic protein [Gossypium hirsutum]

Seq. No.	221870
Seq. ID	LIB3165-019-P1-K1-F9
Method	BLASTX
NCBI GI	g131385
BLAST score	496
E value	2.0e-50
Match length	130
% identity	78
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN)

Seq. No.	221871
Seq. ID	LIB3165-019-P1-K1-G1
Method	BLASTX
NCBI GI	g548774
BLAST score	207

E value 7.0e-17
Match length 40
% identity 95
NCBI Description 60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631) ribosomal protein L7A [Oryza sativa]

Seq. No. 221872
Seq. ID LIB3165-019-P1-K1-G10
Method BLASTX
NCBI GI g1354515
BLAST score 274
E value 3.0e-24
Match length 131
% identity 52
NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No. 221873
Seq. ID LIB3165-019-P1-K1-G2
Method BLASTX
NCBI GI g508304
BLAST score 353
E value 2.0e-33
Match length 79
% identity 80
NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 221874
Seq. ID LIB3165-019-P1-K1-G3
Method BLASTX
NCBI GI g1352821
BLAST score 641
E value 3.0e-67
Match length 124
% identity 99
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221875
Seq. ID LIB3165-019-P1-K1-G6
Method BLASTX
NCBI GI g2160782
BLAST score 324
E value 3.0e-30
Match length 75
% identity 84
NCBI Description (AF001505) putative ammonium transporter OsAMT1p [Oryza sativa]

Seq. No. 221876
Seq. ID LIB3165-019-P1-K1-G7
Method BLASTX
NCBI GI g1168411

BLAST score 264
E value 3.0e-23
Match length 75
% identity 75
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No. 221877
Seq. ID LIB3165-019-P1-K1-G9
Method BLASTX
NCBI GI g1709651
BLAST score 353
E value 1.0e-33
Match length 107
% identity 64
NCBI Description PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209 plastocyanin a precursor - black poplar >gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus nigra]

Seq. No. 221878
Seq. ID LIB3165-019-P1-K1-H10
Method BLASTX
NCBI GI g445613
BLAST score 494
E value 4.0e-50
Match length 123
% identity 75
NCBI Description ribosomal protein L7 [Solanum tuberosum]

Seq. No. 221879
Seq. ID LIB3165-019-P1-K1-H11
Method BLASTX
NCBI GI g729051
BLAST score 551
E value 1.0e-56
Match length 115
% identity 59
NCBI Description CALTRACTIN (CENTRIN) >gi_444342_prf__1906390A caltractin-like protein [Atriplex nummularia]

Seq. No. 221880
Seq. ID LIB3165-019-P1-K1-H12
Method BLASTX
NCBI GI g2708749
BLAST score 244
E value 1.0e-20
Match length 76
% identity 58
NCBI Description (AC003952) putative senescence-assoc. rhodanese-like protein [Arabidopsis thaliana]

Seq. No. 221881
Seq. ID LIB3165-019-P1-K1-H3
Method BLASTX
NCBI GI g4262181
BLAST score 144
E value 5.0e-09

Match length	101
% identity	43
NCBI Description	(AC005508) 37496 [Arabidopsis thaliana]

Seq. No.	221882
Seq. ID	LIB3165-019-P1-K1-H5
Method	BLASTX
NCBI GI	g1352821
BLAST score	552
E value	7.0e-57
Match length	116
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221883
Seq. ID	LIB3165-019-P1-K1-H6
Method	BLASTX
NCBI GI	g4406530
BLAST score	207
E value	2.0e-16
Match length	77
% identity	58
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221884
Seq. ID	LIB3165-019-P1-K1-H7
Method	BLASTX
NCBI GI	g3928760
BLAST score	176
E value	7.0e-13
Match length	75
% identity	48
NCBI Description	(AB011797) homolog to plastid-lipid-associated protein [Citrus unshiu]

Seq. No.	221885
Seq. ID	LIB3165-019-P1-K1-H9
Method	BLASTX
NCBI GI	g82263
BLAST score	236
E value	7.0e-20
Match length	93
% identity	62
NCBI Description	ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome c1 precursor (clone pC(1)3II) - potato

Seq. No.	221886
Seq. ID	LIB3165-020-P1-K1-A1
Method	BLASTX
NCBI GI	g1181599
BLAST score	162
E value	2.0e-11
Match length	83

% identity	48
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.	221887
Seq. ID	LIB3165-020-P1-K1-A11
Method	BLASTX
NCBI GI	g1168411
BLAST score	327
E value	2.0e-30
Match length	87
% identity	79
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	221888
Seq. ID	LIB3165-020-P1-K1-A12
Method	BLASTX
NCBI GI	g1354515
BLAST score	318
E value	2.0e-29
Match length	140
% identity	50
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	221889
Seq. ID	LIB3165-020-P1-K1-A4
Method	BLASTX
NCBI GI	g1352821
BLAST score	612
E value	8.0e-64
Match length	114
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221890
Seq. ID	LIB3165-020-P1-K1-A5
Method	BLASTX
NCBI GI	g3869088
BLAST score	618
E value	2.0e-64
Match length	119
% identity	99
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No.	221891
Seq. ID	LIB3165-020-P1-K1-A6
Method	BLASTX
NCBI GI	g1181599
BLAST score	288
E value	3.0e-26
Match length	83
% identity	69
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.	221892
Seq. ID	LIB3165-020-P1-K1-A7
Method	BLASTX
NCBI GI	g266893
BLAST score	654
E value	8.0e-69
Match length	127
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__S28172 ribulose-bisphosphate carboxylase activase - cucumber >gi_18284_emb_CAA47906_ (X67674) rubisco activase [Cucumis sativus]

Seq. No.	221893
Seq. ID	LIB3165-020-P1-K1-B10
Method	BLASTX
NCBI GI	g399082
BLAST score	199
E value	2.0e-15
Match length	128
% identity	39
NCBI Description	ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR >gi_322713_pir__S28171 H+-transporting ATP synthase (EC 3.6.1.34) delta chain, chloroplast - garden pea >gi_169045 (M94558) ATP synthase delta subunit [Pisum sativum]

Seq. No.	221894
Seq. ID	LIB3165-020-P1-K1-B11
Method	BLASTX
NCBI GI	g2661021
BLAST score	592
E value	1.0e-61
Match length	112
% identity	98
NCBI Description	(AF035255) catalase [Glycine max]

Seq. No.	221895
Seq. ID	LIB3165-020-P1-K1-B12
Method	BLASTX
NCBI GI	g400890
BLAST score	316
E value	4.0e-29
Match length	128
% identity	45
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_282837_pir__S26953 photosystem II 22K protein precursor - spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864) photosystem II 22 kda polypeptide [spinach, Peptide, 274 aa] [Spinacia oleracea]

Seq. No.	221896
Seq. ID	LIB3165-020-P1-K1-B3
Method	BLASTX
NCBI GI	g1352821

BLAST score	627
E value	1.0e-65
Match length	119
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221897
Seq. ID	LIB3165-020-P1-K1-B4
Method	BLASTX
NCBI GI	g4406530
BLAST score	363
E value	1.0e-34
Match length	119
% identity	65
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221898
Seq. ID	LIB3165-020-P1-K1-B5
Method	BLASTX
NCBI GI	g100200
BLAST score	437
E value	3.0e-43
Match length	114
% identity	75
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	221899
Seq. ID	LIB3165-020-P1-K1-B7
Method	BLASTX
NCBI GI	g992706
BLAST score	527
E value	7.0e-54
Match length	100
% identity	92
NCBI Description	(U33758) UBC13 [Arabidopsis thaliana]

Seq. No.	221900
Seq. ID	LIB3165-020-P1-K1-B8
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	221901
Seq. ID	LIB3165-020-P1-K1-C10
Method	BLASTX
NCBI GI	g2914706
BLAST score	355
E value	1.0e-33
Match length	94

% identity	65
NCBI Description	(AC003974) putative homeobox protein [Arabidopsis thaliana]

Seq. No.	221902
Seq. ID	LIB3165-020-P1-K1-C2
Method	BLASTN
NCBI GI	g2687442
BLAST score	94
E value	8.0e-46
Match length	146
% identity	91
NCBI Description	Mitella pentandra large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	221903
Seq. ID	LIB3165-020-P1-K1-C5
Method	BLASTX
NCBI GI	g2191191
BLAST score	242
E value	2.0e-20
Match length	114
% identity	54
NCBI Description	(AF007271) A_TM021B04.14 gene product [Arabidopsis thaliana]

Seq. No.	221904
Seq. ID	LIB3165-020-P1-K1-C8
Method	BLASTX
NCBI GI	g2791834
BLAST score	511
E value	5.0e-52
Match length	97
% identity	100
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No.	221905
Seq. ID	LIB3165-020-P1-K1-C9
Method	BLASTX
NCBI GI	g2738949
BLAST score	547
E value	3.0e-56
Match length	114
% identity	89
NCBI Description	(AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa]

Seq. No.	221906
Seq. ID	LIB3165-020-P1-K1-D1
Method	BLASTX
NCBI GI	g289920
BLAST score	695
E value	1.0e-73
Match length	135
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221907
Seq. ID	LIB3165-020-P1-K1-D10
Method	BLASTX
NCBI GI	g1304227
BLAST score	501
E value	8.0e-51
Match length	128
% identity	70
NCBI Description	(D63781) Epoxide hydrolase [Glycine max] >gi_2764804_emb_CAA55293_ (X78547) epoxide hydrolase [Glycine max]

Seq. No.	221908
Seq. ID	LIB3165-020-P1-K1-D12
Method	BLASTX
NCBI GI	g1352821
BLAST score	246
E value	3.0e-21
Match length	72
% identity	74
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221909
Seq. ID	LIB3165-020-P1-K1-D5
Method	BLASTX
NCBI GI	g4406530
BLAST score	392
E value	5.0e-38
Match length	111
% identity	74
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221910
Seq. ID	LIB3165-020-P1-K1-D8
Method	BLASTX
NCBI GI	g2266992
BLAST score	392
E value	5.0e-38
Match length	131
% identity	51
NCBI Description	(U77412) O-linked GlcNAc transferase [Caenorhabditis elegans]

Seq. No.	221911
Seq. ID	LIB3165-020-P1-K1-E1
Method	BLASTX
NCBI GI	g1345698
BLAST score	637
E value	9.0e-67
Match length	126
% identity	94
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR (CAB-151) (LHCP) >gi_99601_pir__S20917 chlorophyll

a/b-binding protein - upland cotton
>gi_452314_emb_CAA38025_ (X54090) chlorophyll ab binding protein [Gossypium hirsutum]

Seq. No.	221912
Seq. ID	LIB3165-020-P1-K1-E10
Method	BLASTX
NCBI GI	g289920
BLAST score	451
E value	2.0e-45
Match length	84
% identity	100
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221913
Seq. ID	LIB3165-020-P1-K1-E12
Method	BLASTX
NCBI GI	g1352821
BLAST score	597
E value	4.0e-62
Match length	113
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221914
Seq. ID	LIB3165-020-P1-K1-E2
Method	BLASTX
NCBI GI	g289920
BLAST score	719
E value	2.0e-76
Match length	136
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221915
Seq. ID	LIB3165-020-P1-K1-E3
Method	BLASTX
NCBI GI	g289920
BLAST score	723
E value	8.0e-77
Match length	136
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221916
Seq. ID	LIB3165-020-P1-K1-E5
Method	BLASTX
NCBI GI	g3510256
BLAST score	258
E value	3.0e-22

Match length	125
% identity	44
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	221917
Seq. ID	LIB3165-020-P1-K1-F10
Method	BLASTX
NCBI GI	g1352821
BLAST score	590
E value	3.0e-61
Match length	110
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221918
Seq. ID	LIB3165-020-P1-K1-F12
Method	BLASTX
NCBI GI	g2815246
BLAST score	225
E value	2.0e-18
Match length	55
% identity	73
NCBI Description	(X95709) class I type 2 metallothionein [Cicer arietinum]

Seq. No.	221919
Seq. ID	LIB3165-020-P1-K1-F3
Method	BLASTX
NCBI GI	g11638
BLAST score	219
E value	9.0e-38
Match length	107
% identity	81
NCBI Description	(X01647) open reading frame (ORF701) pot. membrane protein (aa 1-487) [Marchantia polymorpha]

Seq. No.	221920
Seq. ID	LIB3165-020-P1-K1-F5
Method	BLASTX
NCBI GI	g289920
BLAST score	727
E value	3.0e-77
Match length	138
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221921
Seq. ID	LIB3165-020-P1-K1-F6
Method	BLASTX
NCBI GI	g2244916
BLAST score	215
E value	3.0e-17
Match length	133

% identity	35
NCBI Description	(Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	221922
Seq. ID	LIB3165-020-P1-K1-F7
Method	BLASTX
NCBI GI	g945081
BLAST score	535
E value	8.0e-55
Match length	134
% identity	78
NCBI Description	(U31094) P21 [Petunia hybrida]

Seq. No.	221923
Seq. ID	LIB3165-020-P1-K1-F8
Method	BLASTX
NCBI GI	g285317
BLAST score	463
E value	2.0e-46
Match length	141
% identity	70
NCBI Description	dihydrolipoamide dehydrogenase (EC 1.8.1.4) - garden pea

Seq. No.	221924
Seq. ID	LIB3165-020-P1-K1-G11
Method	BLASTX
NCBI GI	g1354515
BLAST score	343
E value	2.0e-32
Match length	146
% identity	53
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	221925
Seq. ID	LIB3165-020-P1-K1-G12
Method	BLASTX
NCBI GI	g289920
BLAST score	718
E value	3.0e-76
Match length	134
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221926
Seq. ID	LIB3165-020-P1-K1-G2
Method	BLASTX
NCBI GI	g1168408
BLAST score	597
E value	4.0e-62
Match length	132
% identity	89
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1 >gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828) fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No.	221927
Seq. ID	LIB3165-020-P1-K1-G3
Method	BLASTX
NCBI GI	g1352821
BLAST score	613
E value	6.0e-64
Match length	115
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221928
Seq. ID	LIB3165-020-P1-K1-G6
Method	BLASTX
NCBI GI	g1694621
BLAST score	369
E value	2.0e-35
Match length	114
% identity	68
NCBI Description	(D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]

Seq. No.	221929
Seq. ID	LIB3165-020-P1-K1-H1
Method	BLASTX
NCBI GI	g3063444
BLAST score	529
E value	4.0e-54
Match length	142
% identity	68
NCBI Description	(AC003981) F22O13.5 [Arabidopsis thaliana]

Seq. No.	221930
Seq. ID	LIB3165-020-P1-K1-H12
Method	BLASTX
NCBI GI	g1352821
BLAST score	608
E value	2.0e-63
Match length	124
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221931
Seq. ID	LIB3165-020-P1-K1-H2
Method	BLASTX
NCBI GI	g2995384
BLAST score	286
E value	9.0e-28
Match length	114
% identity	57

NCBI Description	(AJ004810) cytochrome P450 monooxygenase [Zea mays]
Seq. No.	221932
Seq. ID	LIB3165-020-P1-K1-H4
Method	BLASTX
NCBI GI	g2351846
BLAST score	208
E value	2.0e-16
Match length	105
% identity	46
NCBI Description	(U93050) poly(A) binding protein II [Mus musculus]
Seq. No.	221933
Seq. ID	LIB3165-020-P1-K1-H5
Method	BLASTX
NCBI GI	g3738285
BLAST score	506
E value	2.0e-51
Match length	127
% identity	75
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.	221934
Seq. ID	LIB3165-020-P1-K1-H6
Method	BLASTX
NCBI GI	g548437
BLAST score	179
E value	4.0e-13
Match length	133
% identity	36
NCBI Description	OSH1 PROTEIN >gi_1078479_pir__S53463 SWH1 protein (version 1) - yeast (Saccharomyces cerevisiae) >gi_456143 (L28920) Osh1p [Saccharomyces cerevisiae]
Seq. No.	221935
Seq. ID	LIB3165-020-P1-K1-H8
Method	BLASTX
NCBI GI	g231688
BLAST score	668
E value	2.0e-70
Match length	126
% identity	100
NCBI Description	CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC 1.11.1.6) - upland cotton >gi_18488_emb_CAA39998_ (X56675) subunit 2 of cotton catalase [Gossypium hirsutum]
Seq. No.	221936
Seq. ID	LIB3165-020-P1-K1-H9
Method	BLASTX
NCBI GI	g2760834
BLAST score	495
E value	4.0e-50
Match length	132
% identity	74
NCBI Description	(AC003105) putative nitrate transporter [Arabidopsis thaliana]

Seq. No.	221937
Seq. ID	LIB3165-021-P1-K1-A10
Method	BLASTX
NCBI GI	g289920
BLAST score	702
E value	2.0e-74
Match length	133
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221938
Seq. ID	LIB3165-021-P1-K1-A11
Method	BLASTX
NCBI GI	g231688
BLAST score	298
E value	5.0e-27
Match length	57
% identity	100
NCBI Description	CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC 1.11.1.6) - upland cotton >gi_18488_emb_CAA39998_ (X56675) subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No.	221939
Seq. ID	LIB3165-021-P1-K1-A2
Method	BLASTX
NCBI GI	g487046
BLAST score	368
E value	3.0e-35
Match length	130
% identity	62
NCBI Description	photosystem I chain II precursor - wood tobacco >gi_407769_dbj_BAA02871_ (D13718) PSI-D1 precursor [Nicotiana sylvestris]

Seq. No.	221940
Seq. ID	LIB3165-021-P1-K1-A5
Method	BLASTX
NCBI GI	g289920
BLAST score	698
E value	6.0e-74
Match length	133
% identity	97
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221941
Seq. ID	LIB3165-021-P1-K1-A6
Method	BLASTX
NCBI GI	g4406530
BLAST score	364
E value	9.0e-35
Match length	104
% identity	74
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	221942

Seq. ID	LIB3165-021-P1-K1-A8
Method	BLASTX
NCBI GI	g166834
BLAST score	539
E value	2.0e-55
Match length	134
% identity	75
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	221943
Seq. ID	LIB3165-021-P1-K1-B11
Method	BLASTX
NCBI GI	g1352821
BLAST score	544
E value	7.0e-56
Match length	103
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221944
Seq. ID	LIB3165-021-P1-K1-B2
Method	BLASTX
NCBI GI	g2501578
BLAST score	477
E value	5.0e-48
Match length	110
% identity	89
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No.	221945
Seq. ID	LIB3165-021-P1-K1-B3
Method	BLASTX
NCBI GI	g3158474
BLAST score	240
E value	2.0e-24
Match length	70
% identity	88
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]

Seq. No.	221946
Seq. ID	LIB3165-021-P1-K1-B4
Method	BLASTX
NCBI GI	g548653
BLAST score	176
E value	1.0e-12
Match length	94
% identity	45
NCBI Description	50S RIBOSOMAL PROTEIN L12-A, CHLOROPLAST PRECURSOR (CL12-A)

>gi_541895_pir__A53394 ribosomal protein L12.A, chloroplast - Arabidopsis thaliana >gi_468771_emb_CAA48181_ (X68046) ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	221947
Seq. ID	LIB3165-021-P1-K1-B8
Method	BLASTX
NCBI GI	g1076724
BLAST score	554
E value	3.0e-57
Match length	109
% identity	91
NCBI Description	LHCI-680, photosystem I antenna protein - barley >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I antenna protein [Hordeum vulgare]

Seq. No.	221948
Seq. ID	LIB3165-021-P1-K1-B9
Method	BLASTX
NCBI GI	g100196
BLAST score	494
E value	4.0e-50
Match length	109
% identity	83
NCBI Description	chlorophyll a/b-binding protein (cab-11) - tomato

Seq. No.	221949
Seq. ID	LIB3165-021-P1-K1-C12
Method	BLASTX
NCBI GI	g3650033
BLAST score	155
E value	3.0e-10
Match length	81
% identity	41
NCBI Description	(AC005396) unknown protein [Arabidopsis thaliana]

Seq. No.	221950
Seq. ID	LIB3165-021-P1-K1-C7
Method	BLASTX
NCBI GI	g4105697
BLAST score	446
E value	2.0e-44
Match length	113
% identity	69
NCBI Description	(AF049870) thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	221951
Seq. ID	LIB3165-021-P1-K1-C9
Method	BLASTX
NCBI GI	g1777312
BLAST score	461
E value	4.0e-46
Match length	118
% identity	74
NCBI Description	(D30622) novel serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	221952
Seq. ID	LIB3165-021-P1-K1-D1
Method	BLASTX
NCBI GI	g1354515
BLAST score	369
E value	2.0e-35
Match length	139
% identity	57
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	221953
Seq. ID	LIB3165-021-P1-K1-D2
Method	BLASTX
NCBI GI	g1352821
BLAST score	510
E value	7.0e-52
Match length	100
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221954
Seq. ID	LIB3165-021-P1-K1-D3
Method	BLASTX
NCBI GI	g1354515
BLAST score	274
E value	3.0e-24
Match length	134
% identity	48
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	221955
Seq. ID	LIB3165-021-P1-K1-D4
Method	BLASTX
NCBI GI	g2317910
BLAST score	340
E value	6.0e-32
Match length	130
% identity	48
NCBI Description	(U89959) CER1 protein [Arabidopsis thaliana]

Seq. No.	221956
Seq. ID	LIB3165-021-P1-K1-D5
Method	BLASTX
NCBI GI	g4538959
BLAST score	436
E value	3.0e-43
Match length	120
% identity	72
NCBI Description	(AL049488) putative protein [Arabidopsis thaliana]

Seq. No. 221957

Seq. ID	LIB3165-021-P1-K1-D6
Method	BLASTX
NCBI GI	g289920
BLAST score	704
E value	1.0e-74
Match length	133
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221958
Seq. ID	LIB3165-021-P1-K1-D8
Method	BLASTX
NCBI GI	g131399
BLAST score	214
E value	1.0e-17
Match length	87
% identity	55
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi_82277_pir__S00411 photosystem II 10K protein precursor - potato >gi_21489_emb_CAA28450_ (X04753) ST-LS1 protein [Solanum tuberosum]

Seq. No.	221959
Seq. ID	LIB3165-021-P1-K1-D9
Method	BLASTX
NCBI GI	g121353
BLAST score	443
E value	5.0e-44
Match length	115
% identity	76
NCBI Description	GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR (ISOZYME DELTA) (GLUTAMATE-AMMONIA LIGASE) >gi_68596_pir__AJFBQD glutamate--ammonia ligase (EC 6.3.1.2) delta precursor, chloroplast - kidney bean >gi_21005_emb_CAA31234_ (X12738) GS precursor protein [Phaseolus vulgaris]

Seq. No.	221960
Seq. ID	LIB3165-021-P1-K1-E1
Method	BLASTX
NCBI GI	g231496
BLAST score	313
E value	3.0e-36
Match length	87
% identity	92
NCBI Description	ACTIN 58 >gi_100421_pir__S20094 actin - potato >gi_21536_emb_CAA39278_ (X55749) actin [Solanum tuberosum]

Seq. No.	221961
Seq. ID	LIB3165-021-P1-K1-E12
Method	BLASTX
NCBI GI	g120669
BLAST score	497
E value	2.0e-50
Match length	99
% identity	93

NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.	221962
Seq. ID	LIB3165-021-P1-K1-E3
Method	BLASTX
NCBI GI	g115833
BLAST score	419
E value	3.0e-41
Match length	117
% identity	71
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi_170394 (M32605) a-binding protein [Lycopersicon esculentum]
Seq. No.	221963
Seq. ID	LIB3165-021-P1-K1-E5
Method	BLASTX
NCBI GI	g1352821
BLAST score	597
E value	4.0e-62
Match length	111
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	221964
Seq. ID	LIB3165-021-P1-K1-E6
Method	BLASTX
NCBI GI	g3047064
BLAST score	359
E value	4.0e-34
Match length	134
% identity	61
NCBI Description	(AF058825) contains similarity to peptidyl-prolyl cis-trans isomerase (Pfam: pro_isomerase.hmm, score: 23.86 and 28.41 [Arabidopsis thaliana]
Seq. No.	221965
Seq. ID	LIB3165-021-P1-K1-E8
Method	BLASTX
NCBI GI	g1352821
BLAST score	615
E value	3.0e-64
Match length	122
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221966
Seq. ID	LIB3165-021-P1-K1-F11
Method	BLASTX
NCBI GI	g125576
BLAST score	625
E value	2.0e-65
Match length	123
% identity	98
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_99744_pir__S16583 phosphoribulokinase (EC 2.7.1.19) precursor - Arabidopsis thaliana >gi_16441_emb_CAA41155_ (X58149) Ribulose-5-phosphate kinase [Arabidopsis thaliana]

Seq. No.	221967
Seq. ID	LIB3165-021-P1-K1-F2
Method	BLASTX
NCBI GI	g1707943
BLAST score	613
E value	6.0e-64
Match length	126
% identity	94
NCBI Description	GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT PRECURSOR 1 (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) >gi_541977_pir__S41293 glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) - fava bean >gi_440593_emb_CAA54259_ (X76940) ADP-glucose pyrophosphorylase [Vicia faba]

Seq. No.	221968
Seq. ID	LIB3165-021-P1-K1-F3
Method	BLASTX
NCBI GI	g1352821
BLAST score	616
E value	3.0e-64
Match length	124
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221969
Seq. ID	LIB3165-021-P1-K1-F6
Method	BLASTX
NCBI GI	g3914940
BLAST score	423
E value	1.0e-41
Match length	140
% identity	64
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_2529376 (L76556) sedoheptulose-1,7-bisphosphatase

[Spinacia oleracea]

Seq. No.	221970
Seq. ID	LIB3165-021-P1-K1-F8
Method	BLASTX
NCBI GI	g285317
BLAST score	307
E value	4.0e-28
Match length	103
% identity	65
NCBI Description	dihydrolipoamide dehydrogenase (EC 1.8.1.4) - garden pea

Seq. No.	221971
Seq. ID	LIB3165-021-P1-K1-F9
Method	BLASTX
NCBI GI	g1352821
BLAST score	546
E value	4.0e-56
Match length	104
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221972
Seq. ID	LIB3165-021-P1-K1-G1
Method	BLASTX
NCBI GI	g68200
BLAST score	467
E value	8.0e-47
Match length	127
% identity	76
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	221973
Seq. ID	LIB3165-021-P1-K1-G10
Method	BLASTX
NCBI GI	g1709651
BLAST score	450
E value	7.0e-45
Match length	139
% identity	65
NCBI Description	PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209 plastocyanin a precursor - black poplar >gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus nigra]

Seq. No.	221974
Seq. ID	LIB3165-021-P1-K1-G2
Method	BLASTX
NCBI GI	g3451463
BLAST score	240
E value	3.0e-20

Match length	126
% identity	40
NCBI Description	(AL031349) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	221975
Seq. ID	LIB3165-021-P1-K1-G3
Method	BLASTX
NCBI GI	g1781348
BLAST score	286
E value	1.0e-25
Match length	71
% identity	75
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No.	221976
Seq. ID	LIB3165-021-P1-K1-G5
Method	BLASTX
NCBI GI	g81850
BLAST score	417
E value	5.0e-41
Match length	86
% identity	99
NCBI Description	histone H3 (clone pH3c-1) - alfalfa (fragment) >gi_829279_emb_CAA31967_ (X13676) histone H3 (AA 1-120) [Medicago sativa]

Seq. No.	221977
Seq. ID	LIB3165-021-P1-K1-G6
Method	BLASTX
NCBI GI	g68200
BLAST score	566
E value	2.0e-58
Match length	139
% identity	82
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	221978
Seq. ID	LIB3165-021-P1-K1-G7
Method	BLASTN
NCBI GI	g18511
BLAST score	377
E value	0.0e+00
Match length	409
% identity	98
NCBI Description	G.hirsutum light regulated unknown reading frame DNA

Seq. No.	221979
Seq. ID	LIB3165-021-P1-K1-G8
Method	BLASTX
NCBI GI	g4049399
BLAST score	160
E value	7.0e-11
Match length	108
% identity	33

NCBI Description (Y09581) FRO2 [Arabidopsis thaliana]

Seq. No. 221980
Seq. ID LIB3165-021-P1-K1-G9
Method BLASTX
NCBI GI g4406530
BLAST score 341
E value 4.0e-32
Match length 104
% identity 71
NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 221981
Seq. ID LIB3165-021-P1-K1-H1
Method BLASTX
NCBI GI g2252824
BLAST score 211
E value 3.0e-17
Match length 86
% identity 56
NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 221982
Seq. ID LIB3165-021-P1-K1-H11
Method BLASTX
NCBI GI g1352821
BLAST score 605
E value 5.0e-63
Match length 113
% identity 98
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 221983
Seq. ID LIB3165-021-P1-K1-H3
Method BLASTX
NCBI GI g2564237
BLAST score 440
E value 1.0e-43
Match length 103
% identity 78
NCBI Description (Y10112) omega-6 desaturase [Gossypium hirsutum]

Seq. No. 221984
Seq. ID LIB3165-021-P1-K1-H5
Method BLASTX
NCBI GI g3914605
BLAST score 517
E value 1.0e-52
Match length 121
% identity 83
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase -

apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica]

Seq. No.	221985
Seq. ID	LIB3165-021-P1-K1-H7
Method	BLASTX
NCBI GI	g3914603
BLAST score	358
E value	4.0e-34
Match length	88
% identity	77
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No.	221986
Seq. ID	LIB3165-021-P1-K1-H8
Method	BLASTX
NCBI GI	g973313
BLAST score	549
E value	2.0e-56
Match length	113
% identity	91
NCBI Description	(U30250) myo-inositol 1-phosphate synthase isozyme-2 [Arabidopsis thaliana]

Seq. No.	221987
Seq. ID	LIB3165-022-P1-K1-A10
Method	BLASTX
NCBI GI	g2980770
BLAST score	165
E value	2.0e-11
Match length	51
% identity	59
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	221988
Seq. ID	LIB3165-022-P1-K1-A12
Method	BLASTX
NCBI GI	g100200
BLAST score	352
E value	2.0e-33
Match length	99
% identity	70
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	221989
Seq. ID	LIB3165-022-P1-K1-A3
Method	BLASTX
NCBI GI	g1352821
BLAST score	645
E value	1.0e-67
Match length	119
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

09604590 = 09604590

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221990
Seq. ID	LIB3165-022-P1-K1-A5
Method	BLASTX
NCBI GI	g1653089
BLAST score	305
E value	8.0e-28
Match length	89
% identity	63
NCBI Description	(D90911) hypothetical protein [Synechocystis sp.]

Seq. No.	221991
Seq. ID	LIB3165-022-P1-K1-A7
Method	BLASTX
NCBI GI	g125578
BLAST score	341
E value	4.0e-32
Match length	99
% identity	68
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_167266 (M73707) phosphoribulokinase [Mesembryanthemum crystallinum]

Seq. No.	221992
Seq. ID	LIB3165-022-P1-K1-A9
Method	BLASTX
NCBI GI	g2218141
BLAST score	294
E value	1.0e-26
Match length	112
% identity	51
NCBI Description	(AF004914) E8 protein homolog [Lycopersicon esculentum]

Seq. No.	221993
Seq. ID	LIB3165-022-P1-K1-B1
Method	BLASTX
NCBI GI	g1352821
BLAST score	412
E value	1.0e-40
Match length	83
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	221994
Seq. ID	LIB3165-022-P1-K1-B12
Method	BLASTX
NCBI GI	g119150
BLAST score	631
E value	4.0e-66

Match length	124
% identity	95
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_82081_pir__S10507 translation elongation factor eEF-1 alpha chain - tomato >gi_19273_emb_CAA32618_ (X14449) EF 1-alpha (AA 1-448) [Lycopersicon esculentum] >gi_295810_emb_CAA37212_ (X53043) elongation factor 1-alpha [Lycopersicon esculentum]

Seq. No.	221995
Seq. ID	LIB3165-022-P1-K1-B5
Method	BLASTX
NCBI GI	g289920
BLAST score	704
E value	1.0e-74
Match length	134
% identity	97
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	221996
Seq. ID	LIB3165-022-P1-K1-B6
Method	BLASTX
NCBI GI	g131392
BLAST score	291
E value	2.0e-33
Match length	105
% identity	70
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_81479_pir__S00005 photosystem II oxygen-evolving complex protein 2 precursor - spinach >gi_21265_emb_CAA29055_ (X05511) 23 kDa OEC protein [Spinacia oleracea] >gi_225596_prf__1307179A luminal protein 23kD [Spinacia oleracea]

Seq. No.	221997
Seq. ID	LIB3165-022-P1-K1-B7
Method	BLASTX
NCBI GI	g2499710
BLAST score	623
E value	4.0e-65
Match length	132
% identity	84
NCBI Description	PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi_1438075 (L33686) phospholipase D [Ricinus communis]

Seq. No.	221998
Seq. ID	LIB3165-022-P1-K1-B8
Method	BLASTX
NCBI GI	g2281633
BLAST score	189
E value	2.0e-20
Match length	135
% identity	51
NCBI Description	(AF003097) AP2 domain containing protein RAP2.4

[Arabidopsis thaliana]

Seq. No.	221999
Seq. ID	LIB3165-022-P1-K1-B9
Method	BLASTX
NCBI GI	g4406530
BLAST score	346
E value	1.0e-32
Match length	119
% identity	62
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222000
Seq. ID	LIB3165-022-P1-K1-C1
Method	BLASTX
NCBI GI	g289920
BLAST score	601
E value	1.0e-62
Match length	117
% identity	95
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222001
Seq. ID	LIB3165-022-P1-K1-C10
Method	BLASTX
NCBI GI	g2924521
BLAST score	179
E value	4.0e-13
Match length	109
% identity	42
NCBI Description	(AL022023) putative protein [Arabidopsis thaliana]

Seq. No.	222002
Seq. ID	LIB3165-022-P1-K1-C12
Method	BLASTX
NCBI GI	g231610
BLAST score	291
E value	3.0e-26
Match length	105
% identity	62
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]

Seq. No.	222003
Seq. ID	LIB3165-022-P1-K1-C2
Method	BLASTX
NCBI GI	g4103324
BLAST score	367
E value	8.0e-37
Match length	88
% identity	93
NCBI Description	(AF022716) GDP-mannose pyrophosphorylase [Solanum tuberosum]

09604-10000

Seq. No.	222004
Seq. ID	LIB3165-022-P1-K1-C4
Method	BLASTX
NCBI GI	g1666234
BLAST score	324
E value	4.0e-30
Match length	66
% identity	95
NCBI Description	(U76193) actin [Pisum sativum] >gi_1724143 (U81049) actin [Pisum sativum]

Seq. No.	222005
Seq. ID	LIB3165-022-P1-K1-C5
Method	BLASTX
NCBI GI	g4510354
BLAST score	166
E value	1.0e-11
Match length	70
% identity	50
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	222006
Seq. ID	LIB3165-022-P1-K1-C8
Method	BLASTN
NCBI GI	g3510339
BLAST score	34
E value	1.0e-09
Match length	157
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No.	222007
Seq. ID	LIB3165-022-P1-K1-C9
Method	BLASTX
NCBI GI	g1172664
BLAST score	265
E value	4.0e-23
Match length	56
% identity	93
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_419791_pir__S31165 photosystem I chain III precursor - Flaveria trinervia >gi_298482_bbs_127083 photosystem I reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem I subunit III [Flaveria trinervia]

Seq. No.	222008
Seq. ID	LIB3165-022-P1-K1-D10
Method	BLASTX
NCBI GI	g3024020
BLAST score	620
E value	8.0e-65
Match length	124
% identity	94

NCBI Description	INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D) >gi_2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation factor 5A3 [Solanum tuberosum]
Seq. No.	222009
Seq. ID	LIB3165-022-P1-K1-D12
Method	BLASTX
NCBI GI	g2735766
BLAST score	181
E value	3.0e-13
Match length	118
% identity	37
NCBI Description	(AF008652) MADS transcriptional factor; STMADS11 [Solanum tuberosum]
Seq. No.	222010
Seq. ID	LIB3165-022-P1-K1-D2
Method	BLASTX
NCBI GI	g461812
BLAST score	333
E value	4.0e-31
Match length	114
% identity	50
NCBI Description	CYTOCHROME P450 72 (CYPLXXII) (PROBABLE GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081) Cytochrome P-450 protein [Catharanthus roseus] >gi_445604_prf__1909351A cytochrome P450 [Catharanthus roseus]
Seq. No.	222011
Seq. ID	LIB3165-022-P1-K1-D6
Method	BLASTX
NCBI GI	g1362017
BLAST score	179
E value	4.0e-13
Match length	78
% identity	51
NCBI Description	zinc finger protein 4 - Arabidopsis thaliana >gi_790679 (L39647) zinc finger protein [Arabidopsis thaliana]
Seq. No.	222012
Seq. ID	LIB3165-022-P1-K1-D8
Method	BLASTX
NCBI GI	g3738261
BLAST score	209
E value	1.0e-16
Match length	52
% identity	85
NCBI Description	(AB018412) chloroplast phosphoglycerate kinase [Populus nigra]
Seq. No.	222013
Seq. ID	LIB3165-022-P1-K1-D9
Method	BLASTX
NCBI GI	g1352821
BLAST score	580
E value	4.0e-60

Match length	108
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222014
Seq. ID	LIB3165-022-P1-K1-E1
Method	BLASTX
NCBI GI	g113240
BLAST score	129
E value	1.0e-10
Match length	60
% identity	62
NCBI Description	ACTIN 2 >gi_71636_pir__ATRZ2 actin 2 - rice >gi_20329_emb_CAA33873_ (X15864) actin [Oryza sativa]

Seq. No.	222015
Seq. ID	LIB3165-022-P1-K1-E11
Method	BLASTX
NCBI GI	g119931
BLAST score	382
E value	7.0e-37
Match length	109
% identity	69
NCBI Description	FERREDOXIN I PRECURSOR >gi_65740_pir__FEPM1 ferredoxin [2Fe-2S] I precursor - garden pea >gi_169087 (M31713) ferredoxin I precursor [Pisum sativum]

Seq. No.	222016
Seq. ID	LIB3165-022-P1-K1-E2
Method	BLASTX
NCBI GI	g1352821
BLAST score	520
E value	4.0e-53
Match length	102
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222017
Seq. ID	LIB3165-022-P1-K1-E4
Method	BLASTX
NCBI GI	g1168411
BLAST score	154
E value	4.0e-10
Match length	72
% identity	49
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	222018
Seq. ID	LIB3165-022-P1-K1-E5

Method	BLASTX
NCBI GI	g4406530
BLAST score	351
E value	3.0e-33
Match length	94
% identity	77
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222019
Seq. ID	LIB3165-022-P1-K1-E6
Method	BLASTX
NCBI GI	g1769905
BLAST score	390
E value	7.0e-38
Match length	96
% identity	77
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	222020
Seq. ID	LIB3165-022-P1-K1-E7
Method	BLASTX
NCBI GI	g2829892
BLAST score	219
E value	9.0e-18
Match length	109
% identity	51
NCBI Description	(AC002311) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	222021
Seq. ID	LIB3165-022-P1-K1-E9
Method	BLASTX
NCBI GI	g3776572
BLAST score	344
E value	2.0e-32
Match length	99
% identity	70
NCBI Description	(AC005388) ESTs gb_R65052, gb_AA712146, gb_H76533, gb_H76282, gb_AA650771, gb_H76287, gb_AA650887, gb_N37383, gb_Z29721 and gb_Z29722 come from this gene. [Arabidopsis thaliana]

Seq. No.	222022
Seq. ID	LIB3165-022-P1-K1-F1
Method	BLASTX
NCBI GI	g1354517
BLAST score	175
E value	1.0e-12
Match length	39
% identity	85
NCBI Description	(U55838) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	222023
Seq. ID	LIB3165-022-P1-K1-F10
Method	BLASTX
NCBI GI	g1724102

BLAST score	277
E value	6.0e-25
Match length	63
% identity	87
NCBI Description	(U79766) S-adenosyl-L-homocystein hydrolase; SAH [Mesembryanthemum crystallinum]

Seq. No.	222024
Seq. ID	LIB3165-022-P1-K1-F12
Method	BLASTX
NCBI GI	g2129651
BLAST score	558
E value	2.0e-57
Match length	139
% identity	77
NCBI Description	myosin heavy chain ATM2 - Arabidopsis thaliana (fragment) >gi_499045_emb_CAA84065_ (Z34292) myosin [Arabidopsis thaliana]

Seq. No.	222025
Seq. ID	LIB3165-022-P1-K1-F2
Method	BLASTX
NCBI GI	g1439609
BLAST score	321
E value	1.0e-29
Match length	79
% identity	80
NCBI Description	(U62778) delta-tonoplast intrinsic protein [Gossypium hirsutum]

Seq. No.	222026
Seq. ID	LIB3165-022-P1-K1-F4
Method	BLASTX
NCBI GI	g1514977
BLAST score	375
E value	2.0e-36
Match length	93
% identity	74
NCBI Description	(D84669) VM23 [Raphanus sativus]

Seq. No.	222027
Seq. ID	LIB3165-022-P1-K1-F6
Method	BLASTX
NCBI GI	g1199772
BLAST score	298
E value	5.0e-27
Match length	123
% identity	55
NCBI Description	(D83226) extensin like protein [Populus nigra] >gi_1199774_dbj_BAA11855_ (D83227) extensin like protein [Populus nigra]

Seq. No.	222028
Seq. ID	LIB3165-022-P1-K1-F9
Method	BLASTX
NCBI GI	g20729
BLAST score	444

E value	4.0e-44
Match length	123
% identity	74
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	222029
Seq. ID	LIB3165-022-P1-K1-G10
Method	BLASTX
NCBI GI	g430947
BLAST score	420
E value	2.0e-41
Match length	104
% identity	81
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	222030
Seq. ID	LIB3165-022-P1-K1-G11
Method	BLASTX
NCBI GI	g1709846
BLAST score	312
E value	1.0e-28
Match length	129
% identity	47
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_706853 (U04336) 22 kDa component of photosystem II [Lycopersicon esculentum]

Seq. No.	222031
Seq. ID	LIB3165-022-P1-K1-G12
Method	BLASTX
NCBI GI	g131399
BLAST score	547
E value	3.0e-56
Match length	129
% identity	82
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi_82277_pir__S00411 photosystem II 10K protein precursor - potato >gi_21489_emb_CAA28450_ (X04753) ST-LS1 protein [Solanum tuberosum]

Seq. No.	222032
Seq. ID	LIB3165-022-P1-K1-G3
Method	BLASTX
NCBI GI	g3913661
BLAST score	296
E value	8.0e-27
Match length	80
% identity	70
NCBI Description	FERREDOXIN B (FD B) >gi_322807_pir__S28199 ferredoxin [2Fe-2S] B - giant taro >gi_264602_bbs_123934 ferredoxin B isoprotein, Fd B [Alocasia macrorrhiza=elephant ear, Schott, Peptide, 98 aa]

Seq. No.	222033
Seq. ID	LIB3165-022-P1-K1-G4

Method	BLASTX
NCBI GI	g166834
BLAST score	170
E value	2.0e-12
Match length	39
% identity	74
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	222034
Seq. ID	LIB3165-022-P1-K1-G5
Method	BLASTX
NCBI GI	g228403
BLAST score	625
E value	2.0e-65
Match length	138
% identity	90
NCBI Description	glycolate oxidase [Lens culinaris]

Seq. No.	222035
Seq. ID	LIB3165-022-P1-K1-G7
Method	BLASTX
NCBI GI	g289920
BLAST score	346
E value	1.0e-32
Match length	120
% identity	62
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222036
Seq. ID	LIB3165-022-P1-K1-G8
Method	BLASTX
NCBI GI	g886100
BLAST score	559
E value	1.0e-57
Match length	124
% identity	86
NCBI Description	(U27347) putative water channel protein; plasmalemma intrinsic protein; similar to Arabidopsis Pip2a gene product, PIR Accession Number S44084 [Glycine max]

Seq. No.	222037
Seq. ID	LIB3165-022-P1-K1-G9
Method	BLASTX
NCBI GI	g1354515
BLAST score	314
E value	6.0e-29
Match length	138
% identity	51
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	222038
Seq. ID	LIB3165-022-P1-K1-H11
Method	BLASTX

NCBI GI	g119905
BLAST score	662
E value	1.0e-69
Match length	135
% identity	90
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR) >gi_81898_pir__S04030 ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - garden pea >gi_20722_emb_CAA30978_ (X12446) ferredoxin-NADH+ reductase preprotein (AA -52 to 308) [Pisum sativum] >gi_226545_prf__1601517A ferredoxin NADP reductase [Arachis hypogaea]

Seq. No.	222039
Seq. ID	LIB3165-022-P1-K1-H3
Method	BLASTX
NCBI GI	g3850111
BLAST score	240
E value	3.0e-20
Match length	112
% identity	42
NCBI Description	(AL033388) hypothetical integral membrane protein, putative involvement in lipid metabolism [Schizosaccharomyces pombe]

Seq. No.	222040
Seq. ID	LIB3165-022-P1-K1-H6
Method	BLASTX
NCBI GI	g1352821
BLAST score	577
E value	1.0e-60
Match length	118
% identity	92
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222041
Seq. ID	LIB3165-022-P1-K1-H7
Method	BLASTX
NCBI GI	g1352821
BLAST score	558
E value	2.0e-57
Match length	112
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222042
Seq. ID	LIB3165-023-P1-K1-A1
Method	BLASTN
NCBI GI	g2656026
BLAST score	60
E value	5.0e-25

Match length	188
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	222043
Seq. ID	LIB3165-023-P1-K1-A12
Method	BLASTX
NCBI GI	g1352821
BLAST score	743
E value	3.0e-79
Match length	138
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222044
Seq. ID	LIB3165-023-P1-K1-A2
Method	BLASTX
NCBI GI	g400198
BLAST score	217
E value	2.0e-17
Match length	85
% identity	55
NCBI Description	PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T) (LIGHT-REGULATED UNKNOWN 11 KD PROTEIN) >gi_99604_pir__S21023 hypothetical protein - upland cotton >gi_1361978_pir__A57500 photosystem II protein psbT - upland cotton >gi_18512_emb_CAA38027_ (X54092) unknown reading frame [Gossypium hirsutum]

Seq. No.	222045
Seq. ID	LIB3165-023-P1-K1-A4
Method	BLASTX
NCBI GI	g289920
BLAST score	211
E value	9.0e-22
Match length	99
% identity	66
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222046
Seq. ID	LIB3165-023-P1-K1-A6
Method	BLASTX
NCBI GI	g3776572
BLAST score	168
E value	8.0e-12
Match length	131
% identity	46
NCBI Description	(AC005388) ESTs gb_R65052, gb_AA712146, gb_H76533, gb_H76282, gb_AA650771, gb_H76287, gb_AA650887, gb_N37383, gb_Z29721 and gb_Z29722 come from this gene. [Arabidopsis thaliana]

Seq. No.	222047
Seq. ID	LIB3165-023-P1-K1-A7
Method	BLASTX
NCBI GI	g3335350
BLAST score	265
E value	3.0e-23
Match length	119
% identity	31
NCBI Description	(AC004512) Similar to gb_Z84386 anthranilate N-hydroxycinnamoyl/benzoyltransferase from Dianthus caryophyllus. [Arabidopsis thaliana]

Seq. No.	222048
Seq. ID	LIB3165-023-P1-K1-A9
Method	BLASTX
NCBI GI	g4406530
BLAST score	366
E value	6.0e-35
Match length	107
% identity	73
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222049
Seq. ID	LIB3165-023-P1-K1-B1
Method	BLASTX
NCBI GI	g544437
BLAST score	386
E value	2.0e-37
Match length	90
% identity	83
NCBI Description	GLUTATHIONE PEROXIDASE HOMOLOG (SALT-ASSOCIATED PROTEIN) >gi_296358_emb_CAA47018_ (X66377) CIT-SAP [Citrus sinensis]

Seq. No.	222050
Seq. ID	LIB3165-023-P1-K1-B10
Method	BLASTX
NCBI GI	g3183454
BLAST score	247
E value	5.0e-21
Match length	110
% identity	45
NCBI Description	HYPOTHETICAL 30.7 KD PROTEIN IN MCPC-KINA INTERGENIC REGION >gi_2632217_emb_CAA10859_ (AJ222587) YkwC protein [Bacillus subtilis] >gi_2633767_emb_CAB13269_ (Z99111) similar to 3-hydroxyisobutyrate dehydrogenase [Bacillus subtilis]

Seq. No.	222051
Seq. ID	LIB3165-023-P1-K1-B11
Method	BLASTX
NCBI GI	g131399
BLAST score	520
E value	5.0e-53
Match length	128
% identity	79
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi_82277_pir__S00411

photosystem II 10K protein precursor - potato
>gi_21489_emb_CAA28450_ (X04753) ST-LS1 protein [Solanum tuberosum]

Seq. No.	222052
Seq. ID	LIB3165-023-P1-K1-B3
Method	BLASTX
NCBI GI	g4415908
BLAST score	334
E value	5.0e-47
Match length	109
% identity	83
NCBI Description	(AC006282) unknown protein [Arabidopsis thaliana]

Seq. No.	222053
Seq. ID	LIB3165-023-P1-K1-B6
Method	BLASTX
NCBI GI	g289920
BLAST score	711
E value	2.0e-75
Match length	136
% identity	97
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222054
Seq. ID	LIB3165-023-P1-K1-B9
Method	BLASTX
NCBI GI	g4415908
BLAST score	258
E value	2.0e-22
Match length	63
% identity	81
NCBI Description	(AC006282) unknown protein [Arabidopsis thaliana]

Seq. No.	222055
Seq. ID	LIB3165-023-P1-K1-C1
Method	BLASTX
NCBI GI	g3402684
BLAST score	402
E value	3.0e-39
Match length	114
% identity	52
NCBI Description	(AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No.	222056
Seq. ID	LIB3165-023-P1-K1-C12
Method	BLASTX
NCBI GI	g1168411
BLAST score	385
E value	9.0e-44
Match length	122
% identity	82
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	222057
Seq. ID	LIB3165-023-P1-K1-C2

Method	BLASTX
NCBI GI	g3023752
BLAST score	237
E value	6.0e-20
Match length	95
% identity	58
NCBI Description	FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520) ferredoxin-I [Lycopersicon esculentum]

Seq. No.	222058
Seq. ID	LIB3165-023-P1-K1-C3
Method	BLASTX
NCBI GI	g3913649
BLAST score	149
E value	1.0e-15
Match length	83
% identity	58
NCBI Description	FERREDOXIN >gi_404374_bbs_135503 [2Fe-2S] ferredoxin, [2Fe-2S] Fd [Datura stramonium, var. stramonium and var. tatula, Peptide, 97 aa] >gi_1174327_bbs_171862 [2Fe-2S] ferredoxin [Datura fastuosa, leaves, Peptide, 97 aa] >gi_742379_prf__2009392A ferredoxin [Datura stramonium]

Seq. No.	222059
Seq. ID	LIB3165-023-P1-K1-C8
Method	BLASTX
NCBI GI	g3309086
BLAST score	375
E value	8.0e-37
Match length	87
% identity	90
NCBI Description	(AF076253) calcineurin B-like protein 3 [Arabidopsis thaliana]

Seq. No.	222060
Seq. ID	LIB3165-023-P1-K1-D10
Method	BLASTX
NCBI GI	g2791834
BLAST score	268
E value	9.0e-35
Match length	105
% identity	77
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No.	222061
Seq. ID	LIB3165-023-P1-K1-D11
Method	BLASTX
NCBI GI	g1168411
BLAST score	449
E value	2.0e-45
Match length	121
% identity	84
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	222062
Seq. ID	LIB3165-023-P1-K1-D12
Method	BLASTX

NCBI GI	g3935185
BLAST score	412
E value	2.0e-40
Match length	137
% identity	67
NCBI Description	(AC004557) F17L21.28 [Arabidopsis thaliana]

Seq. No.	222063
Seq. ID	LIB3165-023-P1-K1-D4
Method	BLASTX
NCBI GI	g3201969
BLAST score	416
E value	7.0e-41
Match length	122
% identity	61
NCBI Description	(AF068332) submergence induced protein 2A [Oryza sativa]

Seq. No.	222064
Seq. ID	LIB3165-023-P1-K1-D5
Method	BLASTX
NCBI GI	g289920
BLAST score	647
E value	6.0e-68
Match length	124
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222065
Seq. ID	LIB3165-023-P1-K1-D6
Method	BLASTX
NCBI GI	g1488043
BLAST score	267
E value	2.0e-23
Match length	83
% identity	67
NCBI Description	(U63784) PAPS-reductase-like protein [Catharanthus roseus]

Seq. No.	222066
Seq. ID	LIB3165-023-P1-K1-D9
Method	BLASTX
NCBI GI	g4262239
BLAST score	395
E value	2.0e-45
Match length	143
% identity	66
NCBI Description	(AC006200) putative membrane transporter [Arabidopsis thaliana]

Seq. No.	222067
Seq. ID	LIB3165-023-P1-K1-E1
Method	BLASTX
NCBI GI	g417820
BLAST score	155
E value	7.0e-27
Match length	74
% identity	96

NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_167536 (M59858) stearoyl-acyl-carrier protein desaturase [Cucumis sativus]
Seq. No.	222068
Seq. ID	LIB3165-023-P1-K1-E10
Method	BLASTN
NCBI GI	g3241924
BLAST score	40
E value	4.0e-13
Match length	147
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC6, complete sequence [Arabidopsis thaliana]
Seq. No.	222069
Seq. ID	LIB3165-023-P1-K1-E12
Method	BLASTX
NCBI GI	g3293031
BLAST score	452
E value	4.0e-45
Match length	116
% identity	79
NCBI Description	(AJ007574) amino acid carrier [Ricinus communis]
Seq. No.	222070
Seq. ID	LIB3165-023-P1-K1-E2
Method	BLASTX
NCBI GI	g4091806
BLAST score	274
E value	3.0e-24
Match length	88
% identity	44
NCBI Description	(AF052585) CONSTANS-like protein 2 [Malus domestica]
Seq. No.	222071
Seq. ID	LIB3165-023-P1-K1-E4
Method	BLASTX
NCBI GI	g1352821
BLAST score	566
E value	2.0e-58
Match length	127
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	222072
Seq. ID	LIB3165-023-P1-K1-E5
Method	BLASTX
NCBI GI	g4567202
BLAST score	456
E value	1.0e-45
Match length	99
% identity	91

NCBI Description	(AC007168) putative myo-inositol 1-phosphate synthase [Arabidopsis thaliana]

Seq. No.	222073
Seq. ID	LIB3165-023-P1-K1-E7
Method	BLASTX
NCBI GI	g1679658
BLAST score	212
E value	6.0e-17
Match length	91
% identity	53
NCBI Description	(U63726) gamma glutamyl hydrolase [Glycine max]

Seq. No.	222074
Seq. ID	LIB3165-023-P1-K1-F10
Method	BLASTX
NCBI GI	g2641638
BLAST score	569
E value	2.0e-63
Match length	140
% identity	89
NCBI Description	(AF032883) AtJ3 [Arabidopsis thaliana]

Seq. No.	222075
Seq. ID	LIB3165-023-P1-K1-F11
Method	BLASTX
NCBI GI	g3121825
BLAST score	177
E value	2.0e-13
Match length	87
% identity	64
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea]

Seq. No.	222076
Seq. ID	LIB3165-023-P1-K1-F12
Method	BLASTX
NCBI GI	g2499946
BLAST score	143
E value	4.0e-09
Match length	31
% identity	84
NCBI Description	URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_747980 (U22260) UMP synthase [Nicotiana tabacum]

Seq. No.	222077
Seq. ID	LIB3165-023-P1-K1-F3
Method	BLASTX
NCBI GI	g421826
BLAST score	182
E value	2.0e-13
Match length	103
% identity	42
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana

	>gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]
Seq. No.	222078
Seq. ID	LIB3165-023-P1-K1-F4
Method	BLASTX
NCBI GI	g2078386
BLAST score	246
E value	6.0e-21
Match length	129
% identity	30
NCBI Description	(U96623) glyceraldehyde-3-phosphate-dehydrogenase [Selaginella lepidophylla]
Seq. No.	222079
Seq. ID	LIB3165-023-P1-K1-F8
Method	BLASTX
NCBI GI	g1352821
BLAST score	579
E value	6.0e-60
Match length	109
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	222080
Seq. ID	LIB3165-023-P1-K1-G5
Method	BLASTX
NCBI GI	g3860272
BLAST score	262
E value	1.0e-46
Match length	108
% identity	90
NCBI Description	(AC005824) putative suppressor protein [Arabidopsis thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1 protein [Arabidopsis thaliana]
Seq. No.	222081
Seq. ID	LIB3165-023-P1-K1-G7
Method	BLASTX
NCBI GI	g4406530
BLAST score	231
E value	3.0e-31
Match length	98
% identity	73
NCBI Description	(AF126870) rubisco activase [Vigna radiata]
Seq. No.	222082
Seq. ID	LIB3165-023-P1-K1-H10
Method	BLASTX
NCBI GI	g1488043
BLAST score	235
E value	1.0e-19
Match length	73

% identity	68
NCBI Description	(U63784) PAPS-reductase-like protein [Catharanthus roseus]

Seq. No.	222083
Seq. ID	LIB3165-023-P1-K1-H2
Method	BLASTX
NCBI GI	g3676818
BLAST score	190
E value	2.0e-14
Match length	54
% identity	69
NCBI Description	(AF091514) metallothionein homolog [Elaeagnus umbellata]

Seq. No.	222084
Seq. ID	LIB3165-023-P1-K1-H6
Method	BLASTX
NCBI GI	g2435518
BLAST score	146
E value	3.0e-09
Match length	80
% identity	44
NCBI Description	(AF024504) contains similarity to C3HC4-type zinc fingers [Arabidopsis thaliana]

Seq. No.	222085
Seq. ID	LIB3165-023-P1-K1-H9
Method	BLASTX
NCBI GI	g1354515
BLAST score	456
E value	3.0e-47
Match length	139
% identity	66
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	222086
Seq. ID	LIB3165-024-P1-K1-A1
Method	BLASTX
NCBI GI	g120026
BLAST score	188
E value	3.0e-14
Match length	87
% identity	55
NCBI Description	FERREDOXIN PRECURSOR >gi_65746_pir__FEQH ferredoxin [2Fe-2S] precursor - white campion >gi_21362_emb_CAA26281_ (X02432) ferredoxin precursor [Silene latifolia ssp. alba]

Seq. No.	222087
Seq. ID	LIB3165-024-P1-K1-A10
Method	BLASTX
NCBI GI	g2832669
BLAST score	196
E value	4.0e-15
Match length	117
% identity	44
NCBI Description	(AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No.	222088
Seq. ID	LIB3165-024-P1-K1-A12
Method	BLASTX
NCBI GI	g2754849
BLAST score	585
E value	1.0e-60
Match length	133
% identity	83
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

Seq. No.	222089
Seq. ID	LIB3165-024-P1-K1-A5
Method	BLASTX
NCBI GI	g3063392
BLAST score	436
E value	3.0e-43
Match length	116
% identity	76
NCBI Description	(AB012932) Ca2+/H+ exchanger [Vigna radiata]

Seq. No.	222090
Seq. ID	LIB3165-024-P1-K1-A6
Method	BLASTX
NCBI GI	g4091810
BLAST score	379
E value	2.0e-36
Match length	140
% identity	49
NCBI Description	(AF053345) fatty acid elongase 3-ketoacyl-CoA synthase 1 [Arabidopsis thaliana]

Seq. No.	222091
Seq. ID	LIB3165-024-P1-K1-A8
Method	BLASTX
NCBI GI	g1352821
BLAST score	617
E value	2.0e-64
Match length	120
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222092
Seq. ID	LIB3165-024-P1-K1-B1
Method	BLASTX
NCBI GI	g20733
BLAST score	492
E value	9.0e-50
Match length	122
% identity	77
NCBI Description	(X15188) precursor C-terminal fragment (AA -80 to 367) [Pisum sativum]

Seq. No.	222093
Seq. ID	LIB3165-024-P1-K1-B12
Method	BLASTN
NCBI GI	g3985958
BLAST score	37
E value	2.0e-11
Match length	49
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	222094
Seq. ID	LIB3165-024-P1-K1-B2
Method	BLASTX
NCBI GI	g70644
BLAST score	616
E value	2.0e-64
Match length	125
% identity	19
NCBI Description	ubiquitin precursor - common sunflower (fragment)

Seq. No.	222095
Seq. ID	LIB3165-024-P1-K1-B3
Method	BLASTX
NCBI GI	g3242704
BLAST score	156
E value	2.0e-10
Match length	45
% identity	64
NCBI Description	(AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No.	222096
Seq. ID	LIB3165-024-P1-K1-B7
Method	BLASTX
NCBI GI	g2129879
BLAST score	619
E value	8.0e-65
Match length	117
% identity	64
NCBI Description	chlorophyll a/b-binding protein type II precursor, photosystem I - garden pea >gi_602359_emb_CAA57492_ (X81962) Type II chlorophyll a/b binding protein from photosystem I [Pisum sativum]

Seq. No.	222097
Seq. ID	LIB3165-024-P1-K1-B8
Method	BLASTX
NCBI GI	g1352821
BLAST score	492
E value	7.0e-50
Match length	94
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222098
Seq. ID	LIB3165-024-P1-K1-B9
Method	BLASTX
NCBI GI	g3913651
BLAST score	476
E value	7.0e-48
Match length	112
% identity	79
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR (FNR) >gi_2225993_emb_CAA74359_ (Y14032) ferredoxin--NADP(+) reductase [Nicotiana tabacum]

Seq. No.	222099
Seq. ID	LIB3165-024-P1-K1-C2
Method	BLASTX
NCBI GI	g1352821
BLAST score	563
E value	4.0e-58
Match length	107
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222100
Seq. ID	LIB3165-024-P1-K1-C3
Method	BLASTX
NCBI GI	g421826
BLAST score	393
E value	3.0e-38
Match length	120
% identity	63
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	222101
Seq. ID	LIB3165-024-P1-K1-C6
Method	BLASTX
NCBI GI	g4538897
BLAST score	493
E value	7.0e-50
Match length	135
% identity	68
NCBI Description	(AL049482) AX110P-like protein [Arabidopsis thaliana]

Seq. No.	222102
Seq. ID	LIB3165-024-P1-K1-C7
Method	BLASTX
NCBI GI	g1928981
BLAST score	455
E value	2.0e-45
Match length	112
% identity	81

NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	222103
Seq. ID	LIB3165-024-P1-K1-C8
Method	BLASTX
NCBI GI	g2754849
BLAST score	416
E value	2.0e-45
Match length	120
% identity	80
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

Seq. No.	222104
Seq. ID	LIB3165-024-P1-K1-C9
Method	BLASTX
NCBI GI	g1353352
BLAST score	429
E value	2.0e-42
Match length	136
% identity	57
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	222105
Seq. ID	LIB3165-024-P1-K1-D10
Method	BLASTX
NCBI GI	g398992
BLAST score	432
E value	8.0e-43
Match length	100
% identity	76
NCBI Description	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE) (ETHYLENE-FORMING ENZYME) (EFE) (PROTEIN PTOM13) >gi_100205_pir__S16591 ethylene-forming enzyme - tomato >gi_19207_emb_CAA41212_ (X58273) 1-Aminocyclopropane-1-carboxylic acid oxidase [Lycopersicon esculentum]

Seq. No.	222106
Seq. ID	LIB3165-024-P1-K1-D11
Method	BLASTX
NCBI GI	g398992
BLAST score	452
E value	4.0e-45
Match length	105
% identity	75
NCBI Description	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE) (ETHYLENE-FORMING ENZYME) (EFE) (PROTEIN PTOM13) >gi_100205_pir__S16591 ethylene-forming enzyme - tomato >gi_19207_emb_CAA41212_ (X58273) 1-Aminocyclopropane-1-carboxylic acid oxidase [Lycopersicon esculentum]

Seq. No.	222107
Seq. ID	LIB3165-024-P1-K1-D2

Method	BLASTX
NCBI GI	g2055230
BLAST score	339
E value	7.0e-32
Match length	114
% identity	56
NCBI Description	(AB000130) SRC2 [Glycine max]

Seq. No.	222108
Seq. ID	LIB3165-024-P1-K1-D4
Method	BLASTX
NCBI GI	g1352821
BLAST score	512
E value	4.0e-52
Match length	109
% identity	89
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222109
Seq. ID	LIB3165-024-P1-K1-D6
Method	BLASTX
NCBI GI	g131166
BLAST score	557
E value	1.0e-59
Match length	125
% identity	89
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_82100_pir__S00449 photosystem I chain II precursor - tomato >gi_170492 (M21344) photosystem I subunit II protein precursor [Lycopersicon esculentum] >gi_226544_prf__1601516A photosystem I reaction center II [Lycopersicon esculentum]

Seq. No.	222110
Seq. ID	LIB3165-024-P1-K1-D7
Method	BLASTN
NCBI GI	g289919
BLAST score	32
E value	1.0e-08
Match length	83
% identity	82
NCBI Description	Gossypium hirsutum chloroplast photosystem II chlorophyll A/B-binding protein gene, complete cds

Seq. No.	222111
Seq. ID	LIB3165-024-P1-K1-E1
Method	BLASTX
NCBI GI	g1352821
BLAST score	574
E value	2.0e-59
Match length	108
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

	(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	222112
Seq. ID	LIB3165-024-P1-K1-E12
Method	BLASTN
NCBI GI	g18058
BLAST score	82
E value	3.0e-38
Match length	270
% identity	83
NCBI Description	Citrus limon cistron for 26S ribosomal RNA
Seq. No.	222113
Seq. ID	LIB3165-024-P1-K1-E2
Method	BLASTX
NCBI GI	g224293
BLAST score	410
E value	3.0e-40
Match length	86
% identity	97
NCBI Description	histone H4 [Triticum aestivum]
Seq. No.	222114
Seq. ID	LIB3165-024-P1-K1-E3
Method	BLASTX
NCBI GI	g1168408
BLAST score	627
E value	1.0e-65
Match length	134
% identity	92
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1 >gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828) fructose-1,6-bisphosphate aldolase [Pisum sativum]
Seq. No.	222115
Seq. ID	LIB3165-024-P1-K1-E4
Method	BLASTX
NCBI GI	g1172664
BLAST score	234
E value	1.0e-19
Match length	51
% identity	90
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_419791_pir__S31165 photosystem I chain III precursor - Flaveria trinervia >gi_298482_bbs_127083 photosystem I reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem I subunit III [Flaveria trinervia]
Seq. No.	222116
Seq. ID	LIB3165-024-P1-K1-E6
Method	BLASTX

NCBI GI	g4406530
BLAST score	311
E value	1.0e-28
Match length	109
% identity	66
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222117
Seq. ID	LIB3165-024-P1-K1-E8
Method	BLASTX
NCBI GI	g2956690
BLAST score	176
E value	1.0e-12
Match length	104
% identity	29
NCBI Description	(AJ223306) PSBY [Arabidopsis thaliana] >gi_3414928 (AF079800) PsbY precursor [Arabidopsis thaliana]

Seq. No.	222118
Seq. ID	LIB3165-024-P1-K1-E9
Method	BLASTX
NCBI GI	g1730635
BLAST score	152
E value	6.0e-10
Match length	103
% identity	38
NCBI Description	HYPOTHETICAL 40.7 KD PROTEIN IN PIK1-POL2 INTERGENIC REGION >gi_2132777_pir__S60917 probable membrane protein YNL264c - yeast (Saccharomyces cerevisiae) >gi_1045245_emb_CAA63233_ (X92494) ORF N0815 [Saccharomyces cerevisiae] >gi_1302321_emb_CAA96171_ (Z71540) ORF YNL264c [Saccharomyces cerevisiae]

Seq. No.	222119
Seq. ID	LIB3165-024-P1-K1-F1
Method	BLASTX
NCBI GI	g1352821
BLAST score	733
E value	5.0e-78
Match length	136
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222120
Seq. ID	LIB3165-024-P1-K1-F11
Method	BLASTX
NCBI GI	g4406530
BLAST score	340
E value	5.0e-32
Match length	91
% identity	77
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222121
Seq. ID	LIB3165-024-P1-K1-F4
Method	BLASTX
NCBI GI	g3928760
BLAST score	322
E value	8.0e-30
Match length	131
% identity	56
NCBI Description	(AB011797) homolog to plastid-lipid-associated protein [Citrus unshiu]

Seq. No.	222122
Seq. ID	LIB3165-024-P1-K1-F5
Method	BLASTX
NCBI GI	g217909
BLAST score	606
E value	3.0e-63
Match length	128
% identity	93
NCBI Description	(D14044) glycolate oxidase [Cucurbita sp.]

Seq. No.	222123
Seq. ID	LIB3165-024-P1-K1-F6
Method	BLASTX
NCBI GI	g4538944
BLAST score	154
E value	4.0e-10
Match length	45
% identity	67
NCBI Description	(AL049483) putative transcription factor [Arabidopsis thaliana]

Seq. No.	222124
Seq. ID	LIB3165-024-P1-K1-F9
Method	BLASTX
NCBI GI	g2443878
BLAST score	186
E value	6.0e-14
Match length	80
% identity	60
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No.	222125
Seq. ID	LIB3165-024-P1-K1-G1
Method	BLASTX
NCBI GI	g115833
BLAST score	507
E value	1.0e-51
Match length	126
% identity	78
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi_170394 (M32605) a-binding protein [Lycopersicon esculentum]

Seq. No.	222126
Seq. ID	LIB3165-024-P1-K1-G10

Method	BLASTX
NCBI GI	g2494415
BLAST score	498
E value	2.0e-50
Match length	134
% identity	76
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_515747 (L34841) fructose-1,6-bisphosphatase [Glycine max]

Seq. No.	222127
Seq. ID	LIB3165-024-P1-K1-G2
Method	BLASTX
NCBI GI	g3377517
BLAST score	380
E value	1.0e-36
Match length	112
% identity	67
NCBI Description	(AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]

Seq. No.	222128
Seq. ID	LIB3165-024-P1-K1-G4
Method	BLASTX
NCBI GI	g1352821
BLAST score	596
E value	6.0e-62
Match length	119
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222129
Seq. ID	LIB3165-024-P1-K1-G5
Method	BLASTX
NCBI GI	g2129538
BLAST score	504
E value	3.0e-51
Match length	105
% identity	91
NCBI Description	AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232) AT103 [Arabidopsis thaliana]

Seq. No.	222130
Seq. ID	LIB3165-024-P1-K1-G7
Method	BLASTX
NCBI GI	g4406530
BLAST score	335
E value	2.0e-31
Match length	91
% identity	76
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No. 222131

Seq. ID	LIB3165-024-P1-K1-G8
Method	BLASTX
NCBI GI	g3128217
BLAST score	244
E value	9.0e-21
Match length	87
% identity	64
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana] >gi_3337374 (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No.	222132
Seq. ID	LIB3165-024-P1-K1-H1
Method	BLASTX
NCBI GI	g558925
BLAST score	433
E value	6.0e-43
Match length	123
% identity	70
NCBI Description	(U15778) geranylgeranyl pyrophosphate synthase [Lupinus albus]

Seq. No.	222133
Seq. ID	LIB3165-024-P1-K1-H10
Method	BLASTX
NCBI GI	g1352821
BLAST score	513
E value	3.0e-52
Match length	125
% identity	82
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222134
Seq. ID	LIB3165-024-P1-K1-H2
Method	BLASTX
NCBI GI	g2501578
BLAST score	577
E value	9.0e-60
Match length	122
% identity	96
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No.	222135
Seq. ID	LIB3165-024-P1-K1-H3
Method	BLASTX
NCBI GI	g1061040
BLAST score	603
E value	8.0e-63
Match length	127
% identity	85

NCBI Description	(X89867) sterol-C-methyltransferase [Arabidopsis thaliana] >gi_1587694_prf__2207220A sterol C-methyltransferase [Arabidopsis thaliana]
Seq. No.	222136
Seq. ID	LIB3165-024-P1-K1-H4
Method	BLASTN
NCBI GI	g3821780
BLAST score	33
E value	5.0e-09
Match length	48
% identity	51
NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	222137
Seq. ID	LIB3165-024-P1-K1-H5
Method	BLASTX
NCBI GI	g4467115
BLAST score	213
E value	3.0e-21
Match length	70
% identity	77
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]
Seq. No.	222138
Seq. ID	LIB3165-024-P1-K1-H6
Method	BLASTX
NCBI GI	g231496
BLAST score	581
E value	3.0e-60
Match length	129
% identity	89
NCBI Description	ACTIN 58 >gi_100421_pir__S20094 actin - potato >gi_21536_emb_CAA39278_ (X55749) actin [Solanum tuberosum]
Seq. No.	222139
Seq. ID	LIB3165-024-P1-K1-H7
Method	BLASTX
NCBI GI	g2244734
BLAST score	439
E value	8.0e-44
Match length	98
% identity	90
NCBI Description	(D88414) actin [Gossypium hirsutum]
Seq. No.	222140
Seq. ID	LIB3165-025-P1-K1-A12
Method	BLASTX
NCBI GI	g3687652
BLAST score	407
E value	3.0e-44
Match length	98
% identity	92
NCBI Description	(AF047352) rubisco activase precursor [Datisca glomerata]
Seq. No.	222141
Seq. ID	LIB3165-025-P1-K1-A3

Method	BLASTX
NCBI GI	g120663
BLAST score	329
E value	6.0e-51
Match length	135
% identity	75
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR, CHLOROPLAST >gi_66027_pir__DEPMNB glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast - garden pea >gi_309671 (M55147) glyceraldehyde-3-phosphate dehydrogenase B subunit [Pisum sativum]

Seq. No.	222142
Seq. ID	LIB3165-025-P1-K1-A5
Method	BLASTX
NCBI GI	g2129921
BLAST score	167
E value	1.0e-11
Match length	51
% identity	67
NCBI Description	hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]

Seq. No.	222143
Seq. ID	LIB3165-025-P1-K1-A7
Method	BLASTX
NCBI GI	g4468813
BLAST score	281
E value	4.0e-25
Match length	68
% identity	75
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	222144
Seq. ID	LIB3165-025-P1-K1-B1
Method	BLASTX
NCBI GI	g68200
BLAST score	517
E value	1.0e-52
Match length	128
% identity	82
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	222145
Seq. ID	LIB3165-025-P1-K1-B12
Method	BLASTX
NCBI GI	g1352821
BLAST score	399
E value	6.0e-39
Match length	87
% identity	92
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

	precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	222146
Seq. ID	LIB3165-025-P1-K1-B2
Method	BLASTX
NCBI GI	g1168411
BLAST score	448
E value	1.0e-44
Match length	120
% identity	78
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
Seq. No.	222147
Seq. ID	LIB3165-025-P1-K1-B5
Method	BLASTX
NCBI GI	g4102703
BLAST score	400
E value	5.0e-39
Match length	117
% identity	73
NCBI Description	(AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis thaliana]
Seq. No.	222148
Seq. ID	LIB3165-025-P1-K1-C11
Method	BLASTX
NCBI GI	g3694872
BLAST score	441
E value	7.0e-44
Match length	107
% identity	79
NCBI Description	(AF092547) profilin [Ricinus communis]
Seq. No.	222149
Seq. ID	LIB3165-025-P1-K1-C2
Method	BLASTX
NCBI GI	g1130682
BLAST score	447
E value	2.0e-44
Match length	86
% identity	100
NCBI Description	(Z46959) acetohydroxyacid synthase [Gossypium hirsutum]
Seq. No.	222150
Seq. ID	LIB3165-025-P1-K1-C3
Method	BLASTX
NCBI GI	g4106696
BLAST score	241
E value	2.0e-20
Match length	70
% identity	73
NCBI Description	(AB021872) ribosome-sedimenting protein [Pisum sativum]
Seq. No.	222151
Seq. ID	LIB3165-025-P1-K1-D1
Method	BLASTX

NCBI GI	g1352821
BLAST score	620
E value	8.0e-65
Match length	121
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222152
Seq. ID	LIB3165-025-P1-K1-D10
Method	BLASTN
NCBI GI	g18511
BLAST score	162
E value	5.0e-86
Match length	250
% identity	91
NCBI Description	G.hirsutum light regulated unknown reading frame DNA

Seq. No.	222153
Seq. ID	LIB3165-025-P1-K1-D12
Method	BLASTN
NCBI GI	g2264318
BLAST score	34
E value	1.0e-09
Match length	192
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

Seq. No.	222154
Seq. ID	LIB3165-025-P1-K1-D3
Method	BLASTX
NCBI GI	g4454459
BLAST score	190
E value	1.0e-14
Match length	58
% identity	60
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	222155
Seq. ID	LIB3165-025-P1-K1-D5
Method	BLASTX
NCBI GI	g2493494
BLAST score	443
E value	5.0e-44
Match length	110
% identity	75
NCBI Description	SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2) >gi_619351_bbs_153537 CP-MII.2=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436 aa]

Seq. No.	222156
Seq. ID	LIB3165-025-P1-K1-D9

Method	BLASTX
NCBI GI	g4056456
BLAST score	467
E value	7.0e-47
Match length	112
% identity	81
NCBI Description	(AC005990) Strong similarity to gb_U20808 auxin-induced protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF_00107. ESTs gb_T43674, gb_H77006 and gb_AA395179 come from this gene. [Arabidopsis thaliana]

Seq. No.	222157
Seq. ID	LIB3165-025-P1-K1-E10
Method	BLASTX
NCBI GI	g20729
BLAST score	183
E value	5.0e-14
Match length	61
% identity	62
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	222158
Seq. ID	LIB3165-025-P1-K1-E11
Method	BLASTX
NCBI GI	g1055130
BLAST score	186
E value	6.0e-14
Match length	95
% identity	37
NCBI Description	(U39998) coded for by C. elegans cDNA yk92b11.3; coded for by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA yk78c2.3

Seq. No.	222159
Seq. ID	LIB3165-025-P1-K1-E6
Method	BLASTX
NCBI GI	g120663
BLAST score	417
E value	5.0e-41
Match length	116
% identity	72
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR, CHLOROPLAST >gi_66027_pir__DEPMNB glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast - garden pea >gi_309671 (M55147) glyceraldehyde-3-phosphate dehydrogenase B subunit [Pisum sativum]

Seq. No.	222160
Seq. ID	LIB3165-025-P1-K1-F1
Method	BLASTX
NCBI GI	g1872544
BLAST score	285
E value	1.0e-25
Match length	122

% identity	54
NCBI Description	(U89014) early light-induced protein; ELIP [Arabidopsis thaliana]

Seq. No.	222161
Seq. ID	LIB3165-025-P1-K1-F12
Method	BLASTN
NCBI GI	g3821780
BLAST score	33
E value	5.0e-09
Match length	37
% identity	97
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	222162
Seq. ID	LIB3165-025-P1-K1-F6
Method	BLASTN
NCBI GI	g450504
BLAST score	75
E value	3.0e-34
Match length	178
% identity	85
NCBI Description	G.hirsutum rbcS gene for ribulose-1,5-bisphosphate carboxylase, small subunit

Seq. No.	222163
Seq. ID	LIB3165-025-P1-K1-G1
Method	BLASTX
NCBI GI	g1209703
BLAST score	332
E value	5.0e-31
Match length	126
% identity	45
NCBI Description	(U40489) maize gl1 homolog [Arabidopsis thaliana]

Seq. No.	222164
Seq. ID	LIB3165-025-P1-K1-G12
Method	BLASTX
NCBI GI	g3334115
BLAST score	326
E value	2.0e-30
Match length	90
% identity	76
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

Seq. No.	222165
Seq. ID	LIB3165-025-P1-K1-G2
Method	BLASTX
NCBI GI	g4567249
BLAST score	295
E value	1.0e-26
Match length	103
% identity	59
NCBI Description	(AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No.	222166
Seq. ID	LIB3165-025-P1-K1-G6
Method	BLASTX
NCBI GI	g2292917
BLAST score	441
E value	8.0e-44
Match length	129
% identity	67
NCBI Description	(X99851) galactokinase [Arabidopsis thaliana]

Seq. No.	222167
Seq. ID	LIB3165-025-P1-K1-G9
Method	BLASTX
NCBI GI	g3915873
BLAST score	404
E value	1.0e-39
Match length	98
% identity	78
NCBI Description	SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE) (NODULIN-100) >gi_2606081 (AF030231) sucrose synthase [Glycine max]

Seq. No.	222168
Seq. ID	LIB3165-025-P1-K1-H10
Method	BLASTX
NCBI GI	g1352821
BLAST score	596
E value	5.0e-62
Match length	119
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222169
Seq. ID	LIB3165-025-P1-K1-H3
Method	BLASTX
NCBI GI	g132091
BLAST score	245
E value	4.0e-33
Match length	96
% identity	75
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN F1 PRECURSOR (RUBISCO SMALL SUBUNIT F1) >gi_68065_pir__RKRPF1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (gene rbcSF1) - rape >gi_17852_emb_CAA39402_ (X55937) ribulose bisphosphate carboxylase /oxygenase small subunit [Brassica napus]

Seq. No.	222170
Seq. ID	LIB3165-025-P1-K1-H7
Method	BLASTX
NCBI GI	g1354515
BLAST score	335

E value	2.0e-31
Match length	130
% identity	58
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	222171
Seq. ID	LIB3165-026-P1-K1-A10
Method	BLASTX
NCBI GI	g2388583
BLAST score	195
E value	5.0e-15
Match length	87
% identity	55
NCBI Description	(AC000098) Similar to Synechocystis hypothetical protein (gb_D90908). [Arabidopsis thaliana]

Seq. No.	222172
Seq. ID	LIB3165-026-P1-K1-A4
Method	BLASTN
NCBI GI	g3985958
BLAST score	41
E value	1.0e-13
Match length	49
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	222173
Seq. ID	LIB3165-026-P1-K1-A6
Method	BLASTX
NCBI GI	g3153902
BLAST score	321
E value	4.0e-30
Match length	79
% identity	82
NCBI Description	(AF066076) 14-3-3-like protein [Helianthus annuus]

Seq. No.	222174
Seq. ID	LIB3165-026-P1-K1-A8
Method	BLASTX
NCBI GI	g125578
BLAST score	609
E value	1.0e-63
Match length	126
% identity	93
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_167266 (M73707) phosphoribulokinase [Mesembryanthemum crystallinum]

Seq. No.	222175
Seq. ID	LIB3165-026-P1-K1-A9
Method	BLASTX
NCBI GI	g1001135
BLAST score	178
E value	5.0e-13
Match length	48

% identity	75
NCBI Description	(D64001) acetolactate synthase [Synechocystis sp.]
Seq. No.	222176
Seq. ID	LIB3165-026-P1-K1-B10
Method	BLASTX
NCBI GI	g487046
BLAST score	389
E value	1.0e-37
Match length	131
% identity	61
NCBI Description	photosystem I chain II precursor - wood tobacco >gi_407769_dbj_BAA02871_ (D13718) PSI-D1 precursor [Nicotiana sylvestris]
Seq. No.	222177
Seq. ID	LIB3165-026-P1-K1-B11
Method	BLASTX
NCBI GI	g4406530
BLAST score	608
E value	2.0e-63
Match length	127
% identity	87
NCBI Description	(AF126870) rubisco activase [Vigna radiata]
Seq. No.	222178
Seq. ID	LIB3165-026-P1-K1-B12
Method	BLASTX
NCBI GI	g2414160
BLAST score	283
E value	3.0e-25
Match length	90
% identity	53
NCBI Description	(Z99266) F15C11.2 [Caenorhabditis elegans]
Seq. No.	222179
Seq. ID	LIB3165-026-P1-K1-B3
Method	BLASTX
NCBI GI	g3183640
BLAST score	268
E value	1.0e-23
Match length	52
% identity	96
NCBI Description	(AJ005869) transmembrane channel protein [Cicer arietinum]
Seq. No.	222180
Seq. ID	LIB3165-026-P1-K1-B4
Method	BLASTX
NCBI GI	g20729
BLAST score	368
E value	2.0e-35
Match length	103
% identity	73
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]
Seq. No.	222181
Seq. ID	LIB3165-026-P1-K1-B6

Method	BLASTX
NCBI GI	g1352821
BLAST score	593
E value	1.0e-61
Match length	118
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222182
Seq. ID	LIB3165-026-P1-K1-B7
Method	BLASTX
NCBI GI	g1172811
BLAST score	460
E value	3.0e-46
Match length	87
% identity	97
NCBI Description	60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPRESSOR SC34) >gi_1076751_pir__S49575 ribosomal protein L10.e, cytosolic - rice >gi_575355_emb_CAA57339_ (X81691) putative tumor suppresser [Oryza sativa]

Seq. No.	222183
Seq. ID	LIB3165-026-P1-K1-B9
Method	BLASTX
NCBI GI	g3738299
BLAST score	363
E value	1.0e-34
Match length	90
% identity	81
NCBI Description	(AC005309) putative glutaredoxin [Arabidopsis thaliana] >gi_4249395 (AC006072) putative glutaredoxin [Arabidopsis thaliana]

Seq. No.	222184
Seq. ID	LIB3165-026-P1-K1-C10
Method	BLASTX
NCBI GI	g2194137
BLAST score	391
E value	6.0e-38
Match length	125
% identity	68
NCBI Description	(AC002062) ESTs gb_R29947,gb_H76702 come from this gene. [Arabidopsis thaliana]

Seq. No.	222185
Seq. ID	LIB3165-026-P1-K1-C11
Method	BLASTX
NCBI GI	g131385
BLAST score	473
E value	1.0e-47
Match length	127
% identity	78
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN)

Seq. No.	222186
Seq. ID	LIB3165-026-P1-K1-C3
Method	BLASTX
NCBI GI	g3193298
BLAST score	319
E value	2.0e-29
Match length	93
% identity	65
NCBI Description	(AF069298) T14P8.17 gene product [Arabidopsis thaliana]

Seq. No.	222187
Seq. ID	LIB3165-026-P1-K1-C4
Method	BLASTX
NCBI GI	g3721926
BLAST score	244
E value	1.0e-20
Match length	91
% identity	63
NCBI Description	(AB017480) chloroplast FtsH protease [Nicotiana tabacum]

Seq. No.	222188
Seq. ID	LIB3165-026-P1-K1-C5
Method	BLASTX
NCBI GI	g2146797
BLAST score	557
E value	2.0e-57
Match length	134
% identity	43
NCBI Description	protein disulfide-isomerase (EC 5.3.4.1) - Castor bean >gi_1134968 (U41385) protein disulphide isomerase PDI [Ricinus communis] >gi_1587210_prf__2206331A protein disulfide isomerase [Ricinus communis]

Seq. No.	222189
Seq. ID	LIB3165-026-P1-K1-C9
Method	BLASTX
NCBI GI	g4454480
BLAST score	328
E value	1.0e-30
Match length	73
% identity	78
NCBI Description	(AC006234) putative (1-4)-beta-mannan endohydrolase [Arabidopsis thaliana]

Seq. No.	222190
Seq. ID	LIB3165-026-P1-K1-D3
Method	BLASTX
NCBI GI	g441457
BLAST score	513
E value	3.0e-52
Match length	95
% identity	98
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]

Seq. No.	222191
Seq. ID	LIB3165-026-P1-K1-D7
Method	BLASTX
NCBI GI	g1709825
BLAST score	332
E value	4.0e-31
Match length	122
% identity	66
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No.	222192
Seq. ID	LIB3165-026-P1-K1-D8
Method	BLASTX
NCBI GI	g2739365
BLAST score	531
E value	2.0e-54
Match length	118
% identity	79
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	222193
Seq. ID	LIB3165-026-P1-K1-E10
Method	BLASTX
NCBI GI	g1352821
BLAST score	531
E value	2.0e-54
Match length	103
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222194
Seq. ID	LIB3165-026-P1-K1-E11
Method	BLASTX
NCBI GI	g4325041
BLAST score	635
E value	1.0e-66
Match length	128
% identity	95
NCBI Description	(AF117339) FtsH-like protein Pftf precursor [Nicotiana tabacum]

Seq. No.	222195
Seq. ID	LIB3165-026-P1-K1-E5
Method	BLASTX
NCBI GI	g3953471
BLAST score	238
E value	5.0e-20
Match length	68
% identity	68
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No.	222196
Seq. ID	LIB3165-026-P1-K1-E7
Method	BLASTX
NCBI GI	g1781348
BLAST score	209
E value	7.0e-17
Match length	46
% identity	91
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No.	222197
Seq. ID	LIB3165-026-P1-K1-F10
Method	BLASTX
NCBI GI	g289920
BLAST score	696
E value	1.0e-73
Match length	130
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222198
Seq. ID	LIB3165-026-P1-K1-F11
Method	BLASTX
NCBI GI	g131399
BLAST score	441
E value	3.0e-45
Match length	110
% identity	84
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi_82277_pir__S00411 photosystem II 10K protein precursor - potato >gi_21489_emb_CAA28450_ (X04753) ST-LS1 protein [Solanum tuberosum]

Seq. No.	222199
Seq. ID	LIB3165-026-P1-K1-F3
Method	BLASTX
NCBI GI	g3158474
BLAST score	539
E value	3.0e-55
Match length	114
% identity	91
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]

Seq. No.	222200
Seq. ID	LIB3165-026-P1-K1-F4
Method	BLASTX
NCBI GI	g4091806
BLAST score	520
E value	4.0e-53
Match length	117
% identity	85
NCBI Description	(AF052585) CONSTANS-like protein 2 [Malus domestica]

Seq. No.	222201

Seq. ID	LIB3165-026-P1-K1-F5
Method	BLASTX
NCBI GI	g82426
BLAST score	559
E value	1.0e-57
Match length	116
% identity	45
NCBI Description	ubiquitin precursor - barley (fragment) >gi_755763_emb_CAA27751_ (X04133) ubiquitin polyprecursor (171 aa) [Hordeum vulgare]

Seq. No.	222202
Seq. ID	LIB3165-026-P1-K1-F7
Method	BLASTX
NCBI GI	g1651736
BLAST score	199
E value	2.0e-15
Match length	52
% identity	71
NCBI Description	(D90899) cysteine synthase [Synechocystis sp.]

Seq. No.	222203
Seq. ID	LIB3165-026-P1-K1-F8
Method	BLASTX
NCBI GI	g1352821
BLAST score	575
E value	2.0e-59
Match length	116
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222204
Seq. ID	LIB3165-026-P1-K1-F9
Method	BLASTX
NCBI GI	g3785995
BLAST score	153
E value	5.0e-10
Match length	71
% identity	46
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	222205
Seq. ID	LIB3165-026-P1-K1-G10
Method	BLASTX
NCBI GI	g100616
BLAST score	256
E value	4.0e-22
Match length	60
% identity	82
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum

vulgare]

Seq. No.	222206
Seq. ID	LIB3165-026-P1-K1-G12
Method	BLASTX
NCBI GI	g430947
BLAST score	421
E value	2.0e-41
Match length	103
% identity	82
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	222207
Seq. ID	LIB3165-026-P1-K1-G2
Method	BLASTX
NCBI GI	g1532135
BLAST score	279
E value	8.0e-25
Match length	57
% identity	91
NCBI Description	(U49442) chloroplast mRNA-binding protein CSP41 precursor [Spinacia oleracea]

Seq. No.	222208
Seq. ID	LIB3165-026-P1-K1-G5
Method	BLASTX
NCBI GI	g1354515
BLAST score	287
E value	9.0e-26
Match length	132
% identity	48
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	222209
Seq. ID	LIB3165-026-P1-K1-G7
Method	BLASTX
NCBI GI	g1168411
BLAST score	363
E value	1.0e-34
Match length	94
% identity	81
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	222210
Seq. ID	LIB3165-026-P1-K1-G8
Method	BLASTX
NCBI GI	g2827076
BLAST score	278
E value	1.0e-24
Match length	109
% identity	54
NCBI Description	(AF020269) malate dehydrogenase precursor [Medicago sativa]

Seq. No.	222211
Seq. ID	LIB3165-026-P1-K1-H10

Method	BLASTX
NCBI GI	g3024126
BLAST score	537
E value	4.0e-55
Match length	105
% identity	97
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine synthetase 1 [Catharanthus roseus]

Seq. No.	222212
Seq. ID	LIB3165-026-P1-K1-H11
Method	BLASTX
NCBI GI	g3063392
BLAST score	418
E value	4.0e-41
Match length	113
% identity	75
NCBI Description	(AB012932) Ca2+/H+ exchanger [Vigna radiata]

Seq. No.	222213
Seq. ID	LIB3165-026-P1-K1-H2
Method	BLASTX
NCBI GI	g2499967
BLAST score	186
E value	6.0e-14
Match length	110
% identity	43
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV B PRECURSOR (PSI-E B) >gi_632724_bbs_151002 (S72358) photosystem I subunit PSI-E [Nicotiana sylvestris, leaves, Peptide Chloroplast, 143 aa] [Nicotiana sylvestris]

Seq. No.	222214
Seq. ID	LIB3165-026-P1-K1-H3
Method	BLASTX
NCBI GI	g3023752
BLAST score	309
E value	2.0e-28
Match length	109
% identity	61
NCBI Description	FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520) ferredoxin-I [Lycopersicon esculentum]

Seq. No.	222215
Seq. ID	LIB3165-026-P1-K1-H5
Method	BLASTX
NCBI GI	g282833
BLAST score	481
E value	2.0e-48
Match length	110
% identity	89
NCBI Description	phosphoglycerate kinase (EC 2.7.2.3) - spinach (fragment)

Seq. No.	222216
Seq. ID	LIB3165-026-P1-K1-H7

Method	BLASTX
NCBI GI	g166834
BLAST score	641
E value	3.0e-67
Match length	134
% identity	90
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	222217
Seq. ID	LIB3165-026-P1-K1-H8
Method	BLASTX
NCBI GI	g2213597
BLAST score	223
E value	3.0e-18
Match length	61
% identity	72
NCBI Description	(AC000348) T7N9.17 [Arabidopsis thaliana]

Seq. No.	222218
Seq. ID	LIB3165-026-P1-K1-H9
Method	BLASTN
NCBI GI	g1545804
BLAST score	33
E value	4.0e-09
Match length	85
% identity	84
NCBI Description	Nicotiana tabacum mRNA for cytochrome P450 like_TBP, complete cds

Seq. No.	222219
Seq. ID	LIB3165-027-P1-K1-A1
Method	BLASTX
NCBI GI	g2388578
BLAST score	456
E value	1.0e-45
Match length	109
% identity	79
NCBI Description	(AC000098) Similar to Mycobacterium RlpF (gb_Z84395). ESTs gb_T75785,gb_R30580,gb_T04698 come from this gene. [Arabidopsis thaliana]

Seq. No.	222220
Seq. ID	LIB3165-027-P1-K1-A10
Method	BLASTX
NCBI GI	g2708749
BLAST score	278
E value	8.0e-25
Match length	85
% identity	59
NCBI Description	(AC003952) putative senescence-assoc. rhodanese-like protein [Arabidopsis thaliana]

Seq. No.	222221
Seq. ID	LIB3165-027-P1-K1-A11
Method	BLASTX

NCBI GI	g1172558
BLAST score	256
E value	2.0e-22
Match length	85
% identity	60
NCBI Description	OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) >gi_480122_pir__S36454 porin por1 - garden pea >gi_396819_emb_CAA80988_ (Z25540) Porin [Pisum sativum]

Seq. No.	222222
Seq. ID	LIB3165-027-P1-K1-A4
Method	BLASTX
NCBI GI	g2129538
BLAST score	541
E value	1.0e-55
Match length	109
% identity	96
NCBI Description	AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232) AT103 [Arabidopsis thaliana]

Seq. No.	222223
Seq. ID	LIB3165-027-P1-K1-A6
Method	BLASTX
NCBI GI	g2191191
BLAST score	215
E value	2.0e-17
Match length	100
% identity	54
NCBI Description	(AF007271) A_TM021B04.14 gene product [Arabidopsis thaliana]

Seq. No.	222224
Seq. ID	LIB3165-027-P1-K1-A7
Method	BLASTX
NCBI GI	g4468812
BLAST score	426
E value	3.0e-42
Match length	112
% identity	37
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	222225
Seq. ID	LIB3165-027-P1-K1-A8
Method	BLASTX
NCBI GI	g4539324
BLAST score	264
E value	2.0e-25
Match length	124
% identity	55
NCBI Description	(AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No.	222226
Seq. ID	LIB3165-027-P1-K1-A9
Method	BLASTX
NCBI GI	g4406530
BLAST score	315

E value	4.0e-29
Match length	87
% identity	75
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222227
Seq. ID	LIB3165-027-P1-K1-B1
Method	BLASTX
NCBI GI	g2623960
BLAST score	140
E value	7.0e-09
Match length	48
% identity	58
NCBI Description	(Y12599) histone H1 [Apium graveolens]

Seq. No.	222228
Seq. ID	LIB3165-027-P1-K1-B2
Method	BLASTX
NCBI GI	g131399
BLAST score	457
E value	9.0e-46
Match length	105
% identity	82
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi_82277_pir__S00411 photosystem II 10K protein precursor - potato >gi_21489_emb_CAA28450_ (X04753) ST-LS1 protein [Solanum tuberosum]

Seq. No.	222229
Seq. ID	LIB3165-027-P1-K1-B4
Method	BLASTN
NCBI GI	g3869069
BLAST score	44
E value	1.0e-15
Match length	115
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	222230
Seq. ID	LIB3165-027-P1-K1-B6
Method	BLASTX
NCBI GI	g2499931
BLAST score	233
E value	1.0e-19
Match length	66
% identity	74
NCBI Description	ADENINE PHOSPHORIBOSYLTRANSFERASE 2 (APRT) >gi_2129534_pir__S71272 adenine phosphoribosyltransferase (EC 2.4.2.7) - Arabidopsis thaliana >gi_1321681_emb_CAA65609_ (X96866) adenine phosphoribosyltransferase [Arabidopsis thaliana]

Seq. No.	222231
Seq. ID	LIB3165-027-P1-K1-B7
Method	BLASTX

NCBI GI g100200
BLAST score 332
E value 4.0e-31
Match length 95
% identity 68
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato

Seq. No. 222232
Seq. ID LIB3165-027-P1-K1-C1
Method BLASTX
NCBI GI g3024126
BLAST score 444
E value 3.0e-44
Match length 87
% identity 97
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine synthetase 1 [Catharanthus roseus]

Seq. No. 222233
Seq. ID LIB3165-027-P1-K1-C10
Method BLASTX
NCBI GI g1181599
BLAST score 412
E value 2.0e-40
Match length 111
% identity 73
NCBI Description (D83007) subunit of photosystem I [Cucumis sativus]

Seq. No. 222234
Seq. ID LIB3165-027-P1-K1-C11
Method BLASTX
NCBI GI g1361983
BLAST score 268
E value 4.0e-35
Match length 111
% identity 73
NCBI Description ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858_ (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No. 222235
Seq. ID LIB3165-027-P1-K1-C12
Method BLASTX
NCBI GI g132086
BLAST score 159
E value 4.0e-11
Match length 30
% identity 97
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1 PRECURSOR (RUBISCO SMALL SUBUNIT 1) >gi_68053_pir__RKSYS ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor SRS1 - soybean >gi_18742_emb_CAA23736_ (V00458) rubpcase [Glycine max]

Seq. No. 222236
Seq. ID LIB3165-027-P1-K1-C3

Method	BLASTX
NCBI GI	g1352821
BLAST score	391
E value	4.0e-38
Match length	76
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222237
Seq. ID	LIB3165-027-P1-K1-C5
Method	BLASTX
NCBI GI	g710626
BLAST score	261
E value	6.0e-23
Match length	77
% identity	65
NCBI Description	(D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941 (AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis thaliana]

Seq. No.	222238
Seq. ID	LIB3165-027-P1-K1-C6
Method	BLASTX
NCBI GI	g131392
BLAST score	342
E value	2.0e-32
Match length	86
% identity	84
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_81479_pir__S00005 photosystem II oxygen-evolving complex protein 2 precursor - spinach >gi_21265_emb_CAA29055_ (X05511) 23 kDa OEC protein [Spinacia oleracea] >gi_225596_prf__1307179A luminal protein 23kD [Spinacia oleracea]

Seq. No.	222239
Seq. ID	LIB3165-027-P1-K1-C7
Method	BLASTX
NCBI GI	g1174498
BLAST score	362
E value	1.0e-34
Match length	86
% identity	76
NCBI Description	SYNAPTOBREVIN-RELATED PROTEIN >gi_600710 (M90418) formerly called HAT24; synaptobrevin-related protein [Arabidopsis thaliana]

Seq. No.	222240
Seq. ID	LIB3165-027-P1-K1-D1
Method	BLASTX
NCBI GI	g3913651

BLAST score	237
E value	4.0e-20
Match length	69
% identity	70
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR (FNR) >gi_2225993_emb_CAA74359_ (Y14032) ferredoxin--NADP(+) reductase [Nicotiana tabacum]

Seq. No.	222241
Seq. ID	LIB3165-027-P1-K1-D12
Method	BLASTX
NCBI GI	g2580440
BLAST score	271
E value	5.0e-24
Match length	68
% identity	75
NCBI Description	(D87261) PCF2 [Oryza sativa]

Seq. No.	222242
Seq. ID	LIB3165-027-P1-K1-D2
Method	BLASTX
NCBI GI	g1345698
BLAST score	641
E value	2.0e-67
Match length	121
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR (CAB-151) (LHCP) >gi_99601_pir__S20917 chlorophyll a/b-binding protein - upland cotton >gi_452314_emb_CAA38025_ (X54090) chlorophyll ab binding protein [Gossypium hirsutum]

Seq. No.	222243
Seq. ID	LIB3165-027-P1-K1-D4
Method	BLASTX
NCBI GI	g4539422
BLAST score	233
E value	2.0e-19
Match length	88
% identity	62
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]

Seq. No.	222244
Seq. ID	LIB3165-027-P1-K1-D6
Method	BLASTX
NCBI GI	g4539543
BLAST score	565
E value	2.0e-58
Match length	118
% identity	95
NCBI Description	(AJ133422) glyceraldehyde-3-phosphate dehydrogenase [Nicotiana tabacum]

Seq. No.	222245
Seq. ID	LIB3165-027-P1-K1-D7
Method	BLASTN
NCBI GI	g3510339

BLAST score	38
E value	5.0e-12
Match length	128
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No.	222246
Seq. ID	LIB3165-027-P1-K1-D8
Method	BLASTX
NCBI GI	g1694976
BLAST score	384
E value	3.0e-37
Match length	85
% identity	81
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis thaliana]

Seq. No.	222247
Seq. ID	LIB3165-027-P1-K1-D9
Method	BLASTX
NCBI GI	g289920
BLAST score	608
E value	2.0e-63
Match length	115
% identity	97
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222248
Seq. ID	LIB3165-027-P1-K1-E10
Method	BLASTX
NCBI GI	g2970051
BLAST score	303
E value	9.0e-28
Match length	82
% identity	68
NCBI Description	(AB012110) ARG10 [Vigna radiata]

Seq. No.	222249
Seq. ID	LIB3165-027-P1-K1-E11
Method	BLASTX
NCBI GI	g4406530
BLAST score	192
E value	8.0e-15
Match length	65
% identity	65
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222250
Seq. ID	LIB3165-027-P1-K1-E2
Method	BLASTX
NCBI GI	g4406530
BLAST score	582
E value	2.0e-60
Match length	116

% identity	96
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222251
Seq. ID	LIB3165-027-P1-K1-E3
Method	BLASTX
NCBI GI	g1352821
BLAST score	453
E value	2.0e-45
Match length	87
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222252
Seq. ID	LIB3165-027-P1-K1-E4
Method	BLASTX
NCBI GI	g1168411
BLAST score	454
E value	2.0e-45
Match length	113
% identity	82
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	222253
Seq. ID	LIB3165-027-P1-K1-E6
Method	BLASTX
NCBI GI	g441457
BLAST score	462
E value	2.0e-46
Match length	88
% identity	97
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]

Seq. No.	222254
Seq. ID	LIB3165-027-P1-K1-E8
Method	BLASTX
NCBI GI	g1353352
BLAST score	379
E value	1.0e-36
Match length	111
% identity	61
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	222255
Seq. ID	LIB3165-027-P1-K1-F1
Method	BLASTX
NCBI GI	g3738324
BLAST score	217
E value	1.0e-17
Match length	65
% identity	55

NCBI Description	(AC005170) GMP synthase-like protein [Arabidopsis thaliana]

Seq. No.	222256
Seq. ID	LIB3165-027-P1-K1-F10
Method	BLASTX
NCBI GI	g2499497
BLAST score	465
E value	7.0e-47
Match length	96
% identity	96
NCBI Description	PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR >gi_1161600_emb_CAA88841_ (Z48977) phosphoglycerate kinase [Nicotiana tabacum]

Seq. No.	222257
Seq. ID	LIB3165-027-P1-K1-F11
Method	BLASTX
NCBI GI	g266893
BLAST score	573
E value	2.0e-59
Match length	114
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__S28172 ribulose-bisphosphate carboxylase activase - cucumber >gi_18284_emb_CAA47906_ (X67674) rubisco activase [Cucumis sativus]

Seq. No.	222258
Seq. ID	LIB3165-027-P1-K1-F12
Method	BLASTN
NCBI GI	g1669584
BLAST score	43
E value	5.0e-15
Match length	83
% identity	88
NCBI Description	Cucumis sativus mRNA for cytosolic ascorbate peroxidase, complete cds

Seq. No.	222259
Seq. ID	LIB3165-027-P1-K1-F3
Method	BLASTX
NCBI GI	g4206195
BLAST score	202
E value	7.0e-16
Match length	39
% identity	87
NCBI Description	(AF071527) hypothetical protein [Arabidopsis thaliana] >gi_4262169_gb_AAD14469_ (AC005275) hypothetical protein [Arabidopsis thaliana]

Seq. No.	222260
Seq. ID	LIB3165-027-P1-K1-F4
Method	BLASTX
NCBI GI	g289920
BLAST score	549
E value	1.0e-56

Match length	100
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222261
Seq. ID	LIB3165-027-P1-K1-F5
Method	BLASTX
NCBI GI	g629733
BLAST score	403
E value	2.0e-39
Match length	98
% identity	78
NCBI Description	sulfate adenylyltransferase (EC 2.7.7.4) met3-2 - potato >gi_2130000_pir__S67498 sulfate adenylyltransferase (EC 2.7.7.4) (clone StMet3-2) - potato >gi_479090_emb_CAA55655_ (X79053) sulfate adenylyltransferase [Solanum tuberosum]

Seq. No.	222262
Seq. ID	LIB3165-027-P1-K1-F6
Method	BLASTX
NCBI GI	g1352821
BLAST score	474
E value	9.0e-48
Match length	91
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222263
Seq. ID	LIB3165-027-P1-K1-G1
Method	BLASTX
NCBI GI	g832876
BLAST score	255
E value	4.0e-22
Match length	100
% identity	40
NCBI Description	(L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi_1097368_prf__2113407A ascorbate free radical reductase [Lycopersicon esculentum]

Seq. No.	222264
Seq. ID	LIB3165-027-P1-K1-G12
Method	BLASTX
NCBI GI	g1352821
BLAST score	485
E value	5.0e-49
Match length	92
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222265
Seq. ID	LIB3165-027-P1-K1-G5
Method	BLASTX
NCBI GI	g462273
BLAST score	181
E value	2.0e-13
Match length	42
% identity	88
NCBI Description	IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (IGPD) >gi_437213 (U02689) imidazoleglycerolphosphate dehydratase [Arabidopsis thaliana]

Seq. No.	222266
Seq. ID	LIB3165-027-P1-K1-G6
Method	BLASTX
NCBI GI	g1352821
BLAST score	584
E value	1.0e-60
Match length	112
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222267
Seq. ID	LIB3165-027-P1-K1-G7
Method	BLASTX
NCBI GI	g120661
BLAST score	570
E value	5.0e-59
Match length	118
% identity	93
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_170237 (M14417) glyceraldehyde-3-phosphate dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No.	222268
Seq. ID	LIB3165-027-P1-K1-G8
Method	BLASTX
NCBI GI	g266893
BLAST score	624
E value	2.0e-65
Match length	121
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__S28172 ribulose-bisphosphate carboxylase activase - cucumber >gi_18284_emb_CAA47906_ (X67674) rubisco activase [Cucumis sativus]

Seq. No.	222269
Seq. ID	LIB3165-027-P1-K1-G9
Method	BLASTX
NCBI GI	g400890

BLAST score	217
E value	1.0e-17
Match length	107
% identity	54
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_282837_pir__S26953 photosystem II 22K protein precursor - spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864) photosystem II 22 kda polypeptide [spinach, Peptide, 274 aa] [Spinacia oleracea]

Seq. No.	222270
Seq. ID	LIB3165-027-P1-K1-H1
Method	BLASTX
NCBI GI	g70644
BLAST score	238
E value	4.0e-20
Match length	60
% identity	14
NCBI Description	ubiquitin precursor - common sunflower (fragment)

Seq. No.	222271
Seq. ID	LIB3165-027-P1-K1-H4
Method	BLASTX
NCBI GI	g289920
BLAST score	262
E value	4.0e-23
Match length	58
% identity	90
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222272
Seq. ID	LIB3165-028-P1-K1-A1
Method	BLASTX
NCBI GI	g2894599
BLAST score	375
E value	3.0e-36
Match length	80
% identity	79
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	222273
Seq. ID	LIB3165-028-P1-K1-A10
Method	BLASTX
NCBI GI	g4406530
BLAST score	255
E value	7.0e-23
Match length	83
% identity	66
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222274
Seq. ID	LIB3165-028-P1-K1-A11
Method	BLASTX
NCBI GI	g121902
BLAST score	163

E value	3.0e-11
Match length	36
% identity	89
NCBI Description	HISTONE H1.1 >gi_1070594_pir__HSMU11 histone H1.1 - Arabidopsis thaliana >gi_16317_emb_CAA44314_ (X62458) Histone H1 [Arabidopsis thaliana]

Seq. No.	222275
Seq. ID	LIB3165-028-P1-K1-A12
Method	BLASTX
NCBI GI	g4234955
BLAST score	175
E value	1.0e-12
Match length	92
% identity	23
NCBI Description	(AF098971) NBS-LRR-like protein cD8 [Phaseolus vulgaris]

Seq. No.	222276
Seq. ID	LIB3165-028-P1-K1-A3
Method	BLASTX
NCBI GI	g2880043
BLAST score	376
E value	2.0e-36
Match length	101
% identity	73
NCBI Description	(AC002340) putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]

Seq. No.	222277
Seq. ID	LIB3165-028-P1-K1-A7
Method	BLASTX
NCBI GI	g1346155
BLAST score	286
E value	6.0e-26
Match length	66
% identity	83
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_481942_pir__S40212 glycine hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei >gi_437995_emb_CAA81078_ (Z25859) glycine hydroxymethyltransferase [Flaveria pringlei]

Seq. No.	222278
Seq. ID	LIB3165-028-P1-K1-A8
Method	BLASTX
NCBI GI	g549063
BLAST score	375
E value	3.0e-36
Match length	91
% identity	79
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]

Seq. No.	222279

Seq. ID	LIB3165-028-P1-K1-B1
Method	BLASTX
NCBI GI	g2129511
BLAST score	367
E value	2.0e-40
Match length	98
% identity	82
NCBI Description	glycerate dehydrogenase (EC 1.1.1.29) splice form HPR1, microbody - cucurbit >gi_1304042_dbj_BAA08410_ (D49432) hydroxypyruvate reductase [Cucurbita sp.]

Seq. No.	222280
Seq. ID	LIB3165-028-P1-K1-B10
Method	BLASTX
NCBI GI	g115765
BLAST score	498
E value	2.0e-50
Match length	110
% identity	48
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	222281
Seq. ID	LIB3165-028-P1-K1-B12
Method	BLASTX
NCBI GI	g1778095
BLAST score	233
E value	2.0e-19
Match length	113
% identity	44
NCBI Description	(U64903) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris]

Seq. No.	222282
Seq. ID	LIB3165-028-P1-K1-B3
Method	BLASTX
NCBI GI	g131385
BLAST score	518
E value	6.0e-53
Match length	126
% identity	84
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN)

Seq. No.	222283
Seq. ID	LIB3165-028-P1-K1-B4
Method	BLASTX
NCBI GI	g1352821
BLAST score	535

E value	7.0e-55
Match length	102
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222284
Seq. ID	LIB3165-028-P1-K1-B5
Method	BLASTX
NCBI GI	g3063451
BLAST score	304
E value	9.0e-28
Match length	94
% identity	59
NCBI Description	(AC003981) F22O13.13 [Arabidopsis thaliana]

Seq. No.	222285
Seq. ID	LIB3165-028-P1-K1-B8
Method	BLASTX
NCBI GI	g130283
BLAST score	365
E value	6.0e-35
Match length	78
% identity	87
NCBI Description	PLASTOCYANIN >gi_65839_pir__CUUA plastocyanin - Chilean potato-tree >gi_223147_prf__0512261A plastocyanin [Solanum crispum]

Seq. No.	222286
Seq. ID	LIB3165-028-P1-K1-B9
Method	BLASTX
NCBI GI	g1181599
BLAST score	454
E value	2.0e-45
Match length	119
% identity	75
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.	222287
Seq. ID	LIB3165-028-P1-K1-C1
Method	BLASTX
NCBI GI	g2598589
BLAST score	281
E value	4.0e-25
Match length	91
% identity	57
NCBI Description	(Y15367) MtN19 [Medicago truncatula]

Seq. No.	222288
Seq. ID	LIB3165-028-P1-K1-C10
Method	BLASTX
NCBI GI	g400890
BLAST score	246
E value	6.0e-21

Match length	112
% identity	46
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_282837_pir__S26953 photosystem II 22K protein precursor - spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864) photosystem II 22 kda polypeptide [spinach, Peptide, 274 aa] [Spinacia oleracea]

Seq. No.	222289
Seq. ID	LIB3165-028-P1-K1-C3
Method	BLASTX
NCBI GI	g2494415
BLAST score	323
E value	5.0e-30
Match length	101
% identity	73
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_515747 (L34841) fructose-1,6-bisphosphatase [Glycine max]

Seq. No.	222290
Seq. ID	LIB3165-028-P1-K1-C4
Method	BLASTX
NCBI GI	g3928543
BLAST score	220
E value	6.0e-18
Match length	127
% identity	35
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	222291
Seq. ID	LIB3165-028-P1-K1-C5
Method	BLASTX
NCBI GI	g115471
BLAST score	526
E value	8.0e-54
Match length	127
% identity	76
NCBI Description	CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) >gi_100078_pir__S10200 carbonate dehydratase (EC 4.2.1.1) precursor - garden pea >gi_20673_emb_CAA36792_ (X52558) precursor peptide (AA -104 to 224) [Pisum sativum]

Seq. No.	222292
Seq. ID	LIB3165-028-P1-K1-C7
Method	BLASTX
NCBI GI	g121953
BLAST score	167
E value	6.0e-12
Match length	38
% identity	87
NCBI Description	HISTONE H1 >gi_81905_pir__S00033 histone H1.b - garden pea >gi_20762_emb_CAA29123_ (X05636) H1 histone (AA 1-263) [Pisum sativum]

Seq. No.	222293
Seq. ID	LIB3165-028-P1-K1-C9
Method	BLASTX
NCBI GI	g3914605
BLAST score	361
E value	2.0e-34
Match length	122
% identity	60
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase - apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica]

Seq. No.	222294
Seq. ID	LIB3165-028-P1-K1-D10
Method	BLASTX
NCBI GI	g4097547
BLAST score	172
E value	3.0e-12
Match length	34
% identity	44
NCBI Description	(U64906) ATFP3 [Arabidopsis thaliana]

Seq. No.	222295
Seq. ID	LIB3165-028-P1-K1-D12
Method	BLASTX
NCBI GI	g3482925
BLAST score	238
E value	5.0e-20
Match length	77
% identity	62
NCBI Description	(AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi_1143445 [Arabidopsis thaliana]

Seq. No.	222296
Seq. ID	LIB3165-028-P1-K1-D2
Method	BLASTX
NCBI GI	g2662343
BLAST score	420
E value	2.0e-41
Match length	82
% identity	99
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	222297
Seq. ID	LIB3165-028-P1-K1-D3
Method	BLASTX
NCBI GI	g100616
BLAST score	387
E value	1.0e-37
Match length	113
% identity	66
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate

carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	222298
Seq. ID	LIB3165-028-P1-K1-D6
Method	BLASTX
NCBI GI	g4455787
BLAST score	296
E value	8.0e-27
Match length	120
% identity	42
NCBI Description	(AL035536) putative DNA polymerase accessory protein [Schizosaccharomyces pombe]

Seq. No.	222299
Seq. ID	LIB3165-028-P1-K1-D9
Method	BLASTN
NCBI GI	g2687434
BLAST score	327
E value	0.0e+00
Match length	395
% identity	96
NCBI Description	Eucryphia lucida large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	222300
Seq. ID	LIB3165-028-P1-K1-E10
Method	BLASTX
NCBI GI	g228403
BLAST score	475
E value	7.0e-48
Match length	104
% identity	88
NCBI Description	glycolate oxidase [Lens culinaris]

Seq. No.	222301
Seq. ID	LIB3165-028-P1-K1-E11
Method	BLASTX
NCBI GI	g2493689
BLAST score	340
E value	5.0e-32
Match length	73
% identity	90
NCBI Description	PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi_1070377_emb_CAA63670_ (X93203) 10 kDa phosphoprotein [Populus deltoides] >gi_2143326_emb_CAA73768_ (Y13328) 10kDa phosphoprotein [Populus deltoides]

Seq. No.	222302
Seq. ID	LIB3165-028-P1-K1-E4
Method	BLASTX
NCBI GI	g441457
BLAST score	577
E value	8.0e-60
Match length	110
% identity	97

NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]

Seq. No.	222303
Seq. ID	LIB3165-028-P1-K1-E6
Method	BLASTX
NCBI GI	g4406530
BLAST score	353
E value	1.0e-33
Match length	94
% identity	77
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222304
Seq. ID	LIB3165-028-P1-K1-E8
Method	BLASTX
NCBI GI	g131397
BLAST score	224
E value	2.0e-18
Match length	111
% identity	50
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_81480_pir__S00008 photosystem II oxygen-evolving complex protein 3 precursor - spinach >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi_225597_prf__1307179B luminal protein 16kD [Spinacia oleracea]

Seq. No.	222305
Seq. ID	LIB3165-028-P1-K1-F10
Method	BLASTX
NCBI GI	g2244965
BLAST score	262
E value	7.0e-23
Match length	86
% identity	60
NCBI Description	(Z97340) unnamed protein product [Arabidopsis thaliana]

Seq. No.	222306
Seq. ID	LIB3165-028-P1-K1-F11
Method	BLASTX
NCBI GI	g3763916
BLAST score	356
E value	7.0e-34
Match length	127
% identity	50
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana] >gi_4531439_gb_AAD22124.1_AC006224_6 (AC006224) unknown protein [Arabidopsis thaliana]

Seq. No.	222307
Seq. ID	LIB3165-028-P1-K1-F12
Method	BLASTX
NCBI GI	g3702327
BLAST score	195

E value	4.0e-15
Match length	57
% identity	63
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	222308
Seq. ID	LIB3165-028-P1-K1-F2
Method	BLASTX
NCBI GI	g2244906
BLAST score	294
E value	1.0e-26
Match length	108
% identity	57
NCBI Description	(Z97339) indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	222309
Seq. ID	LIB3165-028-P1-K1-F5
Method	BLASTX
NCBI GI	g399082
BLAST score	140
E value	1.0e-08
Match length	89
% identity	38
NCBI Description	ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR >gi_322713_pir__S28171 H+-transporting ATP synthase (EC 3.6.1.34) delta chain, chloroplast - garden pea >gi_169045 (M94558) ATP synthase delta subunit [Pisum sativum]

Seq. No.	222310
Seq. ID	LIB3165-028-P1-K1-F7
Method	BLASTX
NCBI GI	g1172494
BLAST score	142
E value	9.0e-09
Match length	113
% identity	30
NCBI Description	PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE (PHS) (4-ALPHA-HYDROXY-TETRAHYDROPTERIN DEHYDRATASE) (PHENYLALANINE HYDROXYLASE-STIMULATING PROTEIN) (PCD) >gi_476742 (M88627) phenylalanine hydroxylase [Pseudomonas aeruginosa]

Seq. No.	222311
Seq. ID	LIB3165-028-P1-K1-F8
Method	BLASTX
NCBI GI	g1694976
BLAST score	370
E value	2.0e-35
Match length	103
% identity	68
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis thaliana]

Seq. No.	222312
Seq. ID	LIB3165-028-P1-K1-F9

Method	BLASTX
NCBI GI	g4544399
BLAST score	457
E value	1.0e-45
Match length	107
% identity	77
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	222313
Seq. ID	LIB3165-028-P1-K1-G1
Method	BLASTX
NCBI GI	g3885328
BLAST score	578
E value	7.0e-60
Match length	130
% identity	76
NCBI Description	(AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	222314
Seq. ID	LIB3165-028-P1-K1-G10
Method	BLASTX
NCBI GI	g1352821
BLAST score	531
E value	2.0e-54
Match length	100
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222315
Seq. ID	LIB3165-028-P1-K1-G11
Method	BLASTX
NCBI GI	g1168411
BLAST score	327
E value	2.0e-30
Match length	87
% identity	79
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	222316
Seq. ID	LIB3165-028-P1-K1-G12
Method	BLASTX
NCBI GI	g131773
BLAST score	363
E value	1.0e-34
Match length	114
% identity	71
NCBI Description	40S RIBOSOMAL PROTEIN S14 (CLONE MCH2) >gi_82724_pir__B30097 ribosomal protein S14 (clone MCH2) - maize

Seq. No.	222317

Seq. ID	LIB3165-028-P1-K1-G3
Method	BLASTX
NCBI GI	g1871577
BLAST score	237
E value	6.0e-20
Match length	87
% identity	54
NCBI Description	(Y11553) putative 21kD protein precursor [Medicago sativa]

Seq. No.	222318
Seq. ID	LIB3165-028-P1-K1-G4
Method	BLASTX
NCBI GI	g3850778
BLAST score	414
E value	1.0e-40
Match length	99
% identity	79
NCBI Description	(Y18346) gluaredoxin [Lycopersicon esculentum]

Seq. No.	222319
Seq. ID	LIB3165-028-P1-K1-G5
Method	BLASTX
NCBI GI	g3236240
BLAST score	227
E value	2.0e-32
Match length	86
% identity	76
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	222320
Seq. ID	LIB3165-028-P1-K1-G7
Method	BLASTX
NCBI GI	g128188
BLAST score	298
E value	5.0e-27
Match length	115
% identity	59
NCBI Description	NITRATE REDUCTASE 2 (NR2) >gi_66202_pir__RDMUNH nitrate reductase (NADH) (EC 1.6.6.1) 2 - Arabidopsis thaliana >gi_166782 (J03240) nitrate reductase (EC 1.6.6.1) [Arabidopsis thaliana]

Seq. No.	222321
Seq. ID	LIB3165-028-P1-K1-G8
Method	BLASTX
NCBI GI	g508304
BLAST score	352
E value	2.0e-33
Match length	79
% identity	80
NCBI Description	(L22305) corC [Medicago sativa]

Seq. No.	222322
Seq. ID	LIB3165-028-P1-K1-G9
Method	BLASTX
NCBI GI	g1354515
BLAST score	242

E value	1.0e-20
Match length	120
% identity	53
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	222323
Seq. ID	LIB3165-028-P1-K1-H1
Method	BLASTX
NCBI GI	g115506
BLAST score	158
E value	1.0e-10
Match length	79
% identity	20
NCBI Description	CALMODULIN >gi_71688_pir__MCKM calmodulin - Chlamydomonas reinhardtii >gi_167411 (M20729) calmodulin [Chlamydomonas reinhardtii]

Seq. No.	222324
Seq. ID	LIB3165-028-P1-K1-H10
Method	BLASTX
NCBI GI	g266944
BLAST score	488
E value	3.0e-49
Match length	97
% identity	93
NCBI Description	60S RIBOSOMAL PROTEIN L2 (L8) (RIBOSOMAL PROTEIN TL2) >gi_71078_pir__R5TOL8 ribosomal protein L8, cytosolic - tomato >gi_19343_emb_CAA45863_ (X64562) ribosomal protein L2 [Lycopersicon esculentum]

Seq. No.	222325
Seq. ID	LIB3165-028-P1-K1-H12
Method	BLASTX
NCBI GI	g2104949
BLAST score	361
E value	2.0e-34
Match length	102
% identity	70
NCBI Description	(U96716) MAP kinase-like protein [Selaginella lepidophylla]

Seq. No.	222326
Seq. ID	LIB3165-028-P1-K1-H3
Method	BLASTX
NCBI GI	g4335773
BLAST score	283
E value	2.0e-25
Match length	119
% identity	61
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	222327
Seq. ID	LIB3165-028-P1-K1-H4
Method	BLASTX
NCBI GI	g487046
BLAST score	359
E value	3.0e-34

Match length	126
% identity	60
NCBI Description	photosystem I chain II precursor - wood tobacco >gi_407769_dbj_BAA02871_ (D13718) PSI-D1 precursor [Nicotiana sylvestris]

Seq. No.	222328
Seq. ID	LIB3165-028-P1-K1-H7
Method	BLASTX
NCBI GI	g4519539
BLAST score	320
E value	1.0e-29
Match length	88
% identity	74
NCBI Description	(AB016256) NAD-dependent sorbitol dehydrogenase [Malus domestica]

Seq. No.	222329
Seq. ID	LIB3165-028-P1-K1-H8
Method	BLASTX
NCBI GI	g399307
BLAST score	427
E value	3.0e-42
Match length	130
% identity	63
NCBI Description	PRENYL TRANSFERASE >gi_99282_pir__A40433 prephytoene pyrophosphatase dehydrogenase (crtE) homolog - Cyanophora paradoxa >gi_336639 (M37111) prephytoene pyrophosphate dehydrogenase [Cyanophora paradoxa] >gi_1016130 (U30821) prenyl transferase [Cyanophora paradoxa]

Seq. No.	222330
Seq. ID	LIB3165-028-P1-K1-H9
Method	BLASTX
NCBI GI	g4406530
BLAST score	293
E value	2.0e-26
Match length	104
% identity	62
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222331
Seq. ID	LIB3165-030-P1-K1-A11
Method	BLASTX
NCBI GI	g400890
BLAST score	199
E value	1.0e-15
Match length	104
% identity	53
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_282837_pir__S26953 photosystem II 22K protein precursor - spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864) photosystem II 22 kda polypeptide [spinach, Peptide, 274 aa] [Spinacia oleracea]

Seq. No.	222332

Seq. ID	LIB3165-030-P1-K1-A12
Method	BLASTX
NCBI GI	g402753
BLAST score	553
E value	5.0e-57
Match length	119
% identity	93
NCBI Description	(X71439) translation elongation factor EF-G [Glycine max]

Seq. No.	222333
Seq. ID	LIB3165-030-P1-K1-A8
Method	BLASTX
NCBI GI	g2738248
BLAST score	237
E value	5.0e-20
Match length	92
% identity	76
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	222334
Seq. ID	LIB3165-030-P1-K1-B4
Method	BLASTX
NCBI GI	g402753
BLAST score	307
E value	2.0e-28
Match length	98
% identity	68
NCBI Description	(X71439) translation elongation factor EF-G [Glycine max]

Seq. No.	222335
Seq. ID	LIB3165-030-P1-K1-C1
Method	BLASTX
NCBI GI	g3687237
BLAST score	351
E value	2.0e-33
Match length	117
% identity	62
NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No.	222336
Seq. ID	LIB3165-030-P1-K1-C11
Method	BLASTX
NCBI GI	g115472
BLAST score	350
E value	3.0e-33
Match length	86
% identity	77
NCBI Description	CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) >gi_99567_pir__A35163 carbonate dehydratase (EC 4.2.1.1) precursor - spinach chloroplast >gi_170105 (J05403) carbonic anhydrase (EC 4.2.1.1) [Spinacia oleracea]

Seq. No.	222337
Seq. ID	LIB3165-030-P1-K1-C5

Method	BLASTX
NCBI GI	g3776536
BLAST score	108
E value	5.0e-12
Match length	110
% identity	6
NCBI Description	(AF095794) polyubiquitin [Schizosaccharomyces pombe]

Seq. No.	222338
Seq. ID	LIB3165-030-P1-K1-D10
Method	BLASTX
NCBI GI	g289920
BLAST score	345
E value	1.0e-32
Match length	106
% identity	65
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222339
Seq. ID	LIB3165-030-P1-K1-D11
Method	BLASTX
NCBI GI	g20729
BLAST score	242
E value	1.0e-20
Match length	90
% identity	62
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	222340
Seq. ID	LIB3165-030-P1-K1-D4
Method	BLASTX
NCBI GI	g20729
BLAST score	374
E value	5.0e-36
Match length	95
% identity	77
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	222341
Seq. ID	LIB3165-030-P1-K1-D7
Method	BLASTX
NCBI GI	g3193303
BLAST score	342
E value	2.0e-32
Match length	90
% identity	70
NCBI Description	(AF069298) similar to several proteins containing a tandem repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis thaliana]

Seq. No.	222342
Seq. ID	LIB3165-030-P1-K1-E1
Method	BLASTX
NCBI GI	g1352821
BLAST score	290

E value	1.0e-26
Match length	61
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222343
Seq. ID	LIB3165-030-P1-K1-E10
Method	BLASTX
NCBI GI	g1200116
BLAST score	161
E value	1.0e-11
Match length	39
% identity	85
NCBI Description	(X95752) c subunit of V-type ATPase [Nicotiana tabacum]

Seq. No.	222344
Seq. ID	LIB3165-030-P1-K1-E6
Method	BLASTX
NCBI GI	g3882081
BLAST score	558
E value	1.0e-57
Match length	117
% identity	37
NCBI Description	(AJ012552) polyubiquitin [Vicia faba]

Seq. No.	222345
Seq. ID	LIB3165-030-P1-K1-E7
Method	BLASTX
NCBI GI	g3158474
BLAST score	457
E value	8.0e-46
Match length	109
% identity	83
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]

Seq. No.	222346
Seq. ID	LIB3165-030-P1-K1-E9
Method	BLASTX
NCBI GI	g3063392
BLAST score	325
E value	3.0e-30
Match length	93
% identity	73
NCBI Description	(AB012932) Ca2+/H+ exchanger [Vigna radiata]

Seq. No.	222347
Seq. ID	LIB3165-030-P1-K1-F1
Method	BLASTX
NCBI GI	g3687237
BLAST score	296
E value	7.0e-27
Match length	111
% identity	53

NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]
Seq. No.	222348
Seq. ID	LIB3165-030-P1-K1-F12
Method	BLASTX
NCBI GI	g3378650
BLAST score	465
E value	1.0e-46
Match length	121
% identity	70
NCBI Description	(X97606) abscisic acid activated [Medicago sativa]
Seq. No.	222349
Seq. ID	LIB3165-030-P1-K1-F9
Method	BLASTX
NCBI GI	g4406530
BLAST score	240
E value	2.0e-20
Match length	91
% identity	62
NCBI Description	(AF126870) rubisco activase [Vigna radiata]
Seq. No.	222350
Seq. ID	LIB3165-030-P1-K1-G1
Method	BLASTX
NCBI GI	g544437
BLAST score	324
E value	3.0e-30
Match length	74
% identity	86
NCBI Description	GLUTATHIONE PEROXIDASE HOMOLOG (SALT-ASSOCIATED PROTEIN) >gi_296358_emb_CAA47018_ (X66377) CIT-SAP [Citrus sinensis]
Seq. No.	222351
Seq. ID	LIB3165-030-P1-K1-G6
Method	BLASTX
NCBI GI	g3913651
BLAST score	424
E value	7.0e-42
Match length	109
% identity	73
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR (FNR) >gi_2225993_emb_CAA74359_ (Y14032) ferredoxin--NADP(+) reductase [Nicotiana tabacum]
Seq. No.	222352
Seq. ID	LIB3165-030-P1-K1-G8
Method	BLASTX
NCBI GI	g4406530
BLAST score	300
E value	2.0e-27
Match length	83
% identity	75
NCBI Description	(AF126870) rubisco activase [Vigna radiata]
Seq. No.	222353

Seq. ID	LIB3165-030-P1-K1-G9
Method	BLASTX
NCBI GI	g3327394
BLAST score	163
E value	3.0e-11
Match length	50
% identity	56
NCBI Description	(AC004483) putative RNA helicase [Arabidopsis thaliana]

Seq. No.	222354
Seq. ID	LIB3165-030-P1-K1-H1
Method	BLASTX
NCBI GI	g100616
BLAST score	261
E value	8.0e-23
Match length	58
% identity	86
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	222355
Seq. ID	LIB3165-030-P1-K1-H10
Method	BLASTX
NCBI GI	g2506443
BLAST score	447
E value	1.0e-44
Match length	107
% identity	83
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	222356
Seq. ID	LIB3165-030-P1-K1-H12
Method	BLASTX
NCBI GI	g231688
BLAST score	468
E value	4.0e-47
Match length	114
% identity	80
NCBI Description	CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC 1.11.1.6) - upland cotton >gi_18488_emb_CAA39998_ (X56675) subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No.	222357
Seq. ID	LIB3165-030-P1-K1-H2
Method	BLASTX
NCBI GI	g1130684

BLAST score	356
E value	6.0e-34
Match length	85
% identity	84
NCBI Description	(Z46960) acetohydroxyacid synthase [Gossypium hirsutum]

Seq. No.	222358
Seq. ID	LIB3165-030-P1-K1-H3
Method	BLASTX
NCBI GI	g1130684
BLAST score	154
E value	2.0e-10
Match length	63
% identity	56
NCBI Description	(Z46960) acetohydroxyacid synthase [Gossypium hirsutum]

Seq. No.	222359
Seq. ID	LIB3165-031-P1-K1-A1
Method	BLASTX
NCBI GI	g128194
BLAST score	573
E value	2.0e-59
Match length	119
% identity	87
NCBI Description	NITRATE REDUCTASE (NR) >gi_81572_pir__A41667 nitrate reductase (NADH) (EC 1.6.6.1) - winter squash >gi_167499 (M33154) nitrate reductase [Cucurbita maxima]

Seq. No.	222360
Seq. ID	LIB3165-031-P1-K1-A10
Method	BLASTX
NCBI GI	g1352821
BLAST score	682
E value	4.0e-72
Match length	127
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222361
Seq. ID	LIB3165-031-P1-K1-A11
Method	BLASTX
NCBI GI	g3808101
BLAST score	358
E value	4.0e-34
Match length	110
% identity	65
NCBI Description	(AJ012165) chloroplast protease [Capsicum annuum]

Seq. No.	222362
Seq. ID	LIB3165-031-P1-K1-A12
Method	BLASTX
NCBI GI	g3746060
BLAST score	158

E value 1.0e-10
Match length 37
% identity 84
NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 222363
Seq. ID LIB3165-031-P1-K1-A4
Method BLASTX
NCBI GI g1707019
BLAST score 202
E value 6.0e-16
Match length 68
% identity 53
NCBI Description (U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No. 222364
Seq. ID LIB3165-031-P1-K1-A5
Method BLASTX
NCBI GI g131397
BLAST score 258
E value 2.0e-22
Match length 116
% identity 52
NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_81480_pir__S00008 photosystem II oxygen-evolving complex protein 3 precursor - spinach >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi_225597_prf__1307179B luminal protein 16kD [Spinacia oleracea]

Seq. No. 222365
Seq. ID LIB3165-031-P1-K1-A6
Method BLASTX
NCBI GI g68200
BLAST score 488
E value 2.0e-49
Match length 119
% identity 84
NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No. 222366
Seq. ID LIB3165-031-P1-K1-A9
Method BLASTX
NCBI GI g20729
BLAST score 355
E value 8.0e-34
Match length 102
% identity 72
NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No. 222367
Seq. ID LIB3165-031-P1-K1-B12
Method BLASTX

NCBI GI g2465008
BLAST score 285
E value 1.0e-25
Match length 123
% identity 46
NCBI Description (AJ001445) ripening-induced protein [Fragaria vesca]

Seq. No. 222368
Seq. ID LIB3165-031-P1-K1-B3
Method BLASTX
NCBI GI g625547
BLAST score 444
E value 3.0e-44
Match length 119
% identity 71
NCBI Description chlorophyll a/b-binding protein type I - common tobacco >gi_493723_emb_CAA45523_ (X64198) photosystem I light-harvesting chlorophyll a/b-binding protein [Nicotiana tabacum]

Seq. No. 222369
Seq. ID LIB3165-031-P1-K1-B4
Method BLASTX
NCBI GI g4406530
BLAST score 292
E value 2.0e-26
Match length 103
% identity 62
NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 222370
Seq. ID LIB3165-031-P1-K1-B8
Method BLASTX
NCBI GI g3023752
BLAST score 232
E value 2.0e-19
Match length 92
% identity 55
NCBI Description FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520) ferredoxin-I [Lycopersicon esculentum]

Seq. No. 222371
Seq. ID LIB3165-031-P1-K1-B9
Method BLASTX
NCBI GI g1345698
BLAST score 369
E value 2.0e-35
Match length 77
% identity 91
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR (CAB-151) (LHCP) >gi_99601_pir__S20917 chlorophyll a/b-binding protein - upland cotton >gi_452314_emb_CAA38025_ (X54090) chlorophyll ab binding protein [Gossypium hirsutum]

Seq. No. 222372
Seq. ID LIB3165-031-P1-K1-C1

Method	BLASTX
NCBI GI	g2342727
BLAST score	393
E value	3.0e-38
Match length	83
% identity	77
NCBI Description	(AC002341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	222373
Seq. ID	LIB3165-031-P1-K1-C10
Method	BLASTX
NCBI GI	g4539292
BLAST score	452
E value	4.0e-45
Match length	100
% identity	83
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	222374
Seq. ID	LIB3165-031-P1-K1-C12
Method	BLASTX
NCBI GI	g3643090
BLAST score	164
E value	2.0e-11
Match length	93
% identity	46
NCBI Description	(AF075582) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]

Seq. No.	222375
Seq. ID	LIB3165-031-P1-K1-C2
Method	BLASTX
NCBI GI	g1352821
BLAST score	525
E value	1.0e-53
Match length	101
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222376
Seq. ID	LIB3165-031-P1-K1-C4
Method	BLASTN
NCBI GI	g2924257
BLAST score	70
E value	5.0e-31
Match length	182
% identity	94
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	222377
Seq. ID	LIB3165-031-P1-K1-C6
Method	BLASTX

NCBI GI	g3334665
BLAST score	256
E value	4.0e-22
Match length	108
% identity	45
NCBI Description	(Y10492) putative cytochrome P450 [Glycine max]

Seq. No.	222378
Seq. ID	LIB3165-031-P1-K1-C8
Method	BLASTN
NCBI GI	g2623914
BLAST score	322
E value	0.0e+00
Match length	365
% identity	96
NCBI Description	Gossypium darwinii ATPase B subunit (atpB) and ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) genes, chloroplast genes encoding chloroplast proteins, partial cds, and atpB-rbcL intergenic spacer

Seq. No.	222379
Seq. ID	LIB3165-031-P1-K1-D10
Method	BLASTX
NCBI GI	g3095075
BLAST score	177
E value	6.0e-13
Match length	97
% identity	23
NCBI Description	(AF031471) pollen allergen [Juniperus oxycedrus]

Seq. No.	222380
Seq. ID	LIB3165-031-P1-K1-D11
Method	BLASTX
NCBI GI	g115765
BLAST score	404
E value	2.0e-39
Match length	94
% identity	78
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	222381
Seq. ID	LIB3165-031-P1-K1-D12
Method	BLASTX
NCBI GI	g1354515
BLAST score	207
E value	2.0e-16
Match length	84
% identity	56
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	222382
Seq. ID	LIB3165-031-P1-K1-D3
Method	BLASTX
NCBI GI	g20729
BLAST score	297
E value	5.0e-27
Match length	89
% identity	69
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	222383
Seq. ID	LIB3165-031-P1-K1-D4
Method	BLASTX
NCBI GI	g289920
BLAST score	616
E value	2.0e-64
Match length	118
% identity	97
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222384
Seq. ID	LIB3165-031-P1-K1-D5
Method	BLASTX
NCBI GI	g228403
BLAST score	456
E value	1.0e-45
Match length	97
% identity	91
NCBI Description	glycolate oxidase [Lens culinaris]

Seq. No.	222385
Seq. ID	LIB3165-031-P1-K1-D6
Method	BLASTX
NCBI GI	g3687676
BLAST score	560
E value	8.0e-58
Match length	111
% identity	95
NCBI Description	(AF052424) rubisco activase precursor [Datisca glomerata]

Seq. No.	222386
Seq. ID	LIB3165-031-P1-K1-D7
Method	BLASTX
NCBI GI	g1352821
BLAST score	468
E value	5.0e-47
Match length	91
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222387

Seq. ID	LIB3165-031-P1-K1-D8
Method	BLASTN
NCBI GI	g4096078
BLAST score	38
E value	6.0e-12
Match length	62
% identity	90
NCBI Description	Arabidopsis thaliana chromosome I BAC T5A14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	222388
Seq. ID	LIB3165-031-P1-K1-E1
Method	BLASTX
NCBI GI	g289920
BLAST score	585
E value	9.0e-61
Match length	110
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222389
Seq. ID	LIB3165-031-P1-K1-E10
Method	BLASTX
NCBI GI	g100200
BLAST score	415
E value	8.0e-41
Match length	111
% identity	73
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	222390
Seq. ID	LIB3165-031-P1-K1-E11
Method	BLASTX
NCBI GI	g1730512
BLAST score	592
E value	1.0e-61
Match length	125
% identity	97
NCBI Description	PHOSPHOGLYCERATE KINASE, CHLOROPLAST >gi_2129669_pir__S71368 phosphoglycerate kinase - Arabidopsis thaliana (fragment) >gi_1022805 (U37701) phosphoglycerate kinase [Arabidopsis thaliana]

Seq. No.	222391
Seq. ID	LIB3165-031-P1-K1-E12
Method	BLASTX
NCBI GI	g4406530
BLAST score	335
E value	2.0e-31
Match length	90
% identity	77
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222392
Seq. ID	LIB3165-031-P1-K1-E2
Method	BLASTX

NCBI GI	g1213450
BLAST score	230
E value	4.0e-19
Match length	82
% identity	55
NCBI Description	(U48963) isopentenyl pyrophosphate isomerase [Clarkia breweri]

Seq. No.	222393
Seq. ID	LIB3165-031-P1-K1-E3
Method	BLASTX
NCBI GI	g2970654
BLAST score	255
E value	5.0e-22
Match length	99
% identity	63
NCBI Description	(AF052058) ferritin subunit cowpea2 precursor [Vigna unguiculata]

Seq. No.	222394
Seq. ID	LIB3165-031-P1-K1-E4
Method	BLASTN
NCBI GI	g2687437
BLAST score	60
E value	6.0e-26
Match length	72
% identity	96
NCBI Description	Jepsonia parryi large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	222395
Seq. ID	LIB3165-031-P1-K1-E5
Method	BLASTX
NCBI GI	g2924325
BLAST score	189
E value	3.0e-14
Match length	41
% identity	88
NCBI Description	(Z93765) hypothetical protein [Malus domestica]

Seq. No.	222396
Seq. ID	LIB3165-031-P1-K1-E6
Method	BLASTX
NCBI GI	g1352821
BLAST score	330
E value	9.0e-31
Match length	88
% identity	78
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222397
Seq. ID	LIB3165-031-P1-K1-E8
Method	BLASTX

NCBI GI	g4406530
BLAST score	307
E value	4.0e-28
Match length	84
% identity	75
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222398
Seq. ID	LIB3165-031-P1-K1-E9
Method	BLASTX
NCBI GI	g4049353
BLAST score	369
E value	2.0e-35
Match length	109
% identity	69
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	222399
Seq. ID	LIB3165-031-P1-K1-F10
Method	BLASTX
NCBI GI	g3687652
BLAST score	611
E value	8.0e-64
Match length	117
% identity	98
NCBI Description	(AF047352) rubisco activase precursor [Datisca glomerata]

Seq. No.	222400
Seq. ID	LIB3165-031-P1-K1-F2
Method	BLASTX
NCBI GI	g505482
BLAST score	397
E value	8.0e-39
Match length	106
% identity	80
NCBI Description	(X64349) 33 kDa polypeptide of water-oxidizing complex of photosystem II [Nicotiana tabacum]

Seq. No.	222401
Seq. ID	LIB3165-031-P1-K1-F3
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	8.0e-11
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	222402
Seq. ID	LIB3165-031-P1-K1-F5
Method	BLASTX
NCBI GI	g2754849
BLAST score	574
E value	2.0e-59
Match length	122
% identity	91
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase

[Fritillaria agrestis]

Seq. No.	222403
Seq. ID	LIB3165-031-P1-K1-F6
Method	BLASTN
NCBI GI	g2687434
BLAST score	306
E value	1.0e-172
Match length	378
% identity	96
NCBI Description	Eucryphia lucida large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	222404
Seq. ID	LIB3165-031-P1-K1-F8
Method	BLASTX
NCBI GI	g3925703
BLAST score	538
E value	3.0e-55
Match length	122
% identity	87
NCBI Description	(X95905) 14-3-3 protein [Lycopersicon esculentum]

Seq. No.	222405
Seq. ID	LIB3165-031-P1-K1-G1
Method	BLASTX
NCBI GI	g1352821
BLAST score	502
E value	5.0e-51
Match length	95
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222406
Seq. ID	LIB3165-031-P1-K1-G10
Method	BLASTX
NCBI GI	g289920
BLAST score	584
E value	3.0e-61
Match length	116
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222407
Seq. ID	LIB3165-031-P1-K1-G12
Method	BLASTX
NCBI GI	g289920
BLAST score	560
E value	8.0e-58
Match length	117
% identity	97
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No.	222408
Seq. ID	LIB3165-031-P1-K1-G3
Method	BLASTX
NCBI GI	g167367
BLAST score	455
E value	2.0e-45
Match length	120
% identity	74
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	222409
Seq. ID	LIB3165-031-P1-K1-G7
Method	BLASTX
NCBI GI	g1710780
BLAST score	359
E value	3.0e-34
Match length	101
% identity	69
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	222410
Seq. ID	LIB3165-031-P1-K1-G8
Method	BLASTX
NCBI GI	g4406530
BLAST score	349
E value	4.0e-33
Match length	93
% identity	76
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222411
Seq. ID	LIB3165-031-P1-K1-H10
Method	BLASTX
NCBI GI	g231688
BLAST score	453
E value	2.0e-45
Match length	102
% identity	85
NCBI Description	CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC 1.11.1.6) - upland cotton >gi_18488_emb_CAA39998_ (X56675) subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No.	222412
Seq. ID	LIB3165-031-P1-K1-H12
Method	BLASTX
NCBI GI	g2129511
BLAST score	142
E value	1.0e-13
Match length	49
% identity	71
NCBI Description	glycerate dehydrogenase (EC 1.1.1.29) splice form HPR1, microbody - cucurbit >gi_1304042_dbj_BAA08410_ (D49432) hydroxypyruvate reductase [Cucurbita sp.]

Seq. No.	222413
Seq. ID	LIB3165-031-P1-K1-H2
Method	BLASTX
NCBI GI	g1352821
BLAST score	522
E value	3.0e-53
Match length	101
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222414
Seq. ID	LIB3165-031-P1-K1-H3
Method	BLASTX
NCBI GI	g1620898
BLAST score	223
E value	3.0e-18
Match length	60
% identity	73
NCBI Description	(D87957) protein involved in sexual development [Homo sapiens]

Seq. No.	222415
Seq. ID	LIB3165-031-P1-K1-H6
Method	BLASTX
NCBI GI	g118564
BLAST score	415
E value	5.0e-41
Match length	90
% identity	88
NCBI Description	GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE REDUCTASE) (HPR) (GDH) >gi_65955_pir__DEKVG glycerate dehydrogenase (EC 1.1.1.29) - cucumber >gi_18264_emb_CAA41434_ (X58542) NADH-dependent hydroxypyruvate reductase [Cucumis sativus] >gi_18275_emb_CAA32764_ (X14609) NAPH-dependent hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

Seq. No.	222416
Seq. ID	LIB3165-031-P1-K1-H7
Method	BLASTX
NCBI GI	g1352821
BLAST score	455
E value	2.0e-45
Match length	91
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222417

Seq. ID	LIB3165-032-P1-K1-A10
Method	BLASTX
NCBI GI	g1354515
BLAST score	247
E value	4.0e-21
Match length	124
% identity	48
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	222418
Seq. ID	LIB3165-032-P1-K1-A11
Method	BLASTX
NCBI GI	g2511590
BLAST score	236
E value	8.0e-20
Match length	52
% identity	87
NCBI Description	(Y13692) multicatalytic endopeptidase complex, proteasome component, beta subunit [Arabidopsis thaliana] >gi_3421111 (AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis thaliana]

Seq. No.	222419
Seq. ID	LIB3165-032-P1-K1-A3
Method	BLASTN
NCBI GI	g706852
BLAST score	42
E value	2.0e-14
Match length	102
% identity	85
NCBI Description	Lycopersicon esculentum photosystem II 22 kDa component (psbS) gene, complete cds

Seq. No.	222420
Seq. ID	LIB3165-032-P1-K1-A4
Method	BLASTX
NCBI GI	g3036951
BLAST score	431
E value	1.0e-42
Match length	81
% identity	100
NCBI Description	(AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	222421
Seq. ID	LIB3165-032-P1-K1-A5
Method	BLASTX
NCBI GI	g1352821
BLAST score	465
E value	1.0e-46
Match length	88
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222422
Seq. ID	LIB3165-032-P1-K1-A6
Method	BLASTX
NCBI GI	g3289002
BLAST score	199
E value	2.0e-15
Match length	66
% identity	22
NCBI Description	(AF073522) CRP1 [Zea mays]

Seq. No.	222423
Seq. ID	LIB3165-032-P1-K1-B1
Method	BLASTX
NCBI GI	g4406530
BLAST score	315
E value	4.0e-29
Match length	113
% identity	61
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222424
Seq. ID	LIB3165-032-P1-K1-B11
Method	BLASTX
NCBI GI	g100200
BLAST score	442
E value	6.0e-44
Match length	114
% identity	75
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	222425
Seq. ID	LIB3165-032-P1-K1-B2
Method	BLASTX
NCBI GI	g3288821
BLAST score	602
E value	1.0e-62
Match length	128
% identity	88
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana]

Seq. No.	222426
Seq. ID	LIB3165-032-P1-K1-B3
Method	BLASTX
NCBI GI	g2191152
BLAST score	223
E value	2.0e-18
Match length	107
% identity	63
NCBI Description	(AF007269) A_IG002N01.31 gene product [Arabidopsis thaliana]

Seq. No.	222427
Seq. ID	LIB3165-032-P1-K1-B5
Method	BLASTX

NCBI GI	g2738248
BLAST score	512
E value	3.0e-52
Match length	128
% identity	80
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	222428
Seq. ID	LIB3165-032-P1-K1-B6
Method	BLASTX
NCBI GI	g4406530
BLAST score	338
E value	9.0e-32
Match length	114
% identity	64
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222429
Seq. ID	LIB3165-032-P1-K1-B9
Method	BLASTX
NCBI GI	g3913651
BLAST score	376
E value	3.0e-36
Match length	110
% identity	65
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR (FNR) >gi_2225993_emb_CAA74359_ (Y14032) ferredoxin--NADP(+) reductase [Nicotiana tabacum]

Seq. No.	222430
Seq. ID	LIB3165-032-P1-K1-C11
Method	BLASTX
NCBI GI	g100200
BLAST score	573
E value	2.0e-59
Match length	128
% identity	66
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	222431
Seq. ID	LIB3165-032-P1-K1-C12
Method	BLASTX
NCBI GI	g1352821
BLAST score	507
E value	1.0e-51
Match length	98
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222432
Seq. ID	LIB3165-032-P1-K1-C2
Method	BLASTX

NCBI GI	g1352821
BLAST score	574
E value	2.0e-59
Match length	119
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222433
Seq. ID	LIB3165-032-P1-K1-C3
Method	BLASTN
NCBI GI	g2062705
BLAST score	36
E value	9.0e-11
Match length	36
% identity	38
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	222434
Seq. ID	LIB3165-032-P1-K1-C5
Method	BLASTX
NCBI GI	g2493144
BLAST score	422
E value	1.0e-41
Match length	99
% identity	58
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	222435
Seq. ID	LIB3165-032-P1-K1-C7
Method	BLASTX
NCBI GI	g4406530
BLAST score	346
E value	9.0e-33
Match length	93
% identity	76
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222436
Seq. ID	LIB3165-032-P1-K1-C8
Method	BLASTX
NCBI GI	g2129538
BLAST score	220
E value	2.0e-18
Match length	45
% identity	93
NCBI Description	AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232) AT103 [Arabidopsis thaliana]

Seq. No.	222437
Seq. ID	LIB3165-032-P1-K1-D1
Method	BLASTX
NCBI GI	g3334113
BLAST score	333
E value	3.0e-31
Match length	89
% identity	74
NCBI Description	ACYL-COA-BINDING PROTEIN (ACBP) >gi_1006831 (U35015) acyl-CoA-binding protein [Gossypium hirsutum]

Seq. No.	222438
Seq. ID	LIB3165-032-P1-K1-D10
Method	BLASTX
NCBI GI	g4406530
BLAST score	330
E value	8.0e-31
Match length	112
% identity	63
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222439
Seq. ID	LIB3165-032-P1-K1-D11
Method	BLASTX
NCBI GI	g100616
BLAST score	464
E value	1.0e-46
Match length	119
% identity	76
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	222440
Seq. ID	LIB3165-032-P1-K1-D2
Method	BLASTX
NCBI GI	g4056568
BLAST score	298
E value	4.0e-27
Match length	122
% identity	17
NCBI Description	(U90944) PDI-like protein [Zea mays]

Seq. No.	222441
Seq. ID	LIB3165-032-P1-K1-D3
Method	BLASTX
NCBI GI	g1350736
BLAST score	164
E value	2.0e-11
Match length	39
% identity	79
NCBI Description	60S RIBOSOMAL PROTEIN L37 >gi_629673_pir__S44313 ribosomal protein L37 - tomato >gi_483586_emb_CAA55674_ (X79074) ribosomal protein L37 [Lycopersicon esculentum]

Seq. No.	222442
Seq. ID	LIB3165-032-P1-K1-D4
Method	BLASTX
NCBI GI	g1332579
BLAST score	516
E value	1.0e-52
Match length	106
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	222443
Seq. ID	LIB3165-032-P1-K1-D5
Method	BLASTX
NCBI GI	g2924325
BLAST score	307
E value	4.0e-28
Match length	70
% identity	80
NCBI Description	(Z93765) hypothetical protein [Malus domestica]

Seq. No.	222444
Seq. ID	LIB3165-032-P1-K1-D7
Method	BLASTX
NCBI GI	g3850111
BLAST score	144
E value	5.0e-09
Match length	49
% identity	55
NCBI Description	(AL033388) hypothetical integral membrane protein, putative involvement in lipid metabolism [Schizosaccharomyces pombe]

Seq. No.	222445
Seq. ID	LIB3165-032-P1-K1-D8
Method	BLASTX
NCBI GI	g1352821
BLAST score	500
E value	9.0e-51
Match length	97
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222446
Seq. ID	LIB3165-032-P1-K1-D9
Method	BLASTX
NCBI GI	g120661
BLAST score	554
E value	4.0e-57
Match length	121
% identity	88
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_170237 (M14417) glyceraldehyde-3-phosphate dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No.	222447
Seq. ID	LIB3165-032-P1-K1-E1
Method	BLASTX
NCBI GI	g1352821
BLAST score	510
E value	6.0e-52
Match length	98
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222448
Seq. ID	LIB3165-032-P1-K1-E11
Method	BLASTN
NCBI GI	g2564049
BLAST score	40
E value	4.0e-13
Match length	224
% identity	79
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]

Seq. No.	222449
Seq. ID	LIB3165-032-P1-K1-E12
Method	BLASTX
NCBI GI	g3024020
BLAST score	620
E value	7.0e-65
Match length	121
% identity	95
NCBI Description	INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D) >gi_2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation factor 5A3 [Solanum tuberosum]

Seq. No.	222450
Seq. ID	LIB3165-032-P1-K1-E2
Method	BLASTX
NCBI GI	g2493694
BLAST score	248
E value	3.0e-21
Match length	119
% identity	45
NCBI Description	PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII 6.1 KD PROTEIN) >gi_1076268_pir__S53025 photosystem II protein - spinach >gi_728716_emb_CAA59409_ (X85038) protein of photosystem II [Spinacia oleracea]

Seq. No.	222451
Seq. ID	LIB3165-032-P1-K1-E3
Method	BLASTX
NCBI GI	g4220480
BLAST score	390
E value	2.0e-38
Match length	124

% identity	64
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	222452
Seq. ID	LIB3165-032-P1-K1-E6
Method	BLASTX
NCBI GI	g3158476
BLAST score	535
E value	7.0e-55
Match length	117
% identity	86
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	222453
Seq. ID	LIB3165-032-P1-K1-E9
Method	BLASTX
NCBI GI	g1346155
BLAST score	553
E value	5.0e-57
Match length	121
% identity	88
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_481942_pir__S40212 glycine hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei >gi_437995_emb_CAA81078_ (Z25859) glycine hydroxymethyltransferase [Flaveria pringlei]

Seq. No.	222454
Seq. ID	LIB3165-032-P1-K1-F10
Method	BLASTX
NCBI GI	g1632831
BLAST score	442
E value	6.0e-44
Match length	100
% identity	86
NCBI Description	(Z49698) orf [Ricinus communis]

Seq. No.	222455
Seq. ID	LIB3165-032-P1-K1-F11
Method	BLASTX
NCBI GI	g1352821
BLAST score	516
E value	1.0e-52
Match length	100
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222456
Seq. ID	LIB3165-032-P1-K1-F12
Method	BLASTX
NCBI GI	g1507699
BLAST score	271

E value	6.0e-24
Match length	66
% identity	77
NCBI Description	(L81119) COL2 [Arabidopsis thaliana] >gi_1507701 (L81120) COL2 [Arabidopsis thaliana]

Seq. No.	222457
Seq. ID	LIB3165-032-P1-K1-F3
Method	BLASTX
NCBI GI	g100200
BLAST score	390
E value	8.0e-38
Match length	105
% identity	72
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	222458
Seq. ID	LIB3165-032-P1-K1-F6
Method	BLASTX
NCBI GI	g115833
BLAST score	467
E value	7.0e-47
Match length	119
% identity	76
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi_170394 (M32605) a-binding protein [Lycopersicon esculentum]

Seq. No.	222459
Seq. ID	LIB3165-032-P1-K1-F9
Method	BLASTX
NCBI GI	g2765081
BLAST score	449
E value	8.0e-45
Match length	121
% identity	74
NCBI Description	(Y10557) g5bf [Arabidopsis thaliana]

Seq. No.	222460
Seq. ID	LIB3165-032-P1-K1-G10
Method	BLASTX
NCBI GI	g2317910
BLAST score	349
E value	4.0e-33
Match length	122
% identity	51
NCBI Description	(U89959) CER1 protein [Arabidopsis thaliana]

Seq. No.	222461
Seq. ID	LIB3165-032-P1-K1-G11
Method	BLASTX
NCBI GI	g4406777
BLAST score	272
E value	5.0e-24
Match length	70
% identity	73

NCBI Description	(AC006532) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No.	222462
Seq. ID	LIB3165-032-P1-K1-G12
Method	BLASTN
NCBI GI	g2687434
BLAST score	66
E value	7.0e-29
Match length	182
% identity	84
NCBI Description	Eucryphia lucida large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	222463
Seq. ID	LIB3165-032-P1-K1-G2
Method	BLASTX
NCBI GI	g1181615
BLAST score	601
E value	1.0e-62
Match length	128
% identity	90
NCBI Description	(D83078) nitrilase [Nicotiana tabacum]

Seq. No.	222464
Seq. ID	LIB3165-032-P1-K1-G5
Method	BLASTX
NCBI GI	g68200
BLAST score	305
E value	5.0e-28
Match length	93
% identity	70
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	222465
Seq. ID	LIB3165-032-P1-K1-G6
Method	BLASTX
NCBI GI	g68200
BLAST score	469
E value	4.0e-47
Match length	121
% identity	81
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	222466
Seq. ID	LIB3165-032-P1-K1-G7
Method	BLASTN
NCBI GI	g2687435
BLAST score	265
E value	1.0e-147
Match length	305
% identity	97
NCBI Description	Hamamelis virginiana large subunit 26S ribosomal RNA gene,

partial sequence

Seq. No.	222467
Seq. ID	LIB3165-032-P1-K1-G9
Method	BLASTX
NCBI GI	g4406530
BLAST score	346
E value	9.0e-33
Match length	93
% identity	76
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222468
Seq. ID	LIB3165-032-P1-K1-H1
Method	BLASTX
NCBI GI	g228403
BLAST score	195
E value	5.0e-15
Match length	43
% identity	84
NCBI Description	glycolate oxidase [Lens culinaris]

Seq. No.	222469
Seq. ID	LIB3165-032-P1-K1-H10
Method	BLASTX
NCBI GI	g2505874
BLAST score	182
E value	2.0e-13
Match length	57
% identity	63
NCBI Description	(Y12776) putative kinase [Arabidopsis thaliana]

Seq. No.	222470
Seq. ID	LIB3165-032-P1-K1-H12
Method	BLASTX
NCBI GI	g3269292
BLAST score	175
E value	8.0e-13
Match length	80
% identity	49
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	222471
Seq. ID	LIB3165-032-P1-K1-H2
Method	BLASTX
NCBI GI	g121902
BLAST score	158
E value	1.0e-10
Match length	35
% identity	91
NCBI Description	HISTONE H1.1 >gi_1070594_pir__HSMU11 histone H1.1 - Arabidopsis thaliana >gi_16317_emb_CAA44314_ (X62458) Histone H1 [Arabidopsis thaliana]

Seq. No.	222472
Seq. ID	LIB3165-032-P1-K1-H3
Method	BLASTX

NCBI GI g2832669
BLAST score 162
E value 4.0e-11
Match length 102
% identity 43
NCBI Description (AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No. 222473
Seq. ID LIB3165-032-P1-K1-H6
Method BLASTX
NCBI GI g3281850
BLAST score 145
E value 4.0e-09
Match length 83
% identity 43
NCBI Description (AL031004) monogalactosyldiacylglycerol synthase - like protein [Arabidopsis thaliana]

Seq. No. 222474
Seq. ID LIB3165-032-P1-K1-H7
Method BLASTX
NCBI GI g20729
BLAST score 456
E value 1.0e-45
Match length 122
% identity 75
NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No. 222475
Seq. ID LIB3165-032-P1-K1-H8
Method BLASTX
NCBI GI g289920
BLAST score 598
E value 3.0e-62
Match length 110
% identity 99
NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No. 222476
Seq. ID LIB3165-033-P1-K1-A1
Method BLASTX
NCBI GI g3036946
BLAST score 315
E value 3.0e-29
Match length 60
% identity 100
NCBI Description (AB012637) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 222477
Seq. ID LIB3165-033-P1-K1-A10
Method BLASTX
NCBI GI g115470
BLAST score 290
E value 3.0e-26
Match length 107

% identity	58
NCBI Description	CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) >gi_320554_pir__S28412 carbonate dehydratase (EC 4.2.1.1) precursor - Arabidopsis thaliana >gi_14343_emb_CAA46508_ (X65541) carbonic anhydrase [Arabidopsis thaliana]
Seq. No.	222478
Seq. ID	LIB3165-033-P1-K1-A12
Method	BLASTN
NCBI GI	g2687434
BLAST score	49
E value	1.0e-18
Match length	89
% identity	89
NCBI Description	Eucryphia lucida large subunit 26S ribosomal RNA gene, partial sequence
Seq. No.	222479
Seq. ID	LIB3165-033-P1-K1-A2
Method	BLASTN
NCBI GI	g3108248
BLAST score	190
E value	1.0e-102
Match length	268
% identity	94
NCBI Description	Gossypium barbadense clone pXP027 repetitive DNA sequence
Seq. No.	222480
Seq. ID	LIB3165-033-P1-K1-A3
Method	BLASTX
NCBI GI	g3687652
BLAST score	355
E value	6.0e-34
Match length	102
% identity	72
NCBI Description	(AF047352) rubisco activase precursor [Datisca glomerata]
Seq. No.	222481
Seq. ID	LIB3165-033-P1-K1-A5
Method	BLASTX
NCBI GI	g118564
BLAST score	565
E value	2.0e-58
Match length	116
% identity	91
NCBI Description	GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE REDUCTASE) (HPR) (GDH) >gi_65955_pir__DEKVG glycerate dehydrogenase (EC 1.1.1.29) - cucumber >gi_18264_emb_CAA41434_ (X58542) NADH-dependent hydroxypyruvate reductase [Cucumis sativus] >gi_18275_emb_CAA32764_ (X14609) NAPH-dependent hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]
Seq. No.	222482
Seq. ID	LIB3165-033-P1-K1-A6
Method	BLASTX

NCBI GI	g289920
BLAST score	645
E value	9.0e-68
Match length	121
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222483
Seq. ID	LIB3165-033-P1-K1-A8
Method	BLASTX
NCBI GI	g2980887
BLAST score	451
E value	5.0e-45
Match length	119
% identity	71
NCBI Description	(AJ224961) Sucrose carrier [Ricinus communis]

Seq. No.	222484
Seq. ID	LIB3165-033-P1-K1-A9
Method	BLASTX
NCBI GI	g131397
BLAST score	300
E value	2.0e-27
Match length	110
% identity	61
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_81480_pir__S00008 photosystem II oxygen-evolving complex protein 3 precursor - spinach >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi_225597_prf__1307179B luminal protein 16kD [Spinacia oleracea]

Seq. No.	222485
Seq. ID	LIB3165-033-P1-K1-B1
Method	BLASTX
NCBI GI	g1488043
BLAST score	192
E value	1.0e-14
Match length	63
% identity	65
NCBI Description	(U63784) PAPS-reductase-like protein [Catharanthus roseus]

Seq. No.	222486
Seq. ID	LIB3165-033-P1-K1-B2
Method	BLASTX
NCBI GI	g68200
BLAST score	193
E value	8.0e-15
Match length	74
% identity	64
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	222487
Seq. ID	LIB3165-033-P1-K1-B3
Method	BLASTX
NCBI GI	g3080418
BLAST score	260
E value	1.0e-22
Match length	114
% identity	44
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	222488
Seq. ID	LIB3165-033-P1-K1-B5
Method	BLASTX
NCBI GI	g231610
BLAST score	324
E value	4.0e-30
Match length	111
% identity	64
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]

Seq. No.	222489
Seq. ID	LIB3165-033-P1-K1-B6
Method	BLASTX
NCBI GI	g4558563
BLAST score	201
E value	1.0e-15
Match length	96
% identity	46
NCBI Description	(AC007138) putative NifU-like metallocluster assembly factor [Arabidopsis thaliana]

Seq. No.	222490
Seq. ID	LIB3165-033-P1-K1-B8
Method	BLASTX
NCBI GI	g68200
BLAST score	458
E value	7.0e-46
Match length	112
% identity	83
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	222491
Seq. ID	LIB3165-033-P1-K1-C1
Method	BLASTX
NCBI GI	g132168
BLAST score	530
E value	3.0e-54
Match length	126
% identity	77
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_81488_pir__A31082

ribulose-bisphosphate carboxylase activase precursor - spinach >gi_170129 (J03610) rubisco activase precursor [Spinacia oleracea]

Seq. No.	222492
Seq. ID	LIB3165-033-P1-K1-C10
Method	BLASTX
NCBI GI	g289920
BLAST score	457
E value	6.0e-46
Match length	86
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222493
Seq. ID	LIB3165-033-P1-K1-C12
Method	BLASTX
NCBI GI	g430947
BLAST score	409
E value	4.0e-40
Match length	101
% identity	81
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	222494
Seq. ID	LIB3165-033-P1-K1-C3
Method	BLASTX
NCBI GI	g100200
BLAST score	377
E value	2.0e-36
Match length	104
% identity	71
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	222495
Seq. ID	LIB3165-033-P1-K1-C4
Method	BLASTX
NCBI GI	g3850111
BLAST score	149
E value	3.0e-10
Match length	49
% identity	55
NCBI Description	(AL033388) hypothetical integral membrane protein, putative involvement in lipid metabolism [Schizosaccharomyces pombe]

Seq. No.	222496
Seq. ID	LIB3165-033-P1-K1-C5
Method	BLASTX
NCBI GI	g2129921
BLAST score	195
E value	5.0e-15
Match length	51
% identity	75
NCBI Description	hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]

Seq. No.	222497
Seq. ID	LIB3165-033-P1-K1-C6
Method	BLASTX
NCBI GI	g1352821
BLAST score	510
E value	6.0e-52
Match length	98
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222498
Seq. ID	LIB3165-033-P1-K1-C7
Method	BLASTX
NCBI GI	g4262181
BLAST score	160
E value	6.0e-11
Match length	77
% identity	55
NCBI Description	(AC005508) 37496 [Arabidopsis thaliana]

Seq. No.	222499
Seq. ID	LIB3165-033-P1-K1-D10
Method	BLASTX
NCBI GI	g4468813
BLAST score	185
E value	7.0e-14
Match length	100
% identity	42
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	222500
Seq. ID	LIB3165-033-P1-K1-D11
Method	BLASTX
NCBI GI	g2492514
BLAST score	580
E value	3.0e-60
Match length	118
% identity	94
NCBI Description	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR >gi_1483215_emb_CAA68141_ (X99808) chloroplast FtsH protease [Arabidopsis thaliana]

Seq. No.	222501
Seq. ID	LIB3165-033-P1-K1-D12
Method	BLASTX
NCBI GI	g1352821
BLAST score	489
E value	2.0e-49
Match length	105
% identity	92
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222502
Seq. ID	LIB3165-033-P1-K1-D4
Method	BLASTN
NCBI GI	g450504
BLAST score	47
E value	2.0e-17
Match length	51
% identity	98
NCBI Description	G.hirsutum rbcS gene for ribulose-1,5-bisphosphate carboxylase, small subunit

Seq. No.	222503
Seq. ID	LIB3165-033-P1-K1-D6
Method	BLASTX
NCBI GI	g3451067
BLAST score	349
E value	4.0e-33
Match length	92
% identity	76
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	222504
Seq. ID	LIB3165-033-P1-K1-D7
Method	BLASTX
NCBI GI	g1352821
BLAST score	488
E value	2.0e-49
Match length	95
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222505
Seq. ID	LIB3165-033-P1-K1-D8
Method	BLASTX
NCBI GI	g1352821
BLAST score	506
E value	2.0e-51
Match length	98
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222506
Seq. ID	LIB3165-033-P1-K1-D9
Method	BLASTX
NCBI GI	g3298502

BLAST score	389
E value	9.0e-38
Match length	122
% identity	61
NCBI Description	(AB015046) xylulokinase [Homo sapiens]

Seq. No.	222507
Seq. ID	LIB3165-033-P1-K1-E1
Method	BLASTX
NCBI GI	g430947
BLAST score	379
E value	1.0e-36
Match length	95
% identity	80
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	222508
Seq. ID	LIB3165-033-P1-K1-E10
Method	BLASTX
NCBI GI	g3355468
BLAST score	522
E value	2.0e-53
Match length	123
% identity	88
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No.	222509
Seq. ID	LIB3165-033-P1-K1-E12
Method	BLASTX
NCBI GI	g4115931
BLAST score	337
E value	1.0e-31
Match length	124
% identity	59
NCBI Description	(AF118223) contains similarity to Guillardia theta ABC transporter (GB:AF041468) [Arabidopsis thaliana]

Seq. No.	222510
Seq. ID	LIB3165-033-P1-K1-E4
Method	BLASTX
NCBI GI	g4406530
BLAST score	321
E value	9.0e-30
Match length	110
% identity	63
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222511
Seq. ID	LIB3165-033-P1-K1-E5
Method	BLASTX
NCBI GI	g505482
BLAST score	406
E value	9.0e-40
Match length	104
% identity	81

NCBI Description	(X64349) 33 kDa polypeptide of water-oxidizing complex of photosystem II [Nicotiana tabacum]
Seq. No.	222512
Seq. ID	LIB3165-033-P1-K1-E6
Method	BLASTX
NCBI GI	g3914605
BLAST score	471
E value	2.0e-47
Match length	128
% identity	70
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase - apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica]
Seq. No.	222513
Seq. ID	LIB3165-033-P1-K1-F1
Method	BLASTX
NCBI GI	g3292814
BLAST score	153
E value	4.0e-10
Match length	96
% identity	44
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]
Seq. No.	222514
Seq. ID	LIB3165-033-P1-K1-F10
Method	BLASTX
NCBI GI	g1418990
BLAST score	218
E value	1.0e-17
Match length	47
% identity	87
NCBI Description	(Z75524) unknown [Lycopersicon esculentum]
Seq. No.	222515
Seq. ID	LIB3165-033-P1-K1-F11
Method	BLASTX
NCBI GI	g1419090
BLAST score	337
E value	1.0e-31
Match length	96
% identity	70
NCBI Description	(X94968) 37kDa chloroplast inner envelope membrane polypeptide precursor [Nicotiana tabacum]
Seq. No.	222516
Seq. ID	LIB3165-033-P1-K1-F2
Method	BLASTX
NCBI GI	g2245066
BLAST score	212
E value	4.0e-17
Match length	103
% identity	39

NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No. 222517
Seq. ID LIB3165-033-P1-K1-F3
Method BLASTX
NCBI GI g4056469
BLAST score 650
E value 2.0e-68
Match length 124
% identity 98
NCBI Description (AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967, gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t

Seq. No. 222518
Seq. ID LIB3165-033-P1-K1-F4
Method BLASTX
NCBI GI g3288821
BLAST score 436
E value 3.0e-43
Match length 106
% identity 79
NCBI Description (AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana]

Seq. No. 222519
Seq. ID LIB3165-033-P1-K1-F6
Method BLASTX
NCBI GI g100454
BLAST score 532
E value 2.0e-54
Match length 129
% identity 84
NCBI Description photosystem II oxygen-evolving complex protein 1 - potato >gi_809113_emb_CAA35601_ (X17578) 33kDa precursor protein of oxygen-evolving complex [Solanum tuberosum]

Seq. No. 222520
Seq. ID LIB3165-033-P1-K1-F8
Method BLASTX
NCBI GI g2829869
BLAST score 373
E value 6.0e-36
Match length 87
% identity 82
NCBI Description (AC002396) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No. 222521
Seq. ID LIB3165-033-P1-K1-F9
Method BLASTX
NCBI GI g70644
BLAST score 554
E value 4.0e-57
Match length 113

% identity	19
NCBI Description	ubiquitin precursor - common sunflower (fragment)

Seq. No.	222522
Seq. ID	LIB3165-033-P1-K1-G12
Method	BLASTX
NCBI GI	g1168411
BLAST score	514
E value	2.0e-52
Match length	128
% identity	82
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	222523
Seq. ID	LIB3165-033-P1-K1-G4
Method	BLASTX
NCBI GI	g2244844
BLAST score	152
E value	6.0e-10
Match length	118
% identity	40
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	222524
Seq. ID	LIB3165-033-P1-K1-G6
Method	BLASTX
NCBI GI	g100203
BLAST score	185
E value	2.0e-22
Match length	99
% identity	58
NCBI Description	cysteine proteinase (EC 3.4.22.-) precursor - tomato >gi_19195_emb_CAA78403_ (Z14028) pre-pro-cysteine proteinase [Lycopersicon esculentum]

Seq. No.	222525
Seq. ID	LIB3165-033-P1-K1-G9
Method	BLASTX
NCBI GI	g3869088
BLAST score	517
E value	9.0e-53
Match length	100
% identity	98
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No.	222526
Seq. ID	LIB3165-033-P1-K1-H1
Method	BLASTX
NCBI GI	g4106538
BLAST score	472
E value	2.0e-47
Match length	128
% identity	72
NCBI Description	(AF104220) gamma-tocopherol methyltransferase [Arabidopsis thaliana]

Seq. No.	222527

Seq. ID	LIB3165-033-P1-K1-H6
Method	BLASTX
NCBI GI	g1346155
BLAST score	584
E value	1.0e-60
Match length	127
% identity	88
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_481942_pir__S40212 glycine hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei >gi_437995_emb_CAA81078_ (Z25859) glycine hydroxymethyltransferase [Flaveria pringlei]

Seq. No.	222528
Seq. ID	LIB3165-033-P1-K1-H7
Method	BLASTX
NCBI GI	g121083
BLAST score	621
E value	5.0e-65
Match length	123
% identity	92
NCBI Description	GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) >gi_282926_pir__A42109 glycine dehydrogenase (decarboxylating) (EC 1.4.4.2) component P precursor - garden pea >gi_20741_emb_CAA42443_ (X59773) component of aminomethyltransferase [Pisum sativum]

Seq. No.	222529
Seq. ID	LIB3165-033-P1-K1-H9
Method	BLASTX
NCBI GI	g2098705
BLAST score	228
E value	6.0e-19
Match length	98
% identity	48
NCBI Description	(U82973) pectinesterase [Citrus sinensis]

Seq. No.	222530
Seq. ID	LIB3165-034-P1-K1-A1
Method	BLASTX
NCBI GI	g2879867
BLAST score	405
E value	1.0e-39
Match length	110
% identity	70
NCBI Description	(AL021816) 40s ribosomal protein S17 [Schizosaccharomyces pombe]

Seq. No.	222531
Seq. ID	LIB3165-034-P1-K1-A11
Method	BLASTX
NCBI GI	g1352821
BLAST score	546
E value	4.0e-56
Match length	104

% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222532
Seq. ID	LIB3165-034-P1-K1-A2
Method	BLASTX
NCBI GI	g1350944
BLAST score	302
E value	2.0e-27
Match length	78
% identity	79
NCBI Description	40S RIBOSOMAL PROTEIN S17

Seq. No.	222533
Seq. ID	LIB3165-034-P1-K1-A3
Method	BLASTX
NCBI GI	g1706261
BLAST score	428
E value	2.0e-42
Match length	87
% identity	89
NCBI Description	CYSTEINE PROTEINASE 2 PRECURSOR >gi_2118129_pir__S59598 cysteine proteinase 2 precursor - maize >gi_644490_dbj_BAA08245_ (D45403) cysteine proteinase [Zea mays]

Seq. No.	222534
Seq. ID	LIB3165-034-P1-K1-A4
Method	BLASTX
NCBI GI	g1168411
BLAST score	501
E value	6.0e-51
Match length	126
% identity	81
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	222535
Seq. ID	LIB3165-034-P1-K1-A6
Method	BLASTX
NCBI GI	g169039
BLAST score	457
E value	1.0e-45
Match length	104
% identity	86
NCBI Description	(M97477) aldolase [Pisum sativum]

Seq. No.	222536
Seq. ID	LIB3165-034-P1-K1-A7
Method	BLASTX
NCBI GI	g1354515
BLAST score	238
E value	4.0e-20
Match length	121

% identity	48
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	222537
Seq. ID	LIB3165-034-P1-K1-A8
Method	BLASTX
NCBI GI	g100200
BLAST score	603
E value	7.0e-63
Match length	127
% identity	68
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	222538
Seq. ID	LIB3165-034-P1-K1-A9
Method	BLASTX
NCBI GI	g3158474
BLAST score	182
E value	2.0e-13
Match length	53
% identity	70
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]

Seq. No.	222539
Seq. ID	LIB3165-034-P1-K1-B1
Method	BLASTX
NCBI GI	g121953
BLAST score	168
E value	8.0e-12
Match length	41
% identity	83
NCBI Description	HISTONE H1 >gi_81905_pir__S00033 histone H1.b - garden pea >gi_20762_emb_CAA29123_ (X05636) H1 histone (AA 1-263) [Pisum sativum]

Seq. No.	222540
Seq. ID	LIB3165-034-P1-K1-B10
Method	BLASTX
NCBI GI	g81857
BLAST score	215
E value	2.0e-17
Match length	42
% identity	90
NCBI Description	IgE-dependent histamine-releasing factor homolog - alfalfa (fragment) >gi_19658_emb_CAA45349_ (X63872) translationally controlled tumor protein [Medicago sativa]

Seq. No.	222541
Seq. ID	LIB3165-034-P1-K1-B11
Method	BLASTX
NCBI GI	g2653446
BLAST score	380
E value	1.0e-36
Match length	97
% identity	74
NCBI Description	(AB009077) proton pyrophosphatase [Vigna radiata]

Seq. No.	222542
Seq. ID	LIB3165-034-P1-K1-B3
Method	BLASTX
NCBI GI	g3914940
BLAST score	365
E value	6.0e-35
Match length	123
% identity	63
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_2529376 (L76556) sedoheptulose-1,7-bisphosphatase [Spinacia oleracea]

Seq. No.	222543
Seq. ID	LIB3165-034-P1-K1-B5
Method	BLASTX
NCBI GI	g129867
BLAST score	376
E value	3.0e-39
Match length	86
% identity	97
NCBI Description	CYTOCHROME B6-F COMPLEX SUBUNIT 4 (17 KD POLYPEPTIDE) >gi_2924273_emb_CAA77425_ (Z00044) cytochrome b/f complex subunit IV [Nicotiana tabacum]

Seq. No.	222544
Seq. ID	LIB3165-034-P1-K1-B6
Method	BLASTX
NCBI GI	g228210
BLAST score	542
E value	1.0e-55
Match length	134
% identity	75
NCBI Description	granule-bound starch synthase [Solanum tuberosum]

Seq. No.	222545
Seq. ID	LIB3165-034-P1-K1-B8
Method	BLASTX
NCBI GI	g487046
BLAST score	381
E value	8.0e-37
Match length	127
% identity	66
NCBI Description	photosystem I chain II precursor - wood tobacco >gi_407769_dbj_BAA02871_ (D13718) PSI-D1 precursor [Nicotiana sylvestris]

Seq. No.	222546
Seq. ID	LIB3165-034-P1-K1-B9
Method	BLASTX
NCBI GI	g3738316
BLAST score	337
E value	1.0e-31
Match length	90
% identity	70
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	222547
Seq. ID	LIB3165-034-P1-K1-C10
Method	BLASTX
NCBI GI	g2865623
BLAST score	408
E value	4.0e-40
Match length	93
% identity	85
NCBI Description	(AF045286) GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase [Arabidopsis thaliana]

Seq. No.	222548
Seq. ID	LIB3165-034-P1-K1-C11
Method	BLASTX
NCBI GI	g20729
BLAST score	178
E value	4.0e-13
Match length	67
% identity	57
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	222549
Seq. ID	LIB3165-034-P1-K1-C12
Method	BLASTX
NCBI GI	g1181599
BLAST score	399
E value	6.0e-39
Match length	110
% identity	72
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.	222550
Seq. ID	LIB3165-034-P1-K1-C3
Method	BLASTX
NCBI GI	g3269292
BLAST score	289
E value	4.0e-26
Match length	74
% identity	69
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	222551
Seq. ID	LIB3165-034-P1-K1-C5
Method	BLASTX
NCBI GI	g133867
BLAST score	477
E value	5.0e-48
Match length	109
% identity	83
NCBI Description	40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays].

Seq. No.	222552
Seq. ID	LIB3165-034-P1-K1-C7

Method	BLASTX
NCBI GI	g498038
BLAST score	465
E value	1.0e-46
Match length	130
% identity	62
NCBI Description	(L33792) lipid transfer protein [Senecio odorus]

Seq. No.	222553
Seq. ID	LIB3165-034-P1-K1-C9
Method	BLASTX
NCBI GI	g1352821
BLAST score	531
E value	2.0e-54
Match length	102
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222554
Seq. ID	LIB3165-034-P1-K1-D1
Method	BLASTX
NCBI GI	g4249385
BLAST score	371
E value	1.0e-35
Match length	104
% identity	67
NCBI Description	(AC005966) T2K10.11 [Arabidopsis thaliana]

Seq. No.	222555
Seq. ID	LIB3165-034-P1-K1-D11
Method	BLASTX
NCBI GI	g68200
BLAST score	503
E value	4.0e-51
Match length	124
% identity	83
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	222556
Seq. ID	LIB3165-034-P1-K1-D12
Method	BLASTX
NCBI GI	g1352821
BLAST score	677
E value	2.0e-71
Match length	130
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222557
Seq. ID	LIB3165-034-P1-K1-D2
Method	BLASTX
NCBI GI	g3193285
BLAST score	217
E value	1.0e-17
Match length	56
% identity	70
NCBI Description	(AF069298) T14P8.18 gene product [Arabidopsis thaliana]

Seq. No.	222558
Seq. ID	LIB3165-034-P1-K1-D4
Method	BLASTX
NCBI GI	g3121825
BLAST score	301
E value	2.0e-27
Match length	102
% identity	69
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea]

Seq. No.	222559
Seq. ID	LIB3165-034-P1-K1-D5
Method	BLASTX
NCBI GI	g1352821
BLAST score	282
E value	3.0e-25
Match length	54
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222560
Seq. ID	LIB3165-034-P1-K1-D6
Method	BLASTX
NCBI GI	g1168408
BLAST score	169
E value	6.0e-12
Match length	38
% identity	89
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1 >gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828) fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No.	222561
Seq. ID	LIB3165-034-P1-K1-D7
Method	BLASTX
NCBI GI	g430947
BLAST score	444
E value	3.0e-44
Match length	108

% identity	81
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	222562
Seq. ID	LIB3165-034-P1-K1-D9
Method	BLASTX
NCBI GI	g1352821
BLAST score	710
E value	2.0e-75
Match length	133
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222563
Seq. ID	LIB3165-034-P1-K1-E10
Method	BLASTX
NCBI GI	g100490
BLAST score	573
E value	2.0e-59
Match length	115
% identity	28
NCBI Description	polyubiquitin - garden snapdragon (fragment) >gi_16071_emb_CAA48140_ (X67957) ubiquitin [Antirrhinum majus]

Seq. No.	222564
Seq. ID	LIB3165-034-P1-K1-E11
Method	BLASTX
NCBI GI	g68200
BLAST score	323
E value	5.0e-30
Match length	87
% identity	78
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	222565
Seq. ID	LIB3165-034-P1-K1-E12
Method	BLASTX
NCBI GI	g228403
BLAST score	529
E value	4.0e-54
Match length	119
% identity	87
NCBI Description	glycolate oxidase [Lens culinaris]

Seq. No.	222566
Seq. ID	LIB3165-034-P1-K1-E2
Method	BLASTX
NCBI GI	g1781348
BLAST score	564

E value	3.0e-58
Match length	119
% identity	89
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No.	222567
Seq. ID	LIB3165-034-P1-K1-E3
Method	BLASTX
NCBI GI	g3914002
BLAST score	607
E value	3.0e-63
Match length	128
% identity	91
NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_2935279 (AF033862) Lon protease [Arabidopsis thaliana]

Seq. No.	222568
Seq. ID	LIB3165-034-P1-K1-E5
Method	BLASTX
NCBI GI	g2129921
BLAST score	191
E value	1.0e-14
Match length	36
% identity	100
NCBI Description	hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]

Seq. No.	222569
Seq. ID	LIB3165-034-P1-K1-E6
Method	BLASTX
NCBI GI	g2739046
BLAST score	167
E value	1.0e-11
Match length	90
% identity	38
NCBI Description	(AF024652) polyphosphoinositide binding protein Ssh2p [Glycine max]

Seq. No.	222570
Seq. ID	LIB3165-034-P1-K1-E7
Method	BLASTX
NCBI GI	g1483563
BLAST score	423
E value	1.0e-41
Match length	127
% identity	69
NCBI Description	(X99825) leucine aminopeptidase [Petroselinum crispum]

Seq. No.	222571
Seq. ID	LIB3165-034-P1-K1-E8
Method	BLASTX
NCBI GI	g4033838
BLAST score	298
E value	4.0e-27
Match length	103
% identity	60

NCBI Description	(Y18550) sigma-like factor [Arabidopsis thaliana]

Seq. No.	222572
Seq. ID	LIB3165-034-P1-K1-E9
Method	BLASTX
NCBI GI	g2499525
BLAST score	260
E value	1.0e-22
Match length	133
% identity	44
NCBI Description	INTESTINAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER) >gi_1663535 (U51153) intestinal sodium/dicarboxylate cotransporter [Rattus norvegicus]

Seq. No.	222573
Seq. ID	LIB3165-034-P1-K1-F1
Method	BLASTX
NCBI GI	g4455225
BLAST score	237
E value	4.0e-20
Match length	56
% identity	71
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	222574
Seq. ID	LIB3165-034-P1-K1-F10
Method	BLASTX
NCBI GI	g3603401
BLAST score	300
E value	3.0e-27
Match length	74
% identity	69
NCBI Description	(AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No.	222575
Seq. ID	LIB3165-034-P1-K1-F12
Method	BLASTX
NCBI GI	g430947
BLAST score	429
E value	2.0e-42
Match length	106
% identity	80
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	222576
Seq. ID	LIB3165-034-P1-K1-F2
Method	BLASTX
NCBI GI	g3121825
BLAST score	339
E value	7.0e-32
Match length	127
% identity	64
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea]

Seq. No.	222577
Seq. ID	LIB3165-034-P1-K1-F3
Method	BLASTX
NCBI GI	g1352821
BLAST score	593
E value	1.0e-61
Match length	119
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222578
Seq. ID	LIB3165-034-P1-K1-F5
Method	BLASTX
NCBI GI	g100616
BLAST score	236
E value	8.0e-20
Match length	54
% identity	85
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	222579
Seq. ID	LIB3165-034-P1-K1-F6
Method	BLASTX
NCBI GI	g289920
BLAST score	604
E value	6.0e-63
Match length	123
% identity	93
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222580
Seq. ID	LIB3165-034-P1-K1-F7
Method	BLASTX
NCBI GI	g289920
BLAST score	614
E value	4.0e-64
Match length	115
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222581
Seq. ID	LIB3165-034-P1-K1-F8
Method	BLASTN
NCBI GI	g3108329
BLAST score	117
E value	2.0e-59

Match length	117
% identity	100
NCBI Description	Gossypium barbadense clone pXP3-50 repetitive DNA sequence

Seq. No.	222582
Seq. ID	LIB3165-034-P1-K1-G1
Method	BLASTX
NCBI GI	g430947
BLAST score	320
E value	9.0e-30
Match length	83
% identity	80
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	222583
Seq. ID	LIB3165-034-P1-K1-G10
Method	BLASTX
NCBI GI	g3747111
BLAST score	226
E value	1.0e-18
Match length	67
% identity	63
NCBI Description	(AF095641) MTN3 homolog [Arabidopsis thaliana]

Seq. No.	222584
Seq. ID	LIB3165-034-P1-K1-G12
Method	BLASTX
NCBI GI	g2791423
BLAST score	197
E value	3.0e-15
Match length	64
% identity	56
NCBI Description	(AL021185) bcp [Mycobacterium tuberculosis]

Seq. No.	222585
Seq. ID	LIB3165-034-P1-K1-G3
Method	BLASTX
NCBI GI	g3420239
BLAST score	349
E value	4.0e-33
Match length	70
% identity	96
NCBI Description	(AF059484) actin [Gossypium hirsutum]

Seq. No.	222586
Seq. ID	LIB3165-034-P1-K1-G4
Method	BLASTX
NCBI GI	g2979553
BLAST score	184
E value	1.0e-13
Match length	82
% identity	44
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	222587
Seq. ID	LIB3165-034-P1-K1-G7

Method	BLASTX
NCBI GI	g3928543
BLAST score	465
E value	1.0e-46
Match length	114
% identity	71
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	222588
Seq. ID	LIB3165-034-P1-K1-G8
Method	BLASTX
NCBI GI	g2979553
BLAST score	183
E value	1.0e-13
Match length	82
% identity	43
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	222589
Seq. ID	LIB3165-034-P1-K1-G9
Method	BLASTX
NCBI GI	g482311
BLAST score	128
E value	3.0e-14
Match length	67
% identity	63
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No.	222590
Seq. ID	LIB3165-034-P1-K1-H1
Method	BLASTX
NCBI GI	g4324714
BLAST score	407
E value	4.0e-40
Match length	90
% identity	89
NCBI Description	(AF110771) ammonium transporter [Arabidopsis thaliana]

Seq. No.	222591
Seq. ID	LIB3165-034-P1-K1-H11
Method	BLASTX
NCBI GI	g1352821
BLAST score	408
E value	5.0e-40
Match length	81
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222592
Seq. ID	LIB3165-034-P1-K1-H12

Method	BLASTX
NCBI GI	g1181599
BLAST score	356
E value	5.0e-34
Match length	99
% identity	71
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.	222593
Seq. ID	LIB3165-034-P1-K1-H2
Method	BLASTX
NCBI GI	g4262250
BLAST score	286
E value	8.0e-26
Match length	91
% identity	70
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	222594
Seq. ID	LIB3165-034-P1-K1-H3
Method	BLASTX
NCBI GI	g4406530
BLAST score	340
E value	6.0e-32
Match length	115
% identity	63
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222595
Seq. ID	LIB3165-034-P1-K1-H4
Method	BLASTX
NCBI GI	g289920
BLAST score	594
E value	9.0e-62
Match length	124
% identity	90
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222596
Seq. ID	LIB3165-034-P1-K1-H8
Method	BLASTX
NCBI GI	g1352821
BLAST score	402
E value	2.0e-39
Match length	81
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222597
Seq. ID	LIB3165-034-P1-K2-A1
Method	BLASTX
NCBI GI	g2879867

BLAST score	393
E value	3.0e-38
Match length	105
% identity	70
NCBI Description	(AL021816) 40s ribosomal protein S17 [Schizosaccharomyces pombe]

Seq. No.	222598
Seq. ID	LIB3165-034-P1-K2-A11
Method	BLASTX
NCBI GI	g1352821
BLAST score	324
E value	2.0e-30
Match length	63
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222599
Seq. ID	LIB3165-034-P1-K2-A3
Method	BLASTX
NCBI GI	g1706261
BLAST score	418
E value	2.0e-41
Match length	84
% identity	88
NCBI Description	CYSTEINE PROTEINASE 2 PRECURSOR >gi_2118129_pir__S59598 cysteine proteinase 2 precursor - maize >gi_644490_dbj_BAA08245_ (D45403) cysteine proteinase [Zea mays]

Seq. No.	222600
Seq. ID	LIB3165-034-P1-K2-A4
Method	BLASTX
NCBI GI	g1168411
BLAST score	525
E value	1.0e-53
Match length	137
% identity	80
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	222601
Seq. ID	LIB3165-034-P1-K2-A6
Method	BLASTX
NCBI GI	g461501
BLAST score	347
E value	1.0e-60
Match length	131
% identity	90
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE 2, CHLOROPLAST >gi_418803_pir__S29048 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea (fragment)

Seq. No.	222602

Seq. ID	LIB3165-034-P1-K2-A7
Method	BLASTX
NCBI GI	g1354515
BLAST score	177
E value	2.0e-13
Match length	68
% identity	60
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	222603
Seq. ID	LIB3165-034-P1-K2-A8
Method	BLASTX
NCBI GI	g100200
BLAST score	594
E value	8.0e-62
Match length	128
% identity	67
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	222604
Seq. ID	LIB3165-034-P1-K2-A9
Method	BLASTX
NCBI GI	g3158474
BLAST score	255
E value	5.0e-22
Match length	68
% identity	76
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]

Seq. No.	222605
Seq. ID	LIB3165-034-P1-K2-B1
Method	BLASTX
NCBI GI	g121953
BLAST score	172
E value	3.0e-12
Match length	39
% identity	87
NCBI Description	HISTONE H1 >gi_81905_pir__S00033 histone H1.b - garden pea >gi_20762_emb_CAA29123_ (X05636) H1 histone (AA 1-263) [Pisum sativum]

Seq. No.	222606
Seq. ID	LIB3165-034-P1-K2-B10
Method	BLASTX
NCBI GI	g81857
BLAST score	215
E value	2.0e-17
Match length	42
% identity	90
NCBI Description	IgE-dependent histamine-releasing factor homolog - alfalfa (fragment) >gi_19658_emb_CAA45349_ (X63872) translationally controlled tumor protein [Medicago sativa]

Seq. No.	222607
Seq. ID	LIB3165-034-P1-K2-B2
Method	BLASTX

NCBI GI	g1168411
BLAST score	141
E value	7.0e-09
Match length	65
% identity	54
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	222608
Seq. ID	LIB3165-034-P1-K2-B3
Method	BLASTX
NCBI GI	g3914940
BLAST score	307
E value	3.0e-28
Match length	111
% identity	61
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_2529376 (L76556) sedoheptulose-1,7-bisphosphatase [Spinacia oleracea]

Seq. No.	222609
Seq. ID	LIB3165-034-P1-K2-B5
Method	BLASTX
NCBI GI	g129867
BLAST score	360
E value	8.0e-37
Match length	78
% identity	88
NCBI Description	CYTOCHROME B6-F COMPLEX SUBUNIT 4 (17 KD POLYPEPTIDE) >gi_2924273_emb_CAA77425_ (Z00044) cytochrome b/f complex subunit IV [Nicotiana tabacum]

Seq. No.	222610
Seq. ID	LIB3165-034-P1-K2-B6
Method	BLASTX
NCBI GI	g228210
BLAST score	572
E value	3.0e-59
Match length	130
% identity	81
NCBI Description	granule-bound starch synthase [Solanum tuberosum]

Seq. No.	222611
Seq. ID	LIB3165-034-P1-K2-B9
Method	BLASTX
NCBI GI	g3738316
BLAST score	330
E value	8.0e-31
Match length	88
% identity	70
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	222612
Seq. ID	LIB3165-034-P1-K2-C10
Method	BLASTX
NCBI GI	g2865623
BLAST score	387

E value	1.0e-37
Match length	92
% identity	82
NCBI Description	(AF045286) GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase [Arabidopsis thaliana]

Seq. No.	222613
Seq. ID	LIB3165-034-P1-K2-C11
Method	BLASTX
NCBI GI	g20729
BLAST score	270
E value	7.0e-24
Match length	87
% identity	66
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	222614
Seq. ID	LIB3165-034-P1-K2-C12
Method	BLASTX
NCBI GI	g1363479
BLAST score	362
E value	1.0e-34
Match length	98
% identity	73
NCBI Description	photosystem I protein psaL - cucumber >gi_801740_dbj_BAA09047_ (D50456) PsaL [Cucumis sativus]

Seq. No.	222615
Seq. ID	LIB3165-034-P1-K2-C3
Method	BLASTX
NCBI GI	g3269292
BLAST score	291
E value	2.0e-26
Match length	76
% identity	67
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	222616
Seq. ID	LIB3165-034-P1-K2-C5
Method	BLASTX
NCBI GI	g166867
BLAST score	258
E value	1.0e-22
Match length	82
% identity	63
NCBI Description	(J05216) ribosomal protein S11 (probable start codon at bp 67) [Arabidopsis thaliana]

Seq. No.	222617
Seq. ID	LIB3165-034-P1-K2-C7
Method	BLASTX
NCBI GI	g498038
BLAST score	451
E value	5.0e-45
Match length	121
% identity	65

NCBI Description	(L33792) lipid transfer protein [Senecio odorus]

Seq. No.	222618
Seq. ID	LIB3165-034-P1-K2-C9
Method	BLASTX
NCBI GI	g1352821
BLAST score	548
E value	2.0e-56
Match length	115
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222619
Seq. ID	LIB3165-034-P1-K2-D1
Method	BLASTX
NCBI GI	g4249385
BLAST score	385
E value	3.0e-37
Match length	116
% identity	63
NCBI Description	(AC005966) T2K10.11 [Arabidopsis thaliana]

Seq. No.	222620
Seq. ID	LIB3165-034-P1-K2-D11
Method	BLASTX
NCBI GI	g1168411
BLAST score	442
E value	4.0e-44
Match length	109
% identity	83
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	222621
Seq. ID	LIB3165-034-P1-K2-D12
Method	BLASTX
NCBI GI	g1352821
BLAST score	682
E value	5.0e-72
Match length	139
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222622
Seq. ID	LIB3165-034-P1-K2-D5
Method	BLASTX
NCBI GI	g1352821
BLAST score	491
E value	9.0e-50
Match length	96

% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	222623
Seq. ID	LIB3165-034-P1-K2-D7
Method	BLASTX
NCBI GI	g430947
BLAST score	318
E value	1.0e-29
Match length	83
% identity	80
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]
Seq. No.	222624
Seq. ID	LIB3165-034-P1-K2-D9
Method	BLASTX
NCBI GI	g1352821
BLAST score	709
E value	3.0e-75
Match length	139
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	222625
Seq. ID	LIB3165-034-P1-K2-E1
Method	BLASTX
NCBI GI	g4490332
BLAST score	162
E value	4.0e-11
Match length	67
% identity	54
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]
Seq. No.	222626
Seq. ID	LIB3165-034-P1-K2-E10
Method	BLASTX
NCBI GI	g3335355
BLAST score	268
E value	6.0e-24
Match length	66
% identity	21
NCBI Description	(AC004512) Match to polyubiquitin DNA gb_L05401 from A. thaliana. Contains insertion of mitochondrial NADH dehydrogenase gb_X82618 and gb_X98301. May be a pseudogene with an expressed insert. EST gb_AA586248 comes from this region. [Arabi
Seq. No.	222627

Seq. ID	LIB3165-034-P1-K2-E11
Method	BLASTX
NCBI GI	g1168411
BLAST score	271
E value	5.0e-24
Match length	76
% identity	75
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	222628
Seq. ID	LIB3165-034-P1-K2-E12
Method	BLASTX
NCBI GI	g228403
BLAST score	522
E value	3.0e-53
Match length	120
% identity	85
NCBI Description	glycolate oxidase [Lens culinaris]

Seq. No.	222629
Seq. ID	LIB3165-034-P1-K2-E2
Method	BLASTX
NCBI GI	g2407279
BLAST score	451
E value	3.0e-45
Match length	101
% identity	84
NCBI Description	(AF017362) aldolase [Oryza sativa]

Seq. No.	222630
Seq. ID	LIB3165-034-P1-K2-E3
Method	BLASTX
NCBI GI	g3914002
BLAST score	646
E value	8.0e-68
Match length	137
% identity	91
NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_2935279 (AF033862) Lon protease [Arabidopsis thaliana]

Seq. No.	222631
Seq. ID	LIB3165-034-P1-K2-E5
Method	BLASTX
NCBI GI	g2129921
BLAST score	178
E value	6.0e-13
Match length	36
% identity	94
NCBI Description	hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]

Seq. No.	222632
Seq. ID	LIB3165-034-P1-K2-E6
Method	BLASTX
NCBI GI	g2739046
BLAST score	167
E value	1.0e-11

Match length	90
% identity	38
NCBI Description	(AF024652) polyphosphoinositide binding protein Ssh2p [Glycine max]

Seq. No.	222633
Seq. ID	LIB3165-034-P1-K2-E7
Method	BLASTX
NCBI GI	g1483563
BLAST score	328
E value	9.0e-31
Match length	97
% identity	70
NCBI Description	(X99825) leucine aminopeptidase [Petroselinum crispum]

Seq. No.	222634
Seq. ID	LIB3165-034-P1-K2-E8
Method	BLASTX
NCBI GI	g4033838
BLAST score	345
E value	1.0e-32
Match length	123
% identity	59
NCBI Description	(Y18550) sigma-like factor [Arabidopsis thaliana]

Seq. No.	222635
Seq. ID	LIB3165-034-P1-K2-E9
Method	BLASTX
NCBI GI	g2499525
BLAST score	246
E value	5.0e-21
Match length	122
% identity	46
NCBI Description	INTESTINAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER) >gi_1663535 (U51153) intestinal sodium/dicarboxylate cotransporter [Rattus norvegicus]

Seq. No.	222636
Seq. ID	LIB3165-034-P1-K2-F1
Method	BLASTX
NCBI GI	g4455225
BLAST score	399
E value	7.0e-39
Match length	93
% identity	73
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	222637
Seq. ID	LIB3165-034-P1-K2-F10
Method	BLASTX
NCBI GI	g3603401
BLAST score	300
E value	2.0e-27
Match length	74
% identity	69
NCBI Description	(AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No.	222638
Seq. ID	LIB3165-034-P1-K2-F12
Method	BLASTX
NCBI GI	g430947
BLAST score	413
E value	1.0e-40
Match length	103
% identity	81
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	222639
Seq. ID	LIB3165-034-P1-K2-F2
Method	BLASTX
NCBI GI	g3121825
BLAST score	365
E value	7.0e-35
Match length	117
% identity	69
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea]

Seq. No.	222640
Seq. ID	LIB3165-034-P1-K2-F3
Method	BLASTX
NCBI GI	g1352821
BLAST score	543
E value	9.0e-56
Match length	105
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222641
Seq. ID	LIB3165-034-P1-K2-F5
Method	BLASTX
NCBI GI	g100616
BLAST score	286
E value	1.0e-25
Match length	64
% identity	86
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	222642
Seq. ID	LIB3165-034-P1-K2-F6
Method	BLASTX
NCBI GI	g289920
BLAST score	605

E value 5.0e-63
Match length 124
% identity 92
NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No. 222643
Seq. ID LIB3165-034-P1-K2-G1
Method BLASTX
NCBI GI g430947
BLAST score 320
E value 9.0e-30
Match length 83
% identity 80
NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No. 222644
Seq. ID LIB3165-034-P1-K2-G10
Method BLASTX
NCBI GI g1619602
BLAST score 242
E value 2.0e-20
Match length 73
% identity 58
NCBI Description (Y08726) MtN3 [Medicago truncatula]

Seq. No. 222645
Seq. ID LIB3165-034-P1-K2-G12
Method BLASTX
NCBI GI g2791423
BLAST score 215
E value 3.0e-17
Match length 73
% identity 55
NCBI Description (AL021185) bcp [Mycobacterium tuberculosis]

Seq. No. 222646
Seq. ID LIB3165-034-P1-K2-G3
Method BLASTX
NCBI GI g113217
BLAST score 267
E value 1.0e-23
Match length 50
% identity 100
NCBI Description ACTIN 1 >gi_100149_pir__S07002 actin 1 - carrot

Seq. No. 222647
Seq. ID LIB3165-034-P1-K2-G4
Method BLASTX
NCBI GI g2979553
BLAST score 189
E value 3.0e-14
Match length 87
% identity 43
NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	222648
Seq. ID	LIB3165-034-P1-K2-G7
Method	BLASTX
NCBI GI	g3928543
BLAST score	376
E value	3.0e-36
Match length	96
% identity	70
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	222649
Seq. ID	LIB3165-034-P1-K2-G8
Method	BLASTX
NCBI GI	g2979553
BLAST score	194
E value	7.0e-15
Match length	88
% identity	42
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	222650
Seq. ID	LIB3165-034-P1-K2-H1
Method	BLASTX
NCBI GI	g4324714
BLAST score	372
E value	6.0e-36
Match length	89
% identity	83
NCBI Description	(AF110771) ammonium transporter [Arabidopsis thaliana]

Seq. No.	222651
Seq. ID	LIB3165-034-P1-K2-H11
Method	BLASTX
NCBI GI	g1352821
BLAST score	529
E value	4.0e-54
Match length	107
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222652
Seq. ID	LIB3165-034-P1-K2-H12
Method	BLASTX
NCBI GI	g1181599
BLAST score	397
E value	7.0e-39
Match length	110
% identity	72
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.	222653
Seq. ID	LIB3165-034-P1-K2-H2

Method	BLASTX
NCBI GI	g4262250
BLAST score	434
E value	5.0e-43
Match length	124
% identity	75
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	222654
Seq. ID	LIB3165-034-P1-K2-H3
Method	BLASTX
NCBI GI	g4406530
BLAST score	241
E value	5.0e-23
Match length	104
% identity	62
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222655
Seq. ID	LIB3165-034-P1-K2-H4
Method	BLASTX
NCBI GI	g289920
BLAST score	405
E value	1.0e-39
Match length	89
% identity	84
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222656
Seq. ID	LIB3165-034-P1-K2-H6
Method	BLASTX
NCBI GI	g1352821
BLAST score	355
E value	5.0e-34
Match length	68
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222657
Seq. ID	LIB3165-034-P1-K2-H8
Method	BLASTX
NCBI GI	g1352821
BLAST score	402
E value	2.0e-39
Match length	81
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222658
Seq. ID	LIB3165-034-P1-K3-A1
Method	BLASTX
NCBI GI	g1350944
BLAST score	391
E value	6.0e-38
Match length	80
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN S17

Seq. No.	222659
Seq. ID	LIB3165-034-P1-K3-A11
Method	BLASTX
NCBI GI	g1352821
BLAST score	657
E value	4.0e-69
Match length	122
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222660
Seq. ID	LIB3165-034-P1-K3-A3
Method	BLASTX
NCBI GI	g1706261
BLAST score	438
E value	2.0e-43
Match length	87
% identity	90
NCBI Description	CYSTEINE PROTEINASE 2 PRECURSOR >gi_2118129_pir__S59598 cysteine proteinase 2 precursor - maize >gi_644490_dbj_BAA08245_ (D45403) cysteine proteinase [Zea mays]

Seq. No.	222661
Seq. ID	LIB3165-034-P1-K3-A4
Method	BLASTX
NCBI GI	g68200
BLAST score	607
E value	3.0e-63
Match length	146
% identity	84
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	222662
Seq. ID	LIB3165-034-P1-K3-A6
Method	BLASTX
NCBI GI	g1781348
BLAST score	738
E value	1.0e-78
Match length	151
% identity	92

NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]
Seq. No.	222663
Seq. ID	LIB3165-034-P1-K3-A7
Method	BLASTX
NCBI GI	g1354515
BLAST score	243
E value	1.0e-20
Match length	122
% identity	48
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]
Seq. No.	222664
Seq. ID	LIB3165-034-P1-K3-A8
Method	BLASTX
NCBI GI	g100200
BLAST score	290
E value	9.0e-54
Match length	175
% identity	55
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato
Seq. No.	222665
Seq. ID	LIB3165-034-P1-K3-B1
Method	BLASTX
NCBI GI	g121953
BLAST score	181
E value	3.0e-13
Match length	42
% identity	86
NCBI Description	HISTONE H1 >gi_81905_pir__S00033 histone H1.b - garden pea >gi_20762_emb_CAA29123_ (X05636) H1 histone (AA 1-263) [Pisum sativum]
Seq. No.	222666
Seq. ID	LIB3165-034-P1-K3-B10
Method	BLASTX
NCBI GI	g81857
BLAST score	215
E value	2.0e-17
Match length	42
% identity	90
NCBI Description	IgE-dependent histamine-releasing factor homolog - alfalfa (fragment) >gi_19658_emb_CAA45349_ (X63872) translationally controlled tumor protein [Medicago sativa]
Seq. No.	222667
Seq. ID	LIB3165-034-P1-K3-B11
Method	BLASTX
NCBI GI	g1076627
BLAST score	514
E value	3.0e-52
Match length	132
% identity	77
NCBI Description	inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco

	>gi_790479_emb_CAA58701_ (X83730) inorganic pyrophosphatase [Nicotiana tabacum]
Seq. No.	222668
Seq. ID	LIB3165-034-P1-K3-B3
Method	BLASTX
NCBI GI	g1173345
BLAST score	228
E value	5.0e-19
Match length	82
% identity	59
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_1076403_pir__S51838 sedoheptulose-1,7-biphosphatase - Arabidopsis thaliana >gi_786466_bbs_159034 (S74719) sedoheptulose-1,7-bisphosphatase, SBPase {EC 3.1.3.37} [Arabidopsis thaliana, C24, Peptide Chloroplast, 393 aa] [Arabidopsis thaliana]
Seq. No.	222669
Seq. ID	LIB3165-034-P1-K3-B5
Method	BLASTX
NCBI GI	g129867
BLAST score	582
E value	3.0e-60
Match length	110
% identity	100
NCBI Description	CYTOCHROME B6-F COMPLEX SUBUNIT 4 (17 KD POLYPEPTIDE) >gi_2924273_emb_CAA77425_ (Z00044) cytochrome b/f complex subunit IV [Nicotiana tabacum]
Seq. No.	222670
Seq. ID	LIB3165-034-P1-K3-B6
Method	BLASTX
NCBI GI	g2833388
BLAST score	637
E value	1.0e-66
Match length	150
% identity	79
NCBI Description	GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi_629660_pir__S43341 ADPglucose--starch glucosyltransferase (EC 2.4.1.21) precursor - cassava >gi_437042_emb_CAA52273_ (X74160) starch (bacterial glycogen) synthase [Manihot esculenta]
Seq. No.	222671
Seq. ID	LIB3165-034-P1-K3-B8
Method	BLASTX
NCBI GI	g131167
BLAST score	192
E value	6.0e-15
Match length	87
% identity	54
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_100292_pir__S18348 photosystem I chain II precursor - wood tobacco >gi_19748_emb_CAA42623_ (X60008) PSI-D2

[Nicotiana sylvestris]

Seq. No.	222672
Seq. ID	LIB3165-034-P1-K3-C10
Method	BLASTX
NCBI GI	g2865623
BLAST score	581
E value	4.0e-60
Match length	132
% identity	84
NCBI Description	(AF045286) GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase [Arabidopsis thaliana]

Seq. No.	222673
Seq. ID	LIB3165-034-P1-K3-C11
Method	BLASTX
NCBI GI	g20729
BLAST score	443
E value	5.0e-44
Match length	118
% identity	76
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	222674
Seq. ID	LIB3165-034-P1-K3-C12
Method	BLASTX
NCBI GI	g1181599
BLAST score	454
E value	3.0e-45
Match length	119
% identity	75
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.	222675
Seq. ID	LIB3165-034-P1-K3-C3
Method	BLASTX
NCBI GI	g3269292
BLAST score	289
E value	5.0e-26
Match length	74
% identity	69
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	222676
Seq. ID	LIB3165-034-P1-K3-C5
Method	BLASTX
NCBI GI	g133867
BLAST score	584
E value	2.0e-60
Match length	128
% identity	87
NCBI Description	40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays]

Seq. No.	222677

Seq. ID	LIB3165-034-P1-K3-C9
Method	BLASTX
NCBI GI	g1352821
BLAST score	599
E value	3.0e-62
Match length	118
% identity	93
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222678
Seq. ID	LIB3165-034-P1-K3-D1
Method	BLASTX
NCBI GI	g4249385
BLAST score	407
E value	9.0e-40
Match length	125
% identity	62
NCBI Description	(AC005966) T2K10.11 [Arabidopsis thaliana]

Seq. No.	222679
Seq. ID	LIB3165-034-P1-K3-D11
Method	BLASTX
NCBI GI	g1168411
BLAST score	577
E value	1.0e-59
Match length	141
% identity	83
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	222680
Seq. ID	LIB3165-034-P1-K3-D12
Method	BLASTX
NCBI GI	g1352821
BLAST score	746
E value	2.0e-79
Match length	147
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222681
Seq. ID	LIB3165-034-P1-K3-D2
Method	BLASTX
NCBI GI	g3193285
BLAST score	356
E value	9.0e-34
Match length	97
% identity	67
NCBI Description	(AF069298) T14P8.18 gene product [Arabidopsis thaliana]

Seq. No.	222682
Seq. ID	LIB3165-034-P1-K3-D4
Method	BLASTX
NCBI GI	g3121825
BLAST score	378
E value	2.0e-36
Match length	117
% identity	72
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea]

Seq. No.	222683
Seq. ID	LIB3165-034-P1-K3-D5
Method	BLASTX
NCBI GI	g1352821
BLAST score	667
E value	3.0e-70
Match length	122
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222684
Seq. ID	LIB3165-034-P1-K3-D6
Method	BLASTX
NCBI GI	g1168408
BLAST score	251
E value	2.0e-21
Match length	56
% identity	91
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1 >gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828) fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No.	222685
Seq. ID	LIB3165-034-P1-K3-D7
Method	BLASTX
NCBI GI	g430947
BLAST score	486
E value	5.0e-49
Match length	120
% identity	81
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	222686
Seq. ID	LIB3165-034-P1-K3-D9
Method	BLASTX
NCBI GI	g1352821
BLAST score	738
E value	1.0e-78
Match length	139

% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222687
Seq. ID	LIB3165-034-P1-K3-E1
Method	BLASTX
NCBI GI	g4490332
BLAST score	198
E value	3.0e-15
Match length	78
% identity	55
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	222688
Seq. ID	LIB3165-034-P1-K3-E10
Method	BLASTX
NCBI GI	g1800281
BLAST score	680
E value	9.0e-72
Match length	136
% identity	22
NCBI Description	(U82086) polyubiquitin [Fragaria x ananassa]

Seq. No.	222689
Seq. ID	LIB3165-034-P1-K3-E11
Method	BLASTX
NCBI GI	g68200
BLAST score	421
E value	2.0e-41
Match length	108
% identity	80
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	222690
Seq. ID	LIB3165-034-P1-K3-E12
Method	BLASTX
NCBI GI	g228403
BLAST score	618
E value	2.0e-64
Match length	135
% identity	88
NCBI Description	glycolate oxidase [Lens culinaris]

Seq. No.	222691
Seq. ID	LIB3165-034-P1-K3-E2
Method	BLASTX
NCBI GI	g1781348
BLAST score	545
E value	5.0e-56
Match length	119
% identity	87

NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]
Seq. No.	222692
Seq. ID	LIB3165-034-P1-K3-E3
Method	BLASTX
NCBI GI	g3914002
BLAST score	695
E value	2.0e-73
Match length	147
% identity	91
NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_2935279 (AF033862) Lon protease [Arabidopsis thaliana]
Seq. No.	222693
Seq. ID	LIB3165-034-P1-K3-E5
Method	BLASTX
NCBI GI	g2129921
BLAST score	191
E value	2.0e-14
Match length	36
% identity	100
NCBI Description	hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]
Seq. No.	222694
Seq. ID	LIB3165-034-P1-K3-E6
Method	BLASTX
NCBI GI	g2739046
BLAST score	195
E value	7.0e-15
Match length	102
% identity	38
NCBI Description	(AF024652) polyphosphoinositide binding protein Ssh2p [Glycine max]
Seq. No.	222695
Seq. ID	LIB3165-034-P1-K3-E7
Method	BLASTX
NCBI GI	g1483563
BLAST score	563
E value	5.0e-58
Match length	146
% identity	77
NCBI Description	(X99825) leucine aminopeptidase [Petroselinum crispum]
Seq. No.	222696
Seq. ID	LIB3165-034-P1-K3-E8
Method	BLASTX
NCBI GI	g4033838
BLAST score	386
E value	3.0e-37
Match length	134
% identity	60
NCBI Description	(Y18550) sigma-like factor [Arabidopsis thaliana]
Seq. No.	222697

Seq. ID	LIB3165-034-P1-K3-E9
Method	BLASTX
NCBI GI	g2499525
BLAST score	287
E value	1.0e-25
Match length	147
% identity	44
NCBI Description	INTESTINAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER) >gi_1663535 (U51153) intestinal sodium/dicarboxylate cotransporter [Rattus norvegicus]

Seq. No.	222698
Seq. ID	LIB3165-034-P1-K3-F1
Method	BLASTX
NCBI GI	g4455225
BLAST score	358
E value	5.0e-34
Match length	88
% identity	70
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	222699
Seq. ID	LIB3165-034-P1-K3-F10
Method	BLASTX
NCBI GI	g3603401
BLAST score	141
E value	4.0e-17
Match length	66
% identity	61
NCBI Description	(AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No.	222700
Seq. ID	LIB3165-034-P1-K3-F12
Method	BLASTX
NCBI GI	g430947
BLAST score	458
E value	9.0e-46
Match length	114
% identity	81
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	222701
Seq. ID	LIB3165-034-P1-K3-F2
Method	BLASTX
NCBI GI	g3121825
BLAST score	360
E value	3.0e-34
Match length	114
% identity	71
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea]

Seq. No.	222702
Seq. ID	LIB3165-034-P1-K3-F3

Method	BLASTX
NCBI GI	g1352821
BLAST score	655
E value	8.0e-69
Match length	122
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222703
Seq. ID	LIB3165-034-P1-K3-F5
Method	BLASTX
NCBI GI	g100616
BLAST score	270
E value	1.0e-23
Match length	60
% identity	87
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095_(M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	222704
Seq. ID	LIB3165-034-P1-K3-F6
Method	BLASTX
NCBI GI	g289920
BLAST score	540
E value	5.0e-69
Match length	139
% identity	90
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222705
Seq. ID	LIB3165-034-P1-K3-F7
Method	BLASTX
NCBI GI	g289920
BLAST score	718
E value	3.0e-76
Match length	138
% identity	96
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222706
Seq. ID	LIB3165-034-P1-K3-G1
Method	BLASTX
NCBI GI	g430947
BLAST score	455
E value	2.0e-45
Match length	113
% identity	81
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No.	222707
Seq. ID	LIB3165-034-P1-K3-G10
Method	BLASTX
NCBI GI	g1619602
BLAST score	257
E value	3.0e-22
Match length	78
% identity	56
NCBI Description	(Y08726) MtN3 [Medicago truncatula]

Seq. No.	222708
Seq. ID	LIB3165-034-P1-K3-G12
Method	BLASTX
NCBI GI	g2791423
BLAST score	227
E value	1.0e-18
Match length	81
% identity	53
NCBI Description	(AL021185) bcp [Mycobacterium tuberculosis]

Seq. No.	222709
Seq. ID	LIB3165-034-P1-K3-G3
Method	BLASTX
NCBI GI	g1703108
BLAST score	554
E value	5.0e-57
Match length	103
% identity	99
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	222710
Seq. ID	LIB3165-034-P1-K3-G4
Method	BLASTX
NCBI GI	g2979553
BLAST score	201
E value	1.0e-15
Match length	90
% identity	43
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	222711
Seq. ID	LIB3165-034-P1-K3-G7
Method	BLASTX
NCBI GI	g3928543
BLAST score	573
E value	3.0e-59
Match length	136
% identity	73
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	222712
Seq. ID	LIB3165-034-P1-K3-G8
Method	BLASTX
NCBI GI	g2979553
BLAST score	223
E value	3.0e-18
Match length	110
% identity	41
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	222713
Seq. ID	LIB3165-034-P1-K3-G9
Method	BLASTX
NCBI GI	g131384
BLAST score	224
E value	1.0e-18
Match length	68
% identity	69
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_81934_pir__S04132 photosystem II oxygen-evolving complex protein 1 precursor - garden pea >gi_20621_emb_CAA33408_ (X15350) precursor (AA -81 to 248) [Pisum sativum] >gi_344004_dbj_BAA02554_ (D13297) precursor for 33-kDa protein of photosystem II [Pisum sativum] >gi_226937_prf__1611461A O2 evolving complex 33kD protein [Arachis hypogaea]

Seq. No.	222714
Seq. ID	LIB3165-034-P1-K3-H1
Method	BLASTX
NCBI GI	g4324714
BLAST score	437
E value	2.0e-43
Match length	96
% identity	89
NCBI Description	(AF110771) ammonium transporter [Arabidopsis thaliana]

Seq. No.	222715
Seq. ID	LIB3165-034-P1-K3-H11
Method	BLASTX
NCBI GI	g1352821
BLAST score	569
E value	9.0e-59
Match length	109
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222716
Seq. ID	LIB3165-034-P1-K3-H2
Method	BLASTX
NCBI GI	g4262250
BLAST score	445

E value	3.0e-44
Match length	126
% identity	75
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	222717
Seq. ID	LIB3165-034-P1-K3-H3
Method	BLASTX
NCBI GI	g3914605
BLAST score	392
E value	5.0e-38
Match length	130
% identity	62
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase - apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica]

Seq. No.	222718
Seq. ID	LIB3165-034-P1-K3-H4
Method	BLASTX
NCBI GI	g289920
BLAST score	184
E value	2.0e-21
Match length	73
% identity	66
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222719
Seq. ID	LIB3165-034-P1-K3-H6
Method	BLASTX
NCBI GI	g1352821
BLAST score	670
E value	1.0e-70
Match length	130
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222720
Seq. ID	LIB3165-034-P1-K3-H8
Method	BLASTX
NCBI GI	g1352821
BLAST score	403
E value	3.0e-39
Match length	118
% identity	78
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222721
Seq. ID	LIB3165-034-P1-K4-A1
Method	BLASTX
NCBI GI	g133825
BLAST score	400
E value	5.0e-39
Match length	108
% identity	71
NCBI Description	40S RIBOSOMAL PROTEIN S17 >gi_71199_pir__R4HU17 ribosomal protein S17 - human >gi_337501 (M13932) ribosomal protein S17 [Homo sapiens] >gi_337503 (M18000) S17 ribosomal protein [Homo sapiens] >gi_4506693_ref_NP_001012.1_pRPS17_ ribosomal protein S17

Seq. No.	222722
Seq. ID	LIB3165-034-P1-K4-A11
Method	BLASTX
NCBI GI	g1352821
BLAST score	503
E value	4.0e-51
Match length	97
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222723
Seq. ID	LIB3165-034-P1-K4-A3
Method	BLASTX
NCBI GI	g67656
BLAST score	191
E value	5.0e-16
Match length	52
% identity	70
NCBI Description	aleurain (EC 3.4.22.-) precursor - barley

Seq. No.	222724
Seq. ID	LIB3165-034-P1-K4-A4
Method	BLASTX
NCBI GI	g68200
BLAST score	510
E value	5.0e-52
Match length	124
% identity	84
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	222725
Seq. ID	LIB3165-034-P1-K4-A6
Method	BLASTX
NCBI GI	g169039
BLAST score	617

E value	2.0e-64
Match length	126
% identity	92
NCBI Description	(M97477) aldolase [Pisum sativum]

Seq. No.	222726
Seq. ID	LIB3165-034-P1-K4-A7
Method	BLASTX
NCBI GI	g1354515
BLAST score	255
E value	5.0e-22
Match length	125
% identity	49
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	222727
Seq. ID	LIB3165-034-P1-K4-A8
Method	BLASTX
NCBI GI	g100200
BLAST score	603
E value	7.0e-63
Match length	127
% identity	68
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	222728
Seq. ID	LIB3165-034-P1-K4-A9
Method	BLASTX
NCBI GI	g3158474
BLAST score	183
E value	1.0e-13
Match length	53
% identity	70
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]

Seq. No.	222729
Seq. ID	LIB3165-034-P1-K4-B1
Method	BLASTX
NCBI GI	g16314
BLAST score	147
E value	2.0e-09
Match length	32
% identity	94
NCBI Description	(X62456) histone H1-1 [Arabidopsis thaliana]

Seq. No.	222730
Seq. ID	LIB3165-034-P1-K4-B10
Method	BLASTX
NCBI GI	g81857
BLAST score	215
E value	2.0e-17
Match length	42
% identity	90
NCBI Description	IgE-dependent histamine-releasing factor homolog - alfalfa (fragment) >gi_19658_emb_CAA45349_ (X63872) translationally controlled tumor protein [Medicago sativa]

Seq. No.	222731
Seq. ID	LIB3165-034-P1-K4-B11
Method	BLASTX
NCBI GI	g2653446
BLAST score	380
E value	1.0e-36
Match length	97
% identity	74
NCBI Description	(AB009077) proton pyrophosphatase [Vigna radiata]

Seq. No.	222732
Seq. ID	LIB3165-034-P1-K4-B2
Method	BLASTX
NCBI GI	g68200
BLAST score	248
E value	3.0e-21
Match length	88
% identity	64
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	222733
Seq. ID	LIB3165-034-P1-K4-B3
Method	BLASTX
NCBI GI	g3914940
BLAST score	335
E value	2.0e-31
Match length	116
% identity	63
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_2529376 (L76556) sedoheptulose-1,7-bisphosphatase [Spinacia oleracea]

Seq. No.	222734
Seq. ID	LIB3165-034-P1-K4-B5
Method	BLASTX
NCBI GI	g82437
BLAST score	477
E value	4.0e-48
Match length	88
% identity	100
NCBI Description	plastoquinol--plastocyanin reductase (EC 1.10.99.1) 17K protein short form - barley chloroplast (fragment) >gi_1617032_emb_CAA32269_ (X14107) petD [Hordeum vulgare]

Seq. No.	222735
Seq. ID	LIB3165-034-P1-K4-B6
Method	BLASTX
NCBI GI	g228210
BLAST score	563
E value	4.0e-58
Match length	126
% identity	81
NCBI Description	granule-bound starch synthase [Solanum tuberosum]

Seq. No.	222736
Seq. ID	LIB3165-034-P1-K4-B8
Method	BLASTX
NCBI GI	g131167
BLAST score	374
E value	5.0e-36
Match length	124
% identity	66
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_100292_pir__S18348 photosystem I chain II precursor - wood tobacco >gi_19748_emb_CAA42623_ (X60008) PSI-D2 [Nicotiana sylvestris]

Seq. No.	222737
Seq. ID	LIB3165-034-P1-K4-B9
Method	BLASTX
NCBI GI	g3738316
BLAST score	319
E value	1.0e-29
Match length	82
% identity	73
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	222738
Seq. ID	LIB3165-034-P1-K4-C10
Method	BLASTX
NCBI GI	g2865623
BLAST score	461
E value	3.0e-46
Match length	106
% identity	84
NCBI Description	(AF045286) GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase [Arabidopsis thaliana]

Seq. No.	222739
Seq. ID	LIB3165-034-P1-K4-C11
Method	BLASTX
NCBI GI	g20729
BLAST score	323
E value	5.0e-30
Match length	94
% identity	70
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	222740
Seq. ID	LIB3165-034-P1-K4-C12
Method	BLASTX
NCBI GI	g1181599
BLAST score	374
E value	5.0e-36
Match length	103
% identity	72
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.	222741
Seq. ID	LIB3165-034-P1-K4-C3
Method	BLASTX
NCBI GI	g3269292
BLAST score	289
E value	5.0e-26
Match length	74
% identity	69
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	222742
Seq. ID	LIB3165-034-P1-K4-C5
Method	BLASTX
NCBI GI	g133867
BLAST score	451
E value	5.0e-45
Match length	104
% identity	84
NCBI Description	40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays]

Seq. No.	222743
Seq. ID	LIB3165-034-P1-K4-C7
Method	BLASTX
NCBI GI	g498038
BLAST score	454
E value	2.0e-45
Match length	121
% identity	65
NCBI Description	(L33792) lipid transfer protein [Senecio odorus]

Seq. No.	222744
Seq. ID	LIB3165-034-P1-K4-C9
Method	BLASTX
NCBI GI	g1352821
BLAST score	495
E value	3.0e-50
Match length	96
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222745
Seq. ID	LIB3165-034-P1-K4-D1
Method	BLASTX
NCBI GI	g4249385
BLAST score	367
E value	3.0e-35
Match length	102
% identity	69
NCBI Description	(AC005966) T2K10.11 [Arabidopsis thaliana]

Seq. No.	222746

Seq. ID	LIB3165-034-P1-K4-D10
Method	BLASTX
NCBI GI	g1781348
BLAST score	139
E value	5.0e-09
Match length	35
% identity	77
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No.	222747
Seq. ID	LIB3165-034-P1-K4-D11
Method	BLASTX
NCBI GI	g68200
BLAST score	476
E value	5.0e-48
Match length	117
% identity	84
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	222748
Seq. ID	LIB3165-034-P1-K4-D12
Method	BLASTX
NCBI GI	g1352821
BLAST score	640
E value	3.0e-67
Match length	125
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222749
Seq. ID	LIB3165-034-P1-K4-D2
Method	BLASTX
NCBI GI	g3193285
BLAST score	266
E value	3.0e-23
Match length	74
% identity	65
NCBI Description	(AF069298) T14P8.18 gene product [Arabidopsis thaliana]

Seq. No.	222750
Seq. ID	LIB3165-034-P1-K4-D4
Method	BLASTX
NCBI GI	g3121825
BLAST score	262
E value	7.0e-23
Match length	94
% identity	66
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea]

Seq. No.	222751
Seq. ID	LIB3165-034-P1-K4-D5
Method	BLASTX
NCBI GI	g1352821
BLAST score	523
E value	2.0e-53
Match length	99
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222752
Seq. ID	LIB3165-034-P1-K4-D6
Method	BLASTX
NCBI GI	g1168408
BLAST score	145
E value	4.0e-09
Match length	31
% identity	94
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1 >gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828) fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No.	222753
Seq. ID	LIB3165-034-P1-K4-D7
Method	BLASTX
NCBI GI	g430947
BLAST score	411
E value	2.0e-40
Match length	101
% identity	81
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	222754
Seq. ID	LIB3165-034-P1-K4-D9
Method	BLASTX
NCBI GI	g1352821
BLAST score	674
E value	3.0e-71
Match length	126
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222755
Seq. ID	LIB3165-034-P1-K4-E10
Method	BLASTX
NCBI GI	g100490

BLAST score	573
E value	2.0e-59
Match length	115
% identity	28
NCBI Description	polyubiquitin - garden snapdragon (fragment) >gi_16071_emb_CAA48140_ (X67957) ubiquitin [Antirrhinum majus]

Seq. No.	222756
Seq. ID	LIB3165-034-P1-K4-E11
Method	BLASTX
NCBI GI	g68200
BLAST score	318
E value	2.0e-29
Match length	86
% identity	78
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	222757
Seq. ID	LIB3165-034-P1-K4-E12
Method	BLASTX
NCBI GI	g228403
BLAST score	498
E value	1.0e-50
Match length	112
% identity	86
NCBI Description	glycolate oxidase [Lens culinaris]

Seq. No.	222758
Seq. ID	LIB3165-034-P1-K4-E2
Method	BLASTX
NCBI GI	g1781348
BLAST score	564
E value	3.0e-58
Match length	119
% identity	89
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No.	222759
Seq. ID	LIB3165-034-P1-K4-E3
Method	BLASTX
NCBI GI	g3914002
BLAST score	594
E value	8.0e-62
Match length	123
% identity	92
NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_2935279 (AF033862) Lon protease [Arabidopsis thaliana]

Seq. No.	222760
Seq. ID	LIB3165-034-P1-K4-E6
Method	BLASTX
NCBI GI	g2739046
BLAST score	150

E value	9.0e-10
Match length	82
% identity	38
NCBI Description	(AF024652) polyphosphoinositide binding protein Ssh2p [Glycine max]

Seq. No.	222761
Seq. ID	LIB3165-034-P1-K4-E7
Method	BLASTX
NCBI GI	g1483563
BLAST score	406
E value	1.0e-41
Match length	116
% identity	78
NCBI Description	(X99825) leucine aminopeptidase [Petroselinum crispum]

Seq. No.	222762
Seq. ID	LIB3165-034-P1-K4-E8
Method	BLASTX
NCBI GI	g4033838
BLAST score	337
E value	1.0e-31
Match length	111
% identity	63
NCBI Description	(Y18550) sigma-like factor [Arabidopsis thaliana]

Seq. No.	222763
Seq. ID	LIB3165-034-P1-K4-E9
Method	BLASTX
NCBI GI	g2499525
BLAST score	246
E value	5.0e-21
Match length	122
% identity	46
NCBI Description	INTESTINAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER) >gi_1663535 (U51153) intestinal sodium/dicarboxylate cotransporter [Rattus norvegicus]

Seq. No.	222764
Seq. ID	LIB3165-034-P1-K4-F1
Method	BLASTX
NCBI GI	g4455225
BLAST score	346
E value	1.0e-32
Match length	83
% identity	73
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	222765
Seq. ID	LIB3165-034-P1-K4-F10
Method	BLASTX
NCBI GI	g3603401
BLAST score	300
E value	2.0e-27
Match length	74
% identity	69

NCBI Description	(AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No.	222766
Seq. ID	LIB3165-034-P1-K4-F12
Method	BLASTX
NCBI GI	g430947
BLAST score	401
E value	4.0e-39
Match length	99
% identity	81
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	222767
Seq. ID	LIB3165-034-P1-K4-F2
Method	BLASTX
NCBI GI	g3121825
BLAST score	306
E value	5.0e-28
Match length	101
% identity	69
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea]

Seq. No.	222768
Seq. ID	LIB3165-034-P1-K4-F3
Method	BLASTX
NCBI GI	g1352821
BLAST score	557
E value	2.0e-57
Match length	111
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222769
Seq. ID	LIB3165-034-P1-K4-F5
Method	BLASTX
NCBI GI	g100616
BLAST score	222
E value	4.0e-18
Match length	50
% identity	88
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	222770
Seq. ID	LIB3165-034-P1-K4-F6
Method	BLASTX
NCBI GI	g289920

BLAST score	566
E value	2.0e-58
Match length	115
% identity	92
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222771
Seq. ID	LIB3165-034-P1-K4-F7
Method	BLASTX
NCBI GI	g289920
BLAST score	619
E value	9.0e-65
Match length	115
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222772
Seq. ID	LIB3165-034-P1-K4-G1
Method	BLASTX
NCBI GI	g430947
BLAST score	403
E value	2.0e-39
Match length	99
% identity	81
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	222773
Seq. ID	LIB3165-034-P1-K4-G10
Method	BLASTX
NCBI GI	g1619602
BLAST score	207
E value	2.0e-16
Match length	60
% identity	62
NCBI Description	(Y08726) MtN3 [Medicago truncatula]

Seq. No.	222774
Seq. ID	LIB3165-034-P1-K4-G12
Method	BLASTX
NCBI GI	g2791423
BLAST score	189
E value	2.0e-14
Match length	60
% identity	57
NCBI Description	(AL021185) bcp [Mycobacterium tuberculosis]

Seq. No.	222775
Seq. ID	LIB3165-034-P1-K4-G3
Method	BLASTX
NCBI GI	g4139264
BLAST score	432
E value	8.0e-43
Match length	81
% identity	100

NCBI Description	(AF111812) actin [Brassica napus]

Seq. No.	222776
Seq. ID	LIB3165-034-P1-K4-G4
Method	BLASTX
NCBI GI	g2979553
BLAST score	173
E value	2.0e-12
Match length	76
% identity	45
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	222777
Seq. ID	LIB3165-034-P1-K4-G7
Method	BLASTX
NCBI GI	g3928543
BLAST score	459
E value	6.0e-46
Match length	114
% identity	71
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	222778
Seq. ID	LIB3165-034-P1-K4-G8
Method	BLASTX
NCBI GI	g2979553
BLAST score	186
E value	6.0e-14
Match length	82
% identity	44
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	222779
Seq. ID	LIB3165-034-P1-K4-H1
Method	BLASTX
NCBI GI	g4324714
BLAST score	499
E value	1.0e-50
Match length	117
% identity	84
NCBI Description	(AF110771) ammonium transporter [Arabidopsis thaliana]

Seq. No.	222780
Seq. ID	LIB3165-034-P1-K4-H11
Method	BLASTX
NCBI GI	g1352821
BLAST score	468
E value	5.0e-47
Match length	91
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222781
Seq. ID	LIB3165-034-P1-K4-H12
Method	BLASTX
NCBI GI	g1181599
BLAST score	490
E value	1.0e-49
Match length	126
% identity	76
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.	222782
Seq. ID	LIB3165-034-P1-K4-H2
Method	BLASTX
NCBI GI	g4262250
BLAST score	381
E value	8.0e-37
Match length	111
% identity	74
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	222783
Seq. ID	LIB3165-034-P1-K4-H3
Method	BLASTX
NCBI GI	g4406530
BLAST score	310
E value	2.0e-28
Match length	108
% identity	62
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222784
Seq. ID	LIB3165-034-P1-K4-H6
Method	BLASTX
NCBI GI	g1352821
BLAST score	500
E value	9.0e-51
Match length	95
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222785
Seq. ID	LIB3165-034-P1-K4-H8
Method	BLASTX
NCBI GI	g1352821
BLAST score	402
E value	3.0e-39
Match length	96
% identity	84
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222786
Seq. ID	LIB3165-034-P1-K5-A1
Method	BLASTX
NCBI GI	g1350944
BLAST score	329
E value	5.0e-31
Match length	69
% identity	93
NCBI Description	40S RIBOSOMAL PROTEIN S17

Seq. No.	222787
Seq. ID	LIB3165-034-P1-K5-A11
Method	BLASTX
NCBI GI	g1352821
BLAST score	522
E value	2.0e-53
Match length	100
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222788
Seq. ID	LIB3165-034-P1-K5-A4
Method	BLASTX
NCBI GI	g1168411
BLAST score	504
E value	3.0e-51
Match length	122
% identity	84
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	222789
Seq. ID	LIB3165-034-P1-K5-A6
Method	BLASTX
NCBI GI	g169039
BLAST score	614
E value	4.0e-64
Match length	130
% identity	90
NCBI Description	(M97477) aldolase [Pisum sativum]

Seq. No.	222790
Seq. ID	LIB3165-034-P1-K5-A7
Method	BLASTX
NCBI GI	g1354515
BLAST score	238
E value	4.0e-20
Match length	122
% identity	48
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No. 222791

Seq. ID	LIB3165-034-P1-K5-A8
Method	BLASTX
NCBI GI	g100200
BLAST score	474
E value	5.0e-48
Match length	91
% identity	68
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	222792
Seq. ID	LIB3165-034-P1-K5-A9
Method	BLASTX
NCBI GI	g3158474
BLAST score	192
E value	1.0e-14
Match length	58
% identity	67
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]

Seq. No.	222793
Seq. ID	LIB3165-034-P1-K5-B10
Method	BLASTX
NCBI GI	g81857
BLAST score	211
E value	6.0e-17
Match length	42
% identity	88
NCBI Description	IgE-dependent histamine-releasing factor homolog - alfalfa (fragment) >gi_19658_emb_CAA45349_ (X63872) translationally controlled tumor protein [Medicago sativa]

Seq. No.	222794
Seq. ID	LIB3165-034-P1-K5-B11
Method	BLASTX
NCBI GI	g2827755
BLAST score	370
E value	2.0e-35
Match length	97
% identity	73
NCBI Description	INORGANIC PYROPHOSPHATASE, VACUOLAR (PYROPHOSPHATE PHOSPHOHYDROLASE) (PPASE) >gi_951323 (U31467) pyrophosphatase [Vigna radiata]

Seq. No.	222795
Seq. ID	LIB3165-034-P1-K5-B2
Method	BLASTX
NCBI GI	g68200
BLAST score	198
E value	2.0e-15
Match length	75
% identity	59
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	222796
Seq. ID	LIB3165-034-P1-K5-B3

Method	BLASTX
NCBI GI	g3914940
BLAST score	335
E value	2.0e-31
Match length	116
% identity	63
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_2529376 (L76556) sedoheptulose-1,7-bisphosphatase [Spinacia oleracea]

Seq. No.	222797
Seq. ID	LIB3165-034-P1-K5-B5
Method	BLASTX
NCBI GI	g82437
BLAST score	482
E value	1.0e-48
Match length	89
% identity	100
NCBI Description	plastoquinol--plastocyanin reductase (EC 1.10.99.1) 17K protein short form - barley chloroplast (fragment) >gi_1617032_emb_CAA32269_ (X14107) petD [Hordeum vulgare]

Seq. No.	222798
Seq. ID	LIB3165-034-P1-K5-B6
Method	BLASTX
NCBI GI	g228210
BLAST score	572
E value	3.0e-59
Match length	130
% identity	81
NCBI Description	granule-bound starch synthase [Solanum tuberosum]

Seq. No.	222799
Seq. ID	LIB3165-034-P1-K5-B8
Method	BLASTX
NCBI GI	g131167
BLAST score	224
E value	2.0e-18
Match length	112
% identity	52
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_100292_pir__S18348 photosystem I chain II precursor - wood tobacco >gi_19748_emb_CAA42623_ (X60008) PSI-D2 [Nicotiana sylvestris]

Seq. No.	222800
Seq. ID	LIB3165-034-P1-K5-B9
Method	BLASTX
NCBI GI	g3738316
BLAST score	141
E value	5.0e-09
Match length	39
% identity	72
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	222801
Seq. ID	LIB3165-034-P1-K5-C10
Method	BLASTX
NCBI GI	g2865623
BLAST score	385
E value	2.0e-37
Match length	90
% identity	82
NCBI Description	(AF045286) GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase [Arabidopsis thaliana]

Seq. No.	222802
Seq. ID	LIB3165-034-P1-K5-C11
Method	BLASTX
NCBI GI	g20729
BLAST score	332
E value	4.0e-31
Match length	99
% identity	70
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	222803
Seq. ID	LIB3165-034-P1-K5-C12
Method	BLASTX
NCBI GI	g1363479
BLAST score	366
E value	5.0e-35
Match length	99
% identity	74
NCBI Description	photosystem I protein psaL - cucumber >gi_801740_dbj_BAA09047_ (D50456) PsaL [Cucumis sativus]

Seq. No.	222804
Seq. ID	LIB3165-034-P1-K5-C3
Method	BLASTX
NCBI GI	g3269292
BLAST score	271
E value	6.0e-24
Match length	72
% identity	68
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	222805
Seq. ID	LIB3165-034-P1-K5-C5
Method	BLASTX
NCBI GI	g133867
BLAST score	469
E value	4.0e-47
Match length	107
% identity	84
NCBI Description	40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays]

Seq. No.	222806
Seq. ID	LIB3165-034-P1-K5-C7

Method	BLASTX
NCBI GI	g498038
BLAST score	356
E value	4.0e-34
Match length	96
% identity	64
NCBI Description	(L33792) lipid transfer protein [Senecio odorus]

Seq. No.	222807
Seq. ID	LIB3165-034-P1-K5-C9
Method	BLASTX
NCBI GI	g1352821
BLAST score	339
E value	5.0e-32
Match length	94
% identity	80
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222808
Seq. ID	LIB3165-034-P1-K5-D1
Method	BLASTX
NCBI GI	g4249385
BLAST score	360
E value	2.0e-34
Match length	104
% identity	65
NCBI Description	(AC005966) T2K10.11 [Arabidopsis thaliana]

Seq. No.	222809
Seq. ID	LIB3165-034-P1-K5-D10
Method	BLASTX
NCBI GI	g1781348
BLAST score	141
E value	3.0e-09
Match length	35
% identity	83
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No.	222810
Seq. ID	LIB3165-034-P1-K5-D11
Method	BLASTX
NCBI GI	g1168411
BLAST score	502
E value	5.0e-51
Match length	124
% identity	83
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	222811
Seq. ID	LIB3165-034-P1-K5-D12
Method	BLASTX
NCBI GI	g1352821

BLAST score	674
E value	4.0e-71
Match length	130
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222812
Seq. ID	LIB3165-034-P1-K5-D2
Method	BLASTX
NCBI GI	g3193285
BLAST score	270
E value	8.0e-24
Match length	76
% identity	64
NCBI Description	(AF069298) T14P8.18 gene product [Arabidopsis thaliana]

Seq. No.	222813
Seq. ID	LIB3165-034-P1-K5-D4
Method	BLASTX
NCBI GI	g3121825
BLAST score	311
E value	1.0e-28
Match length	121
% identity	64
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea]

Seq. No.	222814
Seq. ID	LIB3165-034-P1-K5-D5
Method	BLASTX
NCBI GI	g1352821
BLAST score	605
E value	5.0e-63
Match length	118
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222815
Seq. ID	LIB3165-034-P1-K5-D6
Method	BLASTX
NCBI GI	g1168408
BLAST score	175
E value	1.0e-12
Match length	38
% identity	92
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1 >gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828)

fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No.	222816
Seq. ID	LIB3165-034-P1-K5-D7
Method	BLASTX
NCBI GI	g430947
BLAST score	423
E value	9.0e-42
Match length	103
% identity	82
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	222817
Seq. ID	LIB3165-034-P1-K5-D9
Method	BLASTX
NCBI GI	g1352821
BLAST score	688
E value	8.0e-73
Match length	128
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222818
Seq. ID	LIB3165-034-P1-K5-E10
Method	BLASTX
NCBI GI	g3603456
BLAST score	538
E value	3.0e-55
Match length	109
% identity	30
NCBI Description	(AF088848) polyubiquitin [Capsicum chinense]

Seq. No.	222819
Seq. ID	LIB3165-034-P1-K5-E11
Method	BLASTX
NCBI GI	g1168411
BLAST score	332
E value	4.0e-31
Match length	89
% identity	79
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	222820
Seq. ID	LIB3165-034-P1-K5-E12
Method	BLASTX
NCBI GI	g228403
BLAST score	512
E value	4.0e-52
Match length	115
% identity	86
NCBI Description	glycolate oxidase [Lens culinaris]

Seq. No.	222821
Seq. ID	LIB3165-034-P1-K5-E2
Method	BLASTX
NCBI GI	g1781348
BLAST score	544
E value	6.0e-56
Match length	119
% identity	87
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No.	222822
Seq. ID	LIB3165-034-P1-K5-E3
Method	BLASTX
NCBI GI	g3914002
BLAST score	571
E value	4.0e-59
Match length	120
% identity	91
NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_2935279 (AF033862) Lon protease [Arabidopsis thaliana]

Seq. No.	222823
Seq. ID	LIB3165-034-P1-K5-E5
Method	BLASTX
NCBI GI	g2129921
BLAST score	184
E value	1.0e-13
Match length	36
% identity	97
NCBI Description	hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]

Seq. No.	222824
Seq. ID	LIB3165-034-P1-K5-E6
Method	BLASTX
NCBI GI	g2739046
BLAST score	162
E value	4.0e-11
Match length	89
% identity	37
NCBI Description	(AF024652) polyphosphoinositide binding protein Ssh2p [Glycine max]

Seq. No.	222825
Seq. ID	LIB3165-034-P1-K5-E7
Method	BLASTX
NCBI GI	g231536
BLAST score	383
E value	1.0e-37
Match length	115
% identity	73
NCBI Description	CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi_99683_pir__S22399 leucyl aminopeptidase (EC 3.4.11.1) - Arabidopsis thaliana >gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase

	[Arabidopsis thaliana] >gi_4115380 (AC005967) putative leucine aminopeptidase [Arabidopsis thaliana]
Seq. No.	222826
Seq. ID	LIB3165-034-P1-K5-E8
Method	BLASTX
NCBI GI	g4033838
BLAST score	325
E value	3.0e-30
Match length	117
% identity	60
NCBI Description	(Y18550) sigma-like factor [Arabidopsis thaliana]
Seq. No.	222827
Seq. ID	LIB3165-034-P1-K5-E9
Method	BLASTX
NCBI GI	g2499525
BLAST score	242
E value	2.0e-20
Match length	122
% identity	47
NCBI Description	INTESTINAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER) >gi_1663535 (U51153) intestinal sodium/dicarboxylate cotransporter [Rattus norvegicus]
Seq. No.	222828
Seq. ID	LIB3165-034-P1-K5-F1
Method	BLASTX
NCBI GI	g4455225
BLAST score	350
E value	3.0e-33
Match length	84
% identity	74
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]
Seq. No.	222829
Seq. ID	LIB3165-034-P1-K5-F10
Method	BLASTX
NCBI GI	g3603401
BLAST score	300
E value	2.0e-27
Match length	74
% identity	69
NCBI Description	(AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]
Seq. No.	222830
Seq. ID	LIB3165-034-P1-K5-F12
Method	BLASTX
NCBI GI	g430947
BLAST score	196
E value	3.0e-30
Match length	101
% identity	75
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	222831
Seq. ID	LIB3165-034-P1-K5-F2
Method	BLASTX
NCBI GI	g3121825
BLAST score	282
E value	3.0e-25
Match length	116
% identity	63
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea]

Seq. No.	222832
Seq. ID	LIB3165-034-P1-K5-F3
Method	BLASTX
NCBI GI	g1352821
BLAST score	532
E value	2.0e-54
Match length	107
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222833
Seq. ID	LIB3165-034-P1-K5-F5
Method	BLASTX
NCBI GI	g100616
BLAST score	243
E value	1.0e-20
Match length	55
% identity	85
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	222834
Seq. ID	LIB3165-034-P1-K5-F6
Method	BLASTX
NCBI GI	g289920
BLAST score	600
E value	2.0e-62
Match length	122
% identity	93
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222835
Seq. ID	LIB3165-034-P1-K5-G1
Method	BLASTX
NCBI GI	g430947
BLAST score	423
E value	1.0e-41

Match length 103
% identity 82
NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No. 222836
Seq. ID LIB3165-034-P1-K5-G10
Method BLASTX
NCBI GI g1619602
BLAST score 217
E value 1.0e-17
Match length 63
% identity 62
NCBI Description (Y08726) MtN3 [Medicago truncatula]

Seq. No. 222837
Seq. ID LIB3165-034-P1-K5-G12
Method BLASTX
NCBI GI g2791423
BLAST score 200
E value 1.0e-15
Match length 67
% identity 55
NCBI Description (AL021185) bcp [Mycobacterium tuberculosis]

Seq. No. 222838
Seq. ID LIB3165-034-P1-K5-G3
Method BLASTX
NCBI GI g4139264
BLAST score 449
E value 9.0e-45
Match length 84
% identity 100
NCBI Description (AF111812) actin [Brassica napus]

Seq. No. 222839
Seq. ID LIB3165-034-P1-K5-G4
Method BLASTX
NCBI GI g2979553
BLAST score 171
E value 3.0e-12
Match length 75
% identity 45
NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No. 222840
Seq. ID LIB3165-034-P1-K5-G7
Method BLASTX
NCBI GI g3928543
BLAST score 426
E value 4.0e-42
Match length 110
% identity 68
NCBI Description (AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No. 222841

Seq. ID	LIB3165-034-P1-K5-G8
Method	BLASTX
NCBI GI	g2979553
BLAST score	191
E value	1.0e-14
Match length	98
% identity	40
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	222842
Seq. ID	LIB3165-034-P1-K5-G9
Method	BLASTX
NCBI GI	g131384
BLAST score	115
E value	1.0e-08
Match length	58
% identity	69
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_81934_pir__S04132 photosystem II oxygen-evolving complex protein 1 precursor - garden pea >gi_20621_emb_CAA33408_ (X15350) precursor (AA -81 to 248) [Pisum sativum] >gi_344004_dbj_BAA02554_ (D13297) precursor for 33-kDa protein of photosystem II [Pisum sativum] >gi_226937_prf__1611461A O2 evolving complex 33kD protein [Arachis hypogaea]

Seq. No.	222843
Seq. ID	LIB3165-034-P1-K5-H1
Method	BLASTX
NCBI GI	g4324714
BLAST score	435
E value	2.0e-43
Match length	92
% identity	91
NCBI Description	(AF110771) ammonium transporter [Arabidopsis thaliana]

Seq. No.	222844
Seq. ID	LIB3165-034-P1-K5-H10
Method	BLASTX
NCBI GI	g3687224
BLAST score	141
E value	1.0e-08
Match length	87
% identity	46
NCBI Description	(AC005169) putative N-acetyl-gamma-glutamyl-phosphate reductase [Arabidopsis thaliana]

Seq. No.	222845
Seq. ID	LIB3165-034-P1-K5-H11
Method	BLASTX
NCBI GI	g1352821
BLAST score	537
E value	4.0e-55
Match length	109
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222846
Seq. ID	LIB3165-034-P1-K5-H12
Method	BLASTX
NCBI GI	g1181599
BLAST score	502
E value	5.0e-51
Match length	130
% identity	76
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.	222847
Seq. ID	LIB3165-034-P1-K5-H2
Method	BLASTX
NCBI GI	g4262250
BLAST score	400
E value	5.0e-39
Match length	115
% identity	75
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	222848
Seq. ID	LIB3165-034-P1-K5-H3
Method	BLASTX
NCBI GI	g4406530
BLAST score	237
E value	5.0e-20
Match length	92
% identity	58
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222849
Seq. ID	LIB3165-034-P1-K5-H4
Method	BLASTX
NCBI GI	g289920
BLAST score	587
E value	6.0e-61
Match length	121
% identity	92
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222850
Seq. ID	LIB3165-034-P1-K5-H6
Method	BLASTX
NCBI GI	g1352821
BLAST score	535
E value	8.0e-55
Match length	109
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222851
Seq. ID	LIB3165-034-P1-K5-H8
Method	BLASTX
NCBI GI	g1352821
BLAST score	406
E value	8.0e-40
Match length	88
% identity	89
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222852
Seq. ID	LIB3165-034-P1-K6-A1
Method	BLASTX
NCBI GI	g2879867
BLAST score	400
E value	5.0e-39
Match length	110
% identity	69
NCBI Description	(AL021816) 40s ribosomal protein S17 [Schizosaccharomyces pombe]

Seq. No.	222853
Seq. ID	LIB3165-034-P1-K6-A2
Method	BLASTX
NCBI GI	g2879867
BLAST score	390
E value	8.0e-38
Match length	113
% identity	65
NCBI Description	(AL021816) 40s ribosomal protein S17 [Schizosaccharomyces pombe]

Seq. No.	222854
Seq. ID	LIB3165-034-P1-K6-A3
Method	BLASTX
NCBI GI	g1706261
BLAST score	438
E value	2.0e-43
Match length	87
% identity	90
NCBI Description	CYSTEINE PROTEINASE 2 PRECURSOR >gi_2118129_pir__S59598 cysteine proteinase 2 precursor - maize >gi_644490_dbj_BAA08245_ (D45403) cysteine proteinase [Zea mays]

Seq. No.	222855
Seq. ID	LIB3165-034-P1-K6-A4
Method	BLASTX
NCBI GI	g68200
BLAST score	533

E value	1.0e-54
Match length	130
% identity	83
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	222856
Seq. ID	LIB3165-034-P1-K6-A6
Method	BLASTX
NCBI GI	g169039
BLAST score	592
E value	1.0e-61
Match length	121
% identity	92
NCBI Description	(M97477) aldolase [Pisum sativum]

Seq. No.	222857
Seq. ID	LIB3165-034-P1-K6-A7
Method	BLASTX
NCBI GI	g1354515
BLAST score	287
E value	9.0e-26
Match length	135
% identity	50
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	222858
Seq. ID	LIB3165-034-P1-K6-A8
Method	BLASTX
NCBI GI	g100200
BLAST score	591
E value	2.0e-61
Match length	128
% identity	67
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	222859
Seq. ID	LIB3165-034-P1-K6-A9
Method	BLASTX
NCBI GI	g3158474
BLAST score	242
E value	2.0e-20
Match length	64
% identity	77
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]

Seq. No.	222860
Seq. ID	LIB3165-034-P1-K6-B1
Method	BLASTX
NCBI GI	g121953
BLAST score	181
E value	2.0e-13
Match length	41
% identity	88
NCBI Description	HISTONE H1 >gi_81905_pir__S00033 histone H1.b - garden pea

>gi_20762_emb_CAA29123_ (X05636) H1 histone (AA 1-263) [Pisum sativum]

Seq. No.	222861
Seq. ID	LIB3165-034-P1-K6-B10
Method	BLASTX
NCBI GI	g81857
BLAST score	215
E value	2.0e-17
Match length	42
% identity	90
NCBI Description	IgE-dependent histamine-releasing factor homolog - alfalfa (fragment) >gi_19658_emb_CAA45349_ (X63872) translationally controlled tumor protein [Medicago sativa]

Seq. No.	222862
Seq. ID	LIB3165-034-P1-K6-B11
Method	BLASTX
NCBI GI	g2827755
BLAST score	425
E value	5.0e-42
Match length	107
% identity	76
NCBI Description	INORGANIC PYROPHOSPHATASE, VACUOLAR (PYROPHOSPHATE PHOSPHOHYDROLASE) (PPASE) >gi_951323 (U31467) pyrophosphatase [Vigna radiata]

Seq. No.	222863
Seq. ID	LIB3165-034-P1-K6-B12
Method	BLASTX
NCBI GI	g730850
BLAST score	145
E value	4.0e-09
Match length	126
% identity	29
NCBI Description	SUR2 PROTEIN (SYRINGOMYCIN RESPONSE PROTEIN 2) >gi_626942_pir__S48533 SUR2 protein - yeast (Saccharomyces cerevisiae) >gi_458718 (U07171) Sur2p [Saccharomyces cerevisiae] >gi_849215 (U28374) Sur2p: syringomycin response protein 2 [Saccharomyces cerevisiae] >gi_1786173 (U10427) Syr2p [Saccharomyces cerevisiae]

Seq. No.	222864
Seq. ID	LIB3165-034-P1-K6-B2
Method	BLASTX
NCBI GI	g68200
BLAST score	230
E value	4.0e-19
Match length	89
% identity	60
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	222865
Seq. ID	LIB3165-034-P1-K6-B3
Method	BLASTX

NCBI GI	g3914940
BLAST score	340
E value	5.0e-32
Match length	115
% identity	63
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_2529376 (L76556) sedoheptulose-1,7-bisphosphatase [Spinacia oleracea]

Seq. No.	222866
Seq. ID	LIB3165-034-P1-K6-B5
Method	BLASTX
NCBI GI	g129867
BLAST score	480
E value	2.0e-48
Match length	93
% identity	97
NCBI Description	CYTOCHROME B6-F COMPLEX SUBUNIT 4 (17 KD POLYPEPTIDE) >gi_2924273_emb_CAA77425_ (Z00044) cytochrome b/f complex subunit IV [Nicotiana tabacum]

Seq. No.	222867
Seq. ID	LIB3165-034-P1-K6-B6
Method	BLASTX
NCBI GI	g228210
BLAST score	578
E value	7.0e-60
Match length	133
% identity	80
NCBI Description	granule-bound starch synthase [Solanum tuberosum]

Seq. No.	222868
Seq. ID	LIB3165-034-P1-K6-B8
Method	BLASTX
NCBI GI	g4263525
BLAST score	309
E value	2.0e-28
Match length	92
% identity	67
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]

Seq. No.	222869
Seq. ID	LIB3165-034-P1-K6-B9
Method	BLASTX
NCBI GI	g3738316
BLAST score	332
E value	5.0e-31
Match length	89
% identity	70
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	222870
Seq. ID	LIB3165-034-P1-K6-C10
Method	BLASTX
NCBI GI	g2865623

BLAST score	502
E value	6.0e-51
Match length	117
% identity	83
NCBI Description	(AF045286) GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase [Arabidopsis thaliana]

Seq. No.	222871
Seq. ID	LIB3165-034-P1-K6-C11
Method	BLASTX
NCBI GI	g20729
BLAST score	346
E value	1.0e-32
Match length	102
% identity	71
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	222872
Seq. ID	LIB3165-034-P1-K6-C12
Method	BLASTX
NCBI GI	g1181599
BLAST score	303
E value	9.0e-28
Match length	88
% identity	68
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.	222873
Seq. ID	LIB3165-034-P1-K6-C3
Method	BLASTX
NCBI GI	g3269292
BLAST score	289
E value	5.0e-26
Match length	74
% identity	69
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	222874
Seq. ID	LIB3165-034-P1-K6-C5
Method	BLASTX
NCBI GI	g133867
BLAST score	339
E value	7.0e-32
Match length	112
% identity	62
NCBI Description	40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays]

Seq. No.	222875
Seq. ID	LIB3165-034-P1-K6-C7
Method	BLASTX
NCBI GI	g498038
BLAST score	416
E value	4.0e-42
Match length	128

% identity	64
NCBI Description	(L33792) lipid transfer protein [Senecio odorus]

Seq. No.	222876
Seq. ID	LIB3165-034-P1-K6-C9
Method	BLASTX
NCBI GI	g1352821
BLAST score	531
E value	2.0e-54
Match length	102
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222877
Seq. ID	LIB3165-034-P1-K6-D1
Method	BLASTX
NCBI GI	g4249385
BLAST score	402
E value	3.0e-39
Match length	112
% identity	66
NCBI Description	(AC005966) T2K10.11 [Arabidopsis thaliana]

Seq. No.	222878
Seq. ID	LIB3165-034-P1-K6-D11
Method	BLASTX
NCBI GI	g1168411
BLAST score	519
E value	5.0e-53
Match length	128
% identity	83
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	222879
Seq. ID	LIB3165-034-P1-K6-D12
Method	BLASTX
NCBI GI	g1352821
BLAST score	671
E value	8.0e-71
Match length	133
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222880
Seq. ID	LIB3165-034-P1-K6-D2
Method	BLASTX
NCBI GI	g3193285
BLAST score	226
E value	1.0e-18

09504016.071000

Match length	69
% identity	61
NCBI Description	(AF069298) T14P8.18 gene product [Arabidopsis thaliana]

Seq. No.	222881
Seq. ID	LIB3165-034-P1-K6-D3
Method	BLASTX
NCBI GI	g4249385
BLAST score	164
E value	2.0e-11
Match length	68
% identity	51
NCBI Description	(AC005966) T2K10.11 [Arabidopsis thaliana]

Seq. No.	222882
Seq. ID	LIB3165-034-P1-K6-D4
Method	BLASTX
NCBI GI	g3121825
BLAST score	319
E value	2.0e-29
Match length	104
% identity	70
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea]

Seq. No.	222883
Seq. ID	LIB3165-034-P1-K6-D5
Method	BLASTX
NCBI GI	g1352821
BLAST score	579
E value	5.0e-60
Match length	112
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222884
Seq. ID	LIB3165-034-P1-K6-D6
Method	BLASTX
NCBI GI	g1168408
BLAST score	173
E value	2.0e-12
Match length	37
% identity	95
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1 >gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828) fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No.	222885
Seq. ID	LIB3165-034-P1-K6-D7
Method	BLASTX
NCBI GI	g430947

BLAST score 450
E value 7.0e-45
Match length 109
% identity 82
NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No. 222886
Seq. ID LIB3165-034-P1-K6-D9
Method BLASTX
NCBI GI g1352821
BLAST score 690
E value 5.0e-73
Match length 131
% identity 95
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 222887
Seq. ID LIB3165-034-P1-K6-E1
Method BLASTX
NCBI GI g4490332
BLAST score 142
E value 9.0e-09
Match length 61
% identity 54
NCBI Description (AL035656) putative protein [Arabidopsis thaliana]

Seq. No. 222888
Seq. ID LIB3165-034-P1-K6-E10
Method BLASTX
NCBI GI g82426
BLAST score 585
E value 1.0e-60
Match length 121
% identity 46
NCBI Description ubiquitin precursor - barley (fragment) >gi_755763_emb_CAA27751_ (X04133) ubiquitin polyprecursor (171 aa) [Hordeum vulgare]

Seq. No. 222889
Seq. ID LIB3165-034-P1-K6-E11
Method BLASTX
NCBI GI g68200
BLAST score 328
E value 1.0e-30
Match length 88
% identity 78
NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No. 222890
Seq. ID LIB3165-034-P1-K6-E12

Method	BLASTX
NCBI GI	g228403
BLAST score	490
E value	1.0e-49
Match length	113
% identity	84
NCBI Description	glycolate oxidase [Lens culinaris]

Seq. No.	222891
Seq. ID	LIB3165-034-P1-K6-E2
Method	BLASTX
NCBI GI	g1781348
BLAST score	546
E value	4.0e-56
Match length	119
% identity	87
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No.	222892
Seq. ID	LIB3165-034-P1-K6-E3
Method	BLASTX
NCBI GI	g3914002
BLAST score	624
E value	3.0e-65
Match length	131
% identity	91
NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_2935279 (AF033862) Lon protease [Arabidopsis thaliana]

Seq. No.	222893
Seq. ID	LIB3165-034-P1-K6-E5
Method	BLASTX
NCBI GI	g2129921
BLAST score	191
E value	1.0e-14
Match length	36
% identity	100
NCBI Description	hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]

Seq. No.	222894
Seq. ID	LIB3165-034-P1-K6-E6
Method	BLASTX
NCBI GI	g2739046
BLAST score	163
E value	3.0e-11
Match length	89
% identity	37
NCBI Description	(AF024652) polyphosphoinositide binding protein Ssh2p [Glycine max]

Seq. No.	222895
Seq. ID	LIB3165-034-P1-K6-E7
Method	BLASTX
NCBI GI	g1483563
BLAST score	365

E value	6.0e-47
Match length	129
% identity	80
NCBI Description	(X99825) leucine aminopeptidase [Petroselinum crispum]

Seq. No.	222896
Seq. ID	LIB3165-034-P1-K6-E8
Method	BLASTX
NCBI GI	g4033838
BLAST score	330
E value	8.0e-31
Match length	114
% identity	61
NCBI Description	(Y18550) sigma-like factor [Arabidopsis thaliana]

Seq. No.	222897
Seq. ID	LIB3165-034-P1-K6-E9
Method	BLASTX
NCBI GI	g2499525
BLAST score	260
E value	1.0e-22
Match length	133
% identity	44
NCBI Description	INTESTINAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER) >gi_1663535 (U51153) intestinal sodium/dicarboxylate cotransporter [Rattus norvegicus]

Seq. No.	222898
Seq. ID	LIB3165-034-P1-K6-F1
Method	BLASTX
NCBI GI	g4455225
BLAST score	392
E value	4.0e-38
Match length	91
% identity	74
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	222899
Seq. ID	LIB3165-034-P1-K6-F10
Method	BLASTX
NCBI GI	g1168728
BLAST score	300
E value	3.0e-27
Match length	112
% identity	50
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_598071 (L37883) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	222900
Seq. ID	LIB3165-034-P1-K6-F12
Method	BLASTX
NCBI GI	g430947
BLAST score	445
E value	3.0e-44
Match length	110
% identity	80

NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	222901
Seq. ID	LIB3165-034-P1-K6-F2
Method	BLASTX
NCBI GI	g3121825
BLAST score	309
E value	2.0e-28
Match length	103
% identity	69
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea]

Seq. No.	222902
Seq. ID	LIB3165-034-P1-K6-F3
Method	BLASTX
NCBI GI	g1352821
BLAST score	605
E value	5.0e-63
Match length	120
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222903
Seq. ID	LIB3165-034-P1-K6-F5
Method	BLASTX
NCBI GI	g100616
BLAST score	236
E value	8.0e-20
Match length	54
% identity	85
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	222904
Seq. ID	LIB3165-034-P1-K6-F6
Method	BLASTX
NCBI GI	g289920
BLAST score	575
E value	2.0e-59
Match length	124
% identity	88
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222905
Seq. ID	LIB3165-034-P1-K6-F7
Method	BLASTX

NCBI GI	g289920
BLAST score	663
E value	7.0e-70
Match length	124
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222906
Seq. ID	LIB3165-034-P1-K6-G1
Method	BLASTX
NCBI GI	g430947
BLAST score	440
E value	1.0e-43
Match length	107
% identity	81
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	222907
Seq. ID	LIB3165-034-P1-K6-G10
Method	BLASTX
NCBI GI	g3747111
BLAST score	229
E value	6.0e-19
Match length	69
% identity	61
NCBI Description	(AF095641) MTN3 homolog [Arabidopsis thaliana]

Seq. No.	222908
Seq. ID	LIB3165-034-P1-K6-G12
Method	BLASTX
NCBI GI	g2791423
BLAST score	217
E value	1.0e-17
Match length	71
% identity	56
NCBI Description	(AL021185) bcp [Mycobacterium tuberculosis]

Seq. No.	222909
Seq. ID	LIB3165-034-P1-K6-G3
Method	BLASTX
NCBI GI	g1703115
BLAST score	420
E value	2.0e-41
Match length	84
% identity	93
NCBI Description	ACTIN 3 >gi_2129526_pir__S68112 actin 3 - Arabidopsis thaliana >gi_1145695 (U39480) actin [Arabidopsis thaliana] >gi_3236244 (AC004684) actin 3 protein [Arabidopsis thaliana]

Seq. No.	222910
Seq. ID	LIB3165-034-P1-K6-G4
Method	BLASTX
NCBI GI	g2979553
BLAST score	184

E value	1.0e-13
Match length	82
% identity	44
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	222911
Seq. ID	LIB3165-034-P1-K6-G7
Method	BLASTX
NCBI GI	g3928543
BLAST score	453
E value	6.0e-46
Match length	122
% identity	66
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	222912
Seq. ID	LIB3165-034-P1-K6-G8
Method	BLASTX
NCBI GI	g3257810
BLAST score	206
E value	3.0e-16
Match length	126
% identity	37
NCBI Description	(AP000006) 307aa long hypothetical phosphoglycerate dehydrogenase [Pyrococcus horikoshii]

Seq. No.	222913
Seq. ID	LIB3165-034-P1-K6-G9
Method	BLASTX
NCBI GI	g482311
BLAST score	111
E value	5.0e-10
Match length	67
% identity	54
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No.	222914
Seq. ID	LIB3165-034-P1-K6-H1
Method	BLASTX
NCBI GI	g4324714
BLAST score	459
E value	6.0e-46
Match length	128
% identity	72
NCBI Description	(AF110771) ammonium transporter [Arabidopsis thaliana]

Seq. No.	222915
Seq. ID	LIB3165-034-P1-K6-H11
Method	BLASTX
NCBI GI	g1352821
BLAST score	527
E value	7.0e-54
Match length	102
% identity	99

NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	222916
Seq. ID	LIB3165-034-P1-K6-H12
Method	BLASTX
NCBI GI	g1181599
BLAST score	394
E value	2.0e-38
Match length	107
% identity	73
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]
Seq. No.	222917
Seq. ID	LIB3165-034-P1-K6-H2
Method	BLASTX
NCBI GI	g4262250
BLAST score	410
E value	3.0e-40
Match length	117
% identity	75
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]
Seq. No.	222918
Seq. ID	LIB3165-034-P1-K6-H3
Method	BLASTX
NCBI GI	g4406530
BLAST score	350
E value	4.0e-33
Match length	116
% identity	65
NCBI Description	(AF126870) rubisco activase [Vigna radiata]
Seq. No.	222919
Seq. ID	LIB3165-034-P1-K6-H4
Method	BLASTX
NCBI GI	g289920
BLAST score	615
E value	3.0e-64
Match length	125
% identity	93
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]
Seq. No.	222920
Seq. ID	LIB3165-034-P1-K6-H6
Method	BLASTX
NCBI GI	g1352821
BLAST score	450
E value	7.0e-45
Match length	89
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

	ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222921
Seq. ID	LIB3165-034-P1-K6-H8
Method	BLASTX
NCBI GI	g1352821
BLAST score	379
E value	1.0e-36
Match length	102
% identity	71
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222922
Seq. ID	LIB3165-036-P1-K1-A1
Method	BLASTX
NCBI GI	g1076524
BLAST score	415
E value	7.0e-41
Match length	120
% identity	62
NCBI Description	chloroplast outer envelope protein OEP86 precursor - garden pea >gi_599958_emb_CAA83453_ (Z31581) chloroplast outer envelope protein 86 [Pisum sativum]

Seq. No.	222923
Seq. ID	LIB3165-036-P1-K1-A10
Method	BLASTX
NCBI GI	g3687303
BLAST score	215
E value	2.0e-17
Match length	95
% identity	41
NCBI Description	(AJ006377) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	222924
Seq. ID	LIB3165-036-P1-K1-A11
Method	BLASTX
NCBI GI	g2493689
BLAST score	287
E value	8.0e-26
Match length	59
% identity	93
NCBI Description	PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi_1070377_emb_CAA63670_ (X93203) 10 kDa phosphoprotein [Populus deltoides] >gi_2143326_emb_CAA73768_ (Y13328) 10kDa phosphoprotein [Populus deltoides]

Seq. No.	222925
Seq. ID	LIB3165-036-P1-K1-A12
Method	BLASTX

NCBI GI g1351408
BLAST score 460
E value 4.0e-46
Match length 121
% identity 73
NCBI Description VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) >gi_1076563_pir__S51117 cystein proteinase - sweet orange >gi_633185_emb_CAA87720_ (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi_1588548_prf__2208463A vascular processing protease [Citrus sinensis]

Seq. No. 222926
Seq. ID LIB3165-036-P1-K1-A3
Method BLASTX
NCBI GI g2495365
BLAST score 624
E value 3.0e-65
Match length 129
% identity 92
NCBI Description HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B heat shock protein HSP81-2 [Arabidopsis thaliana]

Seq. No. 222927
Seq. ID LIB3165-036-P1-K1-A4
Method BLASTX
NCBI GI g3033513
BLAST score 350
E value 4.0e-33
Match length 100
% identity 70
NCBI Description (AF041068) rubisco activase [Phaseolus vulgaris]

Seq. No. 222928
Seq. ID LIB3165-036-P1-K1-A5
Method BLASTX
NCBI GI g2501578
BLAST score 339
E value 7.0e-32
Match length 88
% identity 77
NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No. 222929
Seq. ID LIB3165-036-P1-K1-A7
Method BLASTX
NCBI GI g3914005
BLAST score 278
E value 2.0e-28
Match length 93
% identity 78
NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_1816586 (U85494) LON1 protease [Zea mays]

Seq. No. 222930

Seq. ID	LIB3165-036-P1-K1-A9
Method	BLASTX
NCBI GI	g4490748
BLAST score	155
E value	2.0e-10
Match length	36
% identity	67
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	222931
Seq. ID	LIB3165-036-P1-K1-B1
Method	BLASTX
NCBI GI	g131385
BLAST score	381
E value	9.0e-37
Match length	109
% identity	74
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN)

Seq. No.	222932
Seq. ID	LIB3165-036-P1-K1-B12
Method	BLASTX
NCBI GI	g3834310
BLAST score	349
E value	4.0e-33
Match length	71
% identity	94
NCBI Description	(AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122 come from this gene. [Arabidopsis thaliana]

Seq. No.	222933
Seq. ID	LIB3165-036-P1-K1-B3
Method	BLASTX
NCBI GI	g2924258
BLAST score	556
E value	2.0e-57
Match length	131
% identity	82
NCBI Description	(Z00044) RNA polymerase beta'' subunit [Nicotiana tabacum]

Seq. No.	222934
Seq. ID	LIB3165-036-P1-K1-B4
Method	BLASTX
NCBI GI	g289920
BLAST score	638
E value	7.0e-67
Match length	123
% identity	96
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222935
Seq. ID	LIB3165-036-P1-K1-B6

Method	BLASTX
NCBI GI	g289920
BLAST score	557
E value	4.0e-61
Match length	123
% identity	97
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222936
Seq. ID	LIB3165-036-P1-K1-B7
Method	BLASTX
NCBI GI	g4406530
BLAST score	349
E value	4.0e-33
Match length	93
% identity	76
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222937
Seq. ID	LIB3165-036-P1-K1-B9
Method	BLASTX
NCBI GI	g1170898
BLAST score	293
E value	8.0e-27
Match length	74
% identity	81
NCBI Description	MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR >gi_629659_pir__S44167 malate dehydrogenase, mitochondrial - cider tree >gi_473206_emb_CAA55383_ (X78800) mitochondrial malate dehydrogenase [Eucalyptus gunnii]

Seq. No.	222938
Seq. ID	LIB3165-036-P1-K1-C10
Method	BLASTX
NCBI GI	g228403
BLAST score	476
E value	6.0e-48
Match length	111
% identity	82
NCBI Description	glycolate oxidase [Lens culinaris]

Seq. No.	222939
Seq. ID	LIB3165-036-P1-K1-C11
Method	BLASTX
NCBI GI	g68200
BLAST score	456
E value	1.0e-45
Match length	115
% identity	80
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	222940
Seq. ID	LIB3165-036-P1-K1-C4
Method	BLASTX

NCBI GI	g4406530
BLAST score	152
E value	2.0e-10
Match length	60
% identity	53
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222941
Seq. ID	LIB3165-036-P1-K1-C7
Method	BLASTX
NCBI GI	g1332579
BLAST score	503
E value	4.0e-51
Match length	105
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	222942
Seq. ID	LIB3165-036-P1-K1-C9
Method	BLASTX
NCBI GI	g4512664
BLAST score	306
E value	4.0e-28
Match length	67
% identity	87
NCBI Description	(AC006931) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana] >gi_4544471_gb_AAD22378.1_AC006580_10 (AC006580) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana]

Seq. No.	222943
Seq. ID	LIB3165-036-P1-K1-D10
Method	BLASTX
NCBI GI	g3914603
BLAST score	588
E value	4.0e-61
Match length	126
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No.	222944
Seq. ID	LIB3165-036-P1-K1-D11
Method	BLASTX
NCBI GI	g430947
BLAST score	486
E value	4.0e-49
Match length	119
% identity	82
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	222945
Seq. ID	LIB3165-036-P1-K1-D12
Method	BLASTX

NCBI GI	g1781348
BLAST score	592
E value	1.0e-61
Match length	120
% identity	93
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No.	222946
Seq. ID	LIB3165-036-P1-K1-D2
Method	BLASTX
NCBI GI	g3850111
BLAST score	218
E value	1.0e-17
Match length	72
% identity	54
NCBI Description	(AL033388) hypothetical integral membrane protein, putative involvement in lipid metabolism [Schizosaccharomyces pombe]

Seq. No.	222947
Seq. ID	LIB3165-036-P1-K1-D3
Method	BLASTX
NCBI GI	g2970051
BLAST score	401
E value	4.0e-39
Match length	100
% identity	75
NCBI Description	(AB012110) ARG10 [Vigna radiata]

Seq. No.	222948
Seq. ID	LIB3165-036-P1-K1-D4
Method	BLASTX
NCBI GI	g1168411
BLAST score	381
E value	6.0e-37
Match length	100
% identity	80
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	222949
Seq. ID	LIB3165-036-P1-K1-D5
Method	BLASTX
NCBI GI	g20559
BLAST score	497
E value	2.0e-50
Match length	130
% identity	81
NCBI Description	(X13301) hsp70 (AA 6 - 651) [Petunia x hybrida]

Seq. No.	222950
Seq. ID	LIB3165-036-P1-K1-D6
Method	BLASTX
NCBI GI	g266944
BLAST score	560
E value	8.0e-58
Match length	114
% identity	91

NCBI Description	60S RIBOSOMAL PROTEIN L2 (L8) (RIBOSOMAL PROTEIN TL2) >gi_71078_pir__R5TOL8 ribosomal protein L8, cytosolic - tomato >gi_19343_emb_CAA45863_ (X64562) ribosomal protein L2 [Lycopersicon esculentum]
Seq. No.	222951
Seq. ID	LIB3165-036-P1-K1-D7
Method	BLASTX
NCBI GI	g100615
BLAST score	502
E value	5.0e-51
Match length	126
% identity	77
NCBI Description	ribulose-bisphosphate carboxylase activase A short form precursor - barley >gi_167091 (M55447) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]
Seq. No.	222952
Seq. ID	LIB3165-036-P1-K1-D8
Method	BLASTX
NCBI GI	g3063392
BLAST score	386
E value	2.0e-37
Match length	106
% identity	75
NCBI Description	(AB012932) Ca2+/H+ exchanger [Vigna radiata]
Seq. No.	222953
Seq. ID	LIB3165-036-P1-K1-D9
Method	BLASTX
NCBI GI	g4455180
BLAST score	255
E value	5.0e-22
Match length	106
% identity	51
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]
Seq. No.	222954
Seq. ID	LIB3165-036-P1-K1-E10
Method	BLASTX
NCBI GI	g4539351
BLAST score	185
E value	7.0e-14
Match length	51
% identity	63
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]
Seq. No.	222955
Seq. ID	LIB3165-036-P1-K1-E3
Method	BLASTX
NCBI GI	g100200
BLAST score	371
E value	1.0e-35
Match length	100
% identity	72
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	222956
Seq. ID	LIB3165-036-P1-K1-E4
Method	BLASTX
NCBI GI	g1352821
BLAST score	535
E value	7.0e-55
Match length	101
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222957
Seq. ID	LIB3165-036-P1-K1-E5
Method	BLASTX
NCBI GI	g2190551
BLAST score	272
E value	4.0e-24
Match length	56
% identity	89
NCBI Description	(AC001229) Similar to C. elegans hypothetical protein K07C5.6 (gb_Z71181). ESTs gb_H36844,gb_AA394956 come from this gene. [Arabidopsis thaliana]

Seq. No.	222958
Seq. ID	LIB3165-036-P1-K1-E7
Method	BLASTX
NCBI GI	g2129538
BLAST score	299
E value	3.0e-27
Match length	62
% identity	90
NCBI Description	AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232) AT103 [Arabidopsis thaliana]

Seq. No.	222959
Seq. ID	LIB3165-036-P1-K1-F1
Method	BLASTX
NCBI GI	g100616
BLAST score	419
E value	3.0e-41
Match length	113
% identity	73
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	222960
Seq. ID	LIB3165-036-P1-K1-F11
Method	BLASTX
NCBI GI	g4107276
BLAST score	651
E value	2.0e-68

Match length	125
% identity	89
NCBI Description	(X98506) acetyl-CoA synthetase [Solanum tuberosum]

Seq. No.	222961
Seq. ID	LIB3165-036-P1-K1-F2
Method	BLASTX
NCBI GI	g1181599
BLAST score	421
E value	2.0e-41
Match length	112
% identity	74
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.	222962
Seq. ID	LIB3165-036-P1-K1-F4
Method	BLASTX
NCBI GI	g1353352
BLAST score	183
E value	1.0e-13
Match length	48
% identity	75
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	222963
Seq. ID	LIB3165-036-P1-K1-F6
Method	BLASTX
NCBI GI	g2253415
BLAST score	418
E value	3.0e-41
Match length	81
% identity	90
NCBI Description	(AF007215) stress-induced cysteine proteinase [Lavatera thuringiaca]

Seq. No.	222964
Seq. ID	LIB3165-036-P1-K1-F8
Method	BLASTX
NCBI GI	g2129698
BLAST score	470
E value	3.0e-47
Match length	115
% identity	77
NCBI Description	protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana >gi_1054633_emb_CAA63387_ (X92728) protein kinase [Arabidopsis thaliana]

Seq. No.	222965
Seq. ID	LIB3165-036-P1-K1-G10
Method	BLASTX
NCBI GI	g4406530
BLAST score	312
E value	1.0e-28
Match length	108
% identity	62
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	222966
Seq. ID	LIB3165-036-P1-K1-G11
Method	BLASTX
NCBI GI	g3193286
BLAST score	179
E value	3.0e-13
Match length	55
% identity	58
NCBI Description	(AF069298) T14P8.22 gene product [Arabidopsis thaliana]

Seq. No.	222967
Seq. ID	LIB3165-036-P1-K1-G2
Method	BLASTX
NCBI GI	g445116
BLAST score	405
E value	8.0e-40
Match length	86
% identity	91
NCBI Description	light-harvesting complex IIa protein; [Hordeum vulgare]

Seq. No.	222968
Seq. ID	LIB3165-036-P1-K1-G3
Method	BLASTX
NCBI GI	g1532135
BLAST score	242
E value	2.0e-20
Match length	49
% identity	92
NCBI Description	(U49442) chloroplast mRNA-binding protein CSP41 precursor [Spinacia oleracea]

Seq. No.	222969
Seq. ID	LIB3165-036-P1-K1-G6
Method	BLASTX
NCBI GI	g3687652
BLAST score	577
E value	9.0e-60
Match length	119
% identity	94
NCBI Description	(AF047352) rubisco activase precursor [Datisca glomerata]

Seq. No.	222970
Seq. ID	LIB3165-036-P1-K1-G7
Method	BLASTX
NCBI GI	g1352821
BLAST score	565
E value	2.0e-58
Match length	113
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222971

Seq. ID	LIB3165-036-P1-K1-G9
Method	BLASTX
NCBI GI	g2829204
BLAST score	257
E value	3.0e-22
Match length	107
% identity	50
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	222972
Seq. ID	LIB3165-036-P1-K1-H10
Method	BLASTX
NCBI GI	g82080
BLAST score	489
E value	2.0e-49
Match length	121
% identity	79
NCBI Description	chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf__1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No.	222973
Seq. ID	LIB3165-036-P1-K1-H11
Method	BLASTX
NCBI GI	g267122
BLAST score	442
E value	5.0e-44
Match length	104
% identity	78
NCBI Description	THIOREDOXIN H-TYPE (TRX-H) >gi_478400_pir__JQ2242 thioredoxin h - Arabidopsis thaliana >gi_16552_emb_CAA78462_ (Z14084) Thioredoxin H [Arabidopsis thaliana] >gi_1388080 (U35827) thioredoxin h [Arabidopsis thaliana]

Seq. No.	222974
Seq. ID	LIB3165-036-P1-K1-H12
Method	BLASTX
NCBI GI	g4249382
BLAST score	397
E value	1.0e-38
Match length	91
% identity	82
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	222975
Seq. ID	LIB3165-036-P1-K1-H3
Method	BLASTX
NCBI GI	g100200
BLAST score	379
E value	1.0e-36
Match length	103
% identity	71
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	222976
Seq. ID	LIB3165-036-P1-K1-H4
Method	BLASTX
NCBI GI	g231610
BLAST score	285
E value	1.0e-25
Match length	105
% identity	61
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]

Seq. No.	222977
Seq. ID	LIB3165-036-P1-K1-H6
Method	BLASTX
NCBI GI	g2245005
BLAST score	260
E value	1.0e-22
Match length	103
% identity	53
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	222978
Seq. ID	LIB3165-037-P1-K1-A1
Method	BLASTX
NCBI GI	g1168411
BLAST score	471
E value	3.0e-47
Match length	113
% identity	86
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	222979
Seq. ID	LIB3165-037-P1-K1-A11
Method	BLASTX
NCBI GI	g115813
BLAST score	301
E value	2.0e-27
Match length	98
% identity	63
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE III PRECURSOR (CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	222980
Seq. ID	LIB3165-037-P1-K1-A4
Method	BLASTX
NCBI GI	g1895084
BLAST score	587
E value	6.0e-61
Match length	115
% identity	94
NCBI Description	(U89897) golgi associated protein se-wap41 [Zea mays]

Seq. No.	222981
Seq. ID	LIB3165-037-P1-K1-A5
Method	BLASTX
NCBI GI	g289920
BLAST score	675
E value	3.0e-71
Match length	130
% identity	96
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222982
Seq. ID	LIB3165-037-P1-K1-A7
Method	BLASTX
NCBI GI	g4559339
BLAST score	595
E value	7.0e-62
Match length	136
% identity	85
NCBI Description	(AC007087) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	222983
Seq. ID	LIB3165-037-P1-K1-A8
Method	BLASTX
NCBI GI	g3738285
BLAST score	273
E value	4.0e-24
Match length	69
% identity	74
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	222984
Seq. ID	LIB3165-037-P1-K1-A9
Method	BLASTX
NCBI GI	g3452497
BLAST score	589
E value	4.0e-61
Match length	134
% identity	86
NCBI Description	(Y17796) ketol-acid reductoisomerase [Pisum sativum]

Seq. No.	222985
Seq. ID	LIB3165-037-P1-K1-B1
Method	BLASTX
NCBI GI	g1171866
BLAST score	366
E value	5.0e-35
Match length	111
% identity	64
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR (COMPLEX I-20KD) (CI-20KD) >gi_629601_pir__S48826 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain PSST - wild cabbage >gi_562282_emb_CAA57725_ (X82274) PSST subunit of NADH: ubiquinone oxidoreductase [Brassica oleracea]

Seq. No.	222986

Seq. ID	LIB3165-037-P1-K1-B12
Method	BLASTX
NCBI GI	g3335355
BLAST score	529
E value	3.0e-54
Match length	109
% identity	27
NCBI Description	(AC004512) Match to polyubiquitin DNA gb_L05401 from A. thaliana. Contains insertion of mitochondrial NADH dehydrogenase gb_X82618 and gb_X98301. May be a pseudogene with an expressed insert. EST gb_AA586248 comes from this region. [Arabi

Seq. No.	222987
Seq. ID	LIB3165-037-P1-K1-B2
Method	BLASTX
NCBI GI	g2244847
BLAST score	284
E value	2.0e-25
Match length	88
% identity	61
NCBI Description	(Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No.	222988
Seq. ID	LIB3165-037-P1-K1-B4
Method	BLASTX
NCBI GI	g4545262
BLAST score	234
E value	1.0e-19
Match length	44
% identity	98
NCBI Description	(AF118230) metallothionein-like protein [Gossypium hirsutum]

Seq. No.	222989
Seq. ID	LIB3165-037-P1-K1-B5
Method	BLASTX
NCBI GI	g3694872
BLAST score	239
E value	2.0e-20
Match length	89
% identity	57
NCBI Description	(AF092547) profilin [Ricinus communis]

Seq. No.	222990
Seq. ID	LIB3165-037-P1-K1-B7
Method	BLASTX
NCBI GI	g1352821
BLAST score	555
E value	3.0e-57
Match length	105
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	222991
Seq. ID	LIB3165-037-P1-K1-B8
Method	BLASTX
NCBI GI	g3914605
BLAST score	552
E value	7.0e-57
Match length	122
% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase - apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica]

Seq. No.	222992
Seq. ID	LIB3165-037-P1-K1-C12
Method	BLASTX
NCBI GI	g2970051
BLAST score	461
E value	4.0e-46
Match length	118
% identity	74
NCBI Description	(AB012110) ARG10 [Vigna radiata]

Seq. No.	222993
Seq. ID	LIB3165-037-P1-K1-C7
Method	BLASTX
NCBI GI	g20729
BLAST score	368
E value	3.0e-35
Match length	104
% identity	72
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	222994
Seq. ID	LIB3165-037-P1-K1-C8
Method	BLASTX
NCBI GI	g289920
BLAST score	696
E value	1.0e-73
Match length	133
% identity	96
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	222995
Seq. ID	LIB3165-037-P1-K1-C9
Method	BLASTX
NCBI GI	g4262236
BLAST score	302
E value	1.0e-27
Match length	85
% identity	73
NCBI Description	(AC006200) putative ribose 5-phosphate isomerase

[Arabidopsis thaliana]

Seq. No.	222996
Seq. ID	LIB3165-037-P1-K1-D1
Method	BLASTX
NCBI GI	g20729
BLAST score	385
E value	3.0e-37
Match length	109
% identity	72
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	222997
Seq. ID	LIB3165-037-P1-K1-D4
Method	BLASTX
NCBI GI	g3738298
BLAST score	322
E value	6.0e-30
Match length	107
% identity	55
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana] >gi_4249394 (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.	222998
Seq. ID	LIB3165-037-P1-K1-D6
Method	BLASTX
NCBI GI	g120669
BLAST score	560
E value	9.0e-58
Match length	112
% identity	93
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	222999
Seq. ID	LIB3165-037-P1-K1-D7
Method	BLASTX
NCBI GI	g1814405
BLAST score	151
E value	8.0e-10
Match length	71
% identity	52
NCBI Description	(U84890) putative phosphate permease [Mesembryanthemum crystallinum]

Seq. No.	223000
Seq. ID	LIB3165-037-P1-K1-E1
Method	BLASTX
NCBI GI	g1352821
BLAST score	574
E value	2.0e-59
Match length	108
% identity	98

NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223001
Seq. ID	LIB3165-037-P1-K1-E12
Method	BLASTX
NCBI GI	g1168411
BLAST score	481
E value	2.0e-48
Match length	120
% identity	82
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	223002
Seq. ID	LIB3165-037-P1-K1-E2
Method	BLASTX
NCBI GI	g3738261
BLAST score	352
E value	5.0e-62
Match length	133
% identity	95
NCBI Description	(AB018412) chloroplast phosphoglycerate kinase [Populus nigra]

Seq. No.	223003
Seq. ID	LIB3165-037-P1-K1-E3
Method	BLASTX
NCBI GI	g2275196
BLAST score	437
E value	3.0e-43
Match length	88
% identity	94
NCBI Description	(AC002337) water stress-induced protein, WSI76 isolog [Arabidopsis thaliana]

Seq. No.	223004
Seq. ID	LIB3165-037-P1-K1-E5
Method	BLASTX
NCBI GI	g3738261
BLAST score	264
E value	6.0e-31
Match length	76
% identity	95
NCBI Description	(AB018412) chloroplast phosphoglycerate kinase [Populus nigra]

Seq. No.	223005
Seq. ID	LIB3165-037-P1-K1-E7
Method	BLASTX
NCBI GI	g1352821
BLAST score	539
E value	3.0e-55
Match length	106
% identity	94

NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	223006
Seq. ID	LIB3165-037-P1-K1-E9
Method	BLASTX
NCBI GI	g430947
BLAST score	448
E value	1.0e-44
Match length	109
% identity	82
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]
Seq. No.	223007
Seq. ID	LIB3165-037-P1-K1-F1
Method	BLASTX
NCBI GI	g4455256
BLAST score	544
E value	6.0e-56
Match length	110
% identity	87
NCBI Description	(AL035523) protein-methionine-S-oxide reductase [Arabidopsis thaliana]
Seq. No.	223008
Seq. ID	LIB3165-037-P1-K1-F12
Method	BLASTX
NCBI GI	g1352821
BLAST score	531
E value	2.0e-54
Match length	100
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	223009
Seq. ID	LIB3165-037-P1-K1-F3
Method	BLASTX
NCBI GI	g289920
BLAST score	528
E value	5.0e-54
Match length	107
% identity	93
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]
Seq. No.	223010
Seq. ID	LIB3165-037-P1-K1-F4
Method	BLASTX
NCBI GI	g3150412

BLAST score 336
E value 4.0e-35
Match length 95
% identity 76
NCBI Description (AC004165) putative Fe(II) transport protein [Arabidopsis thaliana] >gi_3420044 (AC004680) putative Fe(II) transport protein [Arabidopsis thaliana]

Seq. No. 223011
Seq. ID LIB3165-037-P1-K1-F5
Method BLASTX
NCBI GI g3080371
BLAST score 285
E value 6.0e-26
Match length 77
% identity 61
NCBI Description (AL022580) putative pectinacetylesterase protein [Arabidopsis thaliana]

Seq. No. 223012
Seq. ID LIB3165-037-P1-K1-F6
Method BLASTX
NCBI GI g3928099
BLAST score 282
E value 4.0e-25
Match length 136
% identity 24
NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

Seq. No. 223013
Seq. ID LIB3165-037-P1-K1-F8
Method BLASTX
NCBI GI g2828292
BLAST score 481
E value 1.0e-48
Match length 114
% identity 77
NCBI Description (AL021687) neoxanthin cleavage enzyme-like protein [Arabidopsis thaliana]

Seq. No. 223014
Seq. ID LIB3165-037-P1-K1-F9
Method BLASTX
NCBI GI g481131
BLAST score 293
E value 2.0e-26
Match length 111
% identity 51
NCBI Description sucrose transport protein SUC2 - Arabidopsis thaliana >gi_407092_emb_CAA53150_ (X75382) sucrose-proton symporter [Arabidopsis thaliana]

Seq. No. 223015
Seq. ID LIB3165-037-P1-K1-G11
Method BLASTX
NCBI GI g1403522
BLAST score 401

E value	4.0e-39
Match length	128
% identity	62
NCBI Description	(X57187) chitinase [Phaseolus vulgaris]

Seq. No.	223016
Seq. ID	LIB3165-037-P1-K1-G2
Method	BLASTX
NCBI GI	g3377802
BLAST score	427
E value	3.0e-42
Match length	102
% identity	79
NCBI Description	(AF075597) Similar to sucrose synthase; T2H3.8 [Arabidopsis thaliana]

Seq. No.	223017
Seq. ID	LIB3165-037-P1-K1-G4
Method	BLASTX
NCBI GI	g1709846
BLAST score	329
E value	1.0e-30
Match length	124
% identity	46
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_706853 (U04336) 22 kDa component of photosystem II [Lycopersicon esculentum]

Seq. No.	223018
Seq. ID	LIB3165-037-P1-K1-G5
Method	BLASTX
NCBI GI	g461550
BLAST score	218
E value	1.0e-17
Match length	47
% identity	98
NCBI Description	ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR >gi_81635_pir__B39732 H+-transporting ATP synthase (EC 3.6.1.34) gamma-1 chain precursor, chloroplast - Arabidopsis thaliana >gi_166632 (M61741) ATP synthase gamma-subunit [Arabidopsis thaliana]

Seq. No.	223019
Seq. ID	LIB3165-037-P1-K1-G7
Method	BLASTX
NCBI GI	g1495259
BLAST score	424
E value	6.0e-42
Match length	119
% identity	65
NCBI Description	(X97826) orf04 [Arabidopsis thaliana]

Seq. No.	223020
Seq. ID	LIB3165-037-P1-K1-G9
Method	BLASTX
NCBI GI	g4406530
BLAST score	342

E value 3.0e-32
Match length 92
% identity 76
NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 223021
Seq. ID LIB3165-037-P1-K1-H11
Method BLASTX
NCBI GI g4406530
BLAST score 350
E value 4.0e-33
Match length 116
% identity 65
NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 223022
Seq. ID LIB3165-037-P1-K1-H2
Method BLASTX
NCBI GI g4455251
BLAST score 341
E value 4.0e-32
Match length 103
% identity 64
NCBI Description (AL035523) magnesium-protoporphyrin IX methyltransferase-like protein [Arabidopsis thaliana]

Seq. No. 223023
Seq. ID LIB3165-037-P1-K1-H5
Method BLASTX
NCBI GI g3738285
BLAST score 159
E value 9.0e-11
Match length 52
% identity 56
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 223024
Seq. ID LIB3165-037-P1-K1-H9
Method BLASTX
NCBI GI g1352821
BLAST score 548
E value 2.0e-56
Match length 105
% identity 99
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223025
Seq. ID LIB3165-038-Q1-K1-A1
Method BLASTX
NCBI GI g3482918
BLAST score 590
E value 3.0e-61
Match length 134

% identity	84
NCBI Description	(AC003970) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	223026
Seq. ID	LIB3165-038-Q1-K1-A12
Method	BLASTX
NCBI GI	g1352821
BLAST score	557
E value	2.0e-57
Match length	108
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223027
Seq. ID	LIB3165-038-Q1-K1-A2
Method	BLASTX
NCBI GI	g20729
BLAST score	348
E value	5.0e-33
Match length	101
% identity	70
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	223028
Seq. ID	LIB3165-038-Q1-K1-A4
Method	BLASTX
NCBI GI	g2827551
BLAST score	199
E value	2.0e-15
Match length	60
% identity	67
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	223029
Seq. ID	LIB3165-038-Q1-K1-A5
Method	BLASTX
NCBI GI	g1352821
BLAST score	621
E value	6.0e-65
Match length	121
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223030
Seq. ID	LIB3165-038-Q1-K1-A6
Method	BLASTX
NCBI GI	g2979553
BLAST score	243

E value	1.0e-20
Match length	117
% identity	45
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	223031
Seq. ID	LIB3165-038-Q1-K1-A8
Method	BLASTX
NCBI GI	g3023752
BLAST score	223
E value	2.0e-18
Match length	92
% identity	55
NCBI Description	FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520) ferredoxin-I [Lycopersicon esculentum]

Seq. No.	223032
Seq. ID	LIB3165-038-Q1-K1-A9
Method	BLASTX
NCBI GI	g131147
BLAST score	150
E value	3.0e-10
Match length	53
% identity	53
NCBI Description	PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2 >gi_72675_pir__A2LVP7 photosystem I P700 apoprotein A2 - liverwort (Marchantia polymorpha) chloroplast >gi_11671_emb_CAA28084_ (X04465) psaB [Marchantia polymorpha]

Seq. No.	223033
Seq. ID	LIB3165-038-Q1-K1-B1
Method	BLASTX
NCBI GI	g4406530
BLAST score	357
E value	6.0e-34
Match length	117
% identity	65
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223034
Seq. ID	LIB3165-038-Q1-K1-B10
Method	BLASTX
NCBI GI	g2765081
BLAST score	395
E value	2.0e-38
Match length	119
% identity	66
NCBI Description	(Y10557) g5bf [Arabidopsis thaliana]

Seq. No.	223035
Seq. ID	LIB3165-038-Q1-K1-B11
Method	BLASTX
NCBI GI	g285317
BLAST score	157
E value	7.0e-11
Match length	77

% identity	53
NCBI Description	dihydrolipoamide dehydrogenase (EC 1.8.1.4) - garden pea

Seq. No.	223036
Seq. ID	LIB3165-038-Q1-K1-B3
Method	BLASTX
NCBI GI	g2827551
BLAST score	182
E value	2.0e-13
Match length	83
% identity	54
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	223037
Seq. ID	LIB3165-038-Q1-K1-B4
Method	BLASTX
NCBI GI	g586858
BLAST score	270
E value	8.0e-24
Match length	118
% identity	46
NCBI Description	HYPOTHETICAL 21.4 KD PROTEIN IN DACA-SERS INTERGENIC REGION >gi_2127020_pir__S66042 hypothetical protein - Bacillus subtilis >gi_467402_dbj_BAA05248_ (D26185) unknown [Bacillus subtilis] >gi_2632279_emb_CAB11788_ (Z99104) similar to hypothetical proteins [Bacillus subtilis]

Seq. No.	223038
Seq. ID	LIB3165-038-Q1-K1-B6
Method	BLASTX
NCBI GI	g2244905
BLAST score	388
E value	1.0e-37
Match length	112
% identity	61
NCBI Description	(Z97339) indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	223039
Seq. ID	LIB3165-038-Q1-K1-B7
Method	BLASTX
NCBI GI	g4559372
BLAST score	228
E value	6.0e-19
Match length	57
% identity	81
NCBI Description	(AC006585) putative CONSTANS protein [Arabidopsis thaliana]

Seq. No.	223040
Seq. ID	LIB3165-038-Q1-K1-B9
Method	BLASTX
NCBI GI	g1352821
BLAST score	193
E value	5.0e-15
Match length	51
% identity	76
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223041
Seq. ID	LIB3165-038-Q1-K1-C10
Method	BLASTX
NCBI GI	g4406530
BLAST score	328
E value	1.0e-30
Match length	91
% identity	75
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223042
Seq. ID	LIB3165-038-Q1-K1-C12
Method	BLASTX
NCBI GI	g1352821
BLAST score	481
E value	2.0e-48
Match length	98
% identity	92
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223043
Seq. ID	LIB3165-038-Q1-K1-C3
Method	BLASTX
NCBI GI	g3319921
BLAST score	283
E value	3.0e-25
Match length	105
% identity	58
NCBI Description	(AJ223388) Hev b 3 [Hevea brasiliensis] >gi_3319923_emb_CAA11304_ (AJ223389) Hev b 3 [Hevea brasiliensis] >gi_3319925_emb_CAA11305_ (AJ223390) Hev b 3 [Hevea brasiliensis] >gi_3818475 (AF051317) small rubber particle protein [Hevea brasiliensis]

Seq. No.	223044
Seq. ID	LIB3165-038-Q1-K1-C4
Method	BLASTX
NCBI GI	g2970051
BLAST score	316
E value	4.0e-29
Match length	75
% identity	81
NCBI Description	(AB012110) ARG10 [Vigna radiata]

Seq. No.	223045
Seq. ID	LIB3165-038-Q1-K1-C5
Method	BLASTX
NCBI GI	g2739375

BLAST score 192
E value 1.0e-14
Match length 102
% identity 47
NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

Seq. No. 223046
Seq. ID LIB3165-038-Q1-K1-C7
Method BLASTX
NCBI GI g133085
BLAST score 183
E value 1.0e-13
Match length 110
% identity 45
NCBI Description 50S RIBOSOMAL PROTEIN L12, CHLOROPLAST PRECURSOR (CL12) >gi_71136_pir__R7SP12 ribosomal protein L12, chloroplast - spinach >gi_170115 (J02849) ribosomal L12 precursor [Spinacia oleracea]

Seq. No. 223047
Seq. ID LIB3165-038-Q1-K1-C9
Method BLASTX
NCBI GI g3913651
BLAST score 569
E value 8.0e-59
Match length 139
% identity 76
NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR (FNR) >gi_2225993_emb_CAA74359_ (Y14032) ferredoxin--NADP(+) reductase [Nicotiana tabacum]

Seq. No. 223048
Seq. ID LIB3165-038-Q1-K1-D1
Method BLASTX
NCBI GI g1255954
BLAST score 534
E value 1.0e-54
Match length 118
% identity 83
NCBI Description (Z70677) thioredoxin [Ricinus communis]

Seq. No. 223049
Seq. ID LIB3165-038-Q1-K1-D11
Method BLASTX
NCBI GI g117822
BLAST score 392
E value 4.0e-38
Match length 74
% identity 100
NCBI Description CYTOCHROME B6 >gi_65635_pir__CBNT6 plastoquinol--plastocyanin reductase (EC 1.10.99.1) cytochrome b6 - common tobacco chloroplast >gi_11858_emb_CAA77375_ (Z00044) cytochrome b6 [Nicotiana tabacum] >gi_225226_prf__1211235BH cytochrome b6 [Nicotiana tabacum]

Seq. No. 223050

Seq. ID	LIB3165-038-Q1-K1-D12
Method	BLASTX
NCBI GI	g2493694
BLAST score	261
E value	1.0e-22
Match length	105
% identity	54
NCBI Description	PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII 6.1 KD PROTEIN) >gi_1076268_pir__S53025 photosystem II protein - spinach >gi_728716_emb_CAA59409_ (X85038) protein of photosystem II [Spinacia oleracea]

Seq. No.	223051
Seq. ID	LIB3165-038-Q1-K1-D7
Method	BLASTX
NCBI GI	g1352821
BLAST score	588
E value	5.0e-61
Match length	111
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223052
Seq. ID	LIB3165-038-Q1-K1-D8
Method	BLASTX
NCBI GI	g282865
BLAST score	627
E value	1.0e-65
Match length	136
% identity	87
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	223053
Seq. ID	LIB3165-038-Q1-K1-E1
Method	BLASTX
NCBI GI	g1352821
BLAST score	636
E value	1.0e-66
Match length	123
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223054
Seq. ID	LIB3165-038-Q1-K1-E10
Method	BLASTX
NCBI GI	g1360088

BLAST score	310
E value	2.0e-28
Match length	88
% identity	65
NCBI Description	(X97947) Zn finger protein [Nicotiana tabacum]

Seq. No.	223055
Seq. ID	LIB3165-038-Q1-K1-E11
Method	BLASTX
NCBI GI	g4056568
BLAST score	249
E value	2.0e-21
Match length	91
% identity	18
NCBI Description	(U90944) PDI-like protein [Zea mays]

Seq. No.	223056
Seq. ID	LIB3165-038-Q1-K1-E12
Method	BLASTX
NCBI GI	g3334138
BLAST score	267
E value	2.0e-23
Match length	99
% identity	53
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin [Glycine max]

Seq. No.	223057
Seq. ID	LIB3165-038-Q1-K1-E2
Method	BLASTX
NCBI GI	g4572673
BLAST score	483
E value	1.0e-48
Match length	117
% identity	77
NCBI Description	(AC006954) putative sarcosine oxidase [Arabidopsis thaliana]

Seq. No.	223058
Seq. ID	LIB3165-038-Q1-K1-E3
Method	BLASTX
NCBI GI	g945081
BLAST score	541
E value	2.0e-55
Match length	135
% identity	78
NCBI Description	(U31094) P21 [Petunia hybrida]

Seq. No.	223059
Seq. ID	LIB3165-038-Q1-K1-E6
Method	BLASTX
NCBI GI	g4512653
BLAST score	298
E value	4.0e-39
Match length	126
% identity	71
NCBI Description	(AC007048) unknown protein [Arabidopsis thaliana]

Seq. No.	223060
Seq. ID	LIB3165-038-Q1-K1-E7
Method	BLASTX
NCBI GI	g4406530
BLAST score	242
E value	4.0e-26
Match length	111
% identity	64
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223061
Seq. ID	LIB3165-038-Q1-K1-E8
Method	BLASTX
NCBI GI	g3668085
BLAST score	142
E value	8.0e-09
Match length	76
% identity	42
NCBI Description	(AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No.	223062
Seq. ID	LIB3165-038-Q1-K1-E9
Method	BLASTX
NCBI GI	g2811025
BLAST score	187
E value	8.0e-28
Match length	105
% identity	68
NCBI Description	ASPARTIC PROTEINASE PRECURSOR >gi_1944181_dbj_BAA19607_ (AB002695) aspartic endopeptidase [Cucurbita pepo]

Seq. No.	223063
Seq. ID	LIB3165-038-Q1-K1-F1
Method	BLASTX
NCBI GI	g1332579
BLAST score	509
E value	9.0e-57
Match length	121
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	223064
Seq. ID	LIB3165-038-Q1-K1-F11
Method	BLASTX
NCBI GI	g289920
BLAST score	680
E value	7.0e-72
Match length	128
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	223065
Seq. ID	LIB3165-038-Q1-K1-F2
Method	BLASTX
NCBI GI	g421843

BLAST score	457
E value	9.0e-46
Match length	111
% identity	74
NCBI Description	protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana >gi_217861_dbj_BAA01715_ (D10909) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	223066
Seq. ID	LIB3165-038-Q1-K1-F3
Method	BLASTX
NCBI GI	g464986
BLAST score	514
E value	2.0e-52
Match length	95
% identity	98
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No.	223067
Seq. ID	LIB3165-038-Q1-K1-F4
Method	BLASTX
NCBI GI	g3319921
BLAST score	184
E value	2.0e-21
Match length	109
% identity	54
NCBI Description	(AJ223388) Hev b 3 [Hevea brasiliensis] >gi_3319923_emb_CAA11304_ (AJ223389) Hev b 3 [Hevea brasiliensis] >gi_3319925_emb_CAA11305_ (AJ223390) Hev b 3 [Hevea brasiliensis] >gi_3818475 (AF051317) small rubber particle protein [Hevea brasiliensis]

Seq. No.	223068
Seq. ID	LIB3165-038-Q1-K1-F5
Method	BLASTX
NCBI GI	g20729
BLAST score	452
E value	1.0e-45
Match length	129
% identity	76
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	223069
Seq. ID	LIB3165-038-Q1-K1-F9
Method	BLASTX
NCBI GI	g2677828
BLAST score	393

E value	3.0e-38
Match length	114
% identity	67
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	223070
Seq. ID	LIB3165-038-Q1-K1-G1
Method	BLASTX
NCBI GI	g3822036
BLAST score	214
E value	3.0e-17
Match length	93
% identity	49
NCBI Description	(AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]

Seq. No.	223071
Seq. ID	LIB3165-038-Q1-K1-G12
Method	BLASTX
NCBI GI	g1723730
BLAST score	184
E value	1.0e-13
Match length	80
% identity	51
NCBI Description	HYPOTHETICAL 78.8 KD PROTEIN IN ATF2-RNR4 INTERGENIC REGION >gi_2131694_pir__S64492 hypothetical protein YGR178c - yeast (Saccharomyces cerevisiae) >gi_1323315_emb_CAA97204_ (Z72963) PBP1 [Saccharomyces cerevisiae] >gi_2737884 (U46931) Mrs16p [Saccharomyces cerevisiae]

Seq. No.	223072
Seq. ID	LIB3165-038-Q1-K1-G2
Method	BLASTX
NCBI GI	g1871577
BLAST score	314
E value	7.0e-29
Match length	115
% identity	49
NCBI Description	(Y11553) putative 21kD protein precursor [Medicago sativa]

Seq. No.	223073
Seq. ID	LIB3165-038-Q1-K1-G4
Method	BLASTX
NCBI GI	g3618316
BLAST score	226
E value	1.0e-18
Match length	113
% identity	44
NCBI Description	(AB001886) zinc finger protein [Oryza sativa]

Seq. No.	223074
Seq. ID	LIB3165-038-Q1-K1-G6
Method	BLASTX
NCBI GI	g3402713
BLAST score	415
E value	9.0e-41
Match length	122
% identity	69

NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]
Seq. No.	223075
Seq. ID	LIB3165-038-Q1-K1-G7
Method	BLASTX
NCBI GI	g3023752
BLAST score	281
E value	4.0e-25
Match length	111
% identity	54
NCBI Description	FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520) ferredoxin-I [Lycopersicon esculentum]
Seq. No.	223076
Seq. ID	LIB3165-038-Q1-K1-G8
Method	BLASTX
NCBI GI	g1617206
BLAST score	400
E value	5.0e-39
Match length	122
% identity	66
NCBI Description	(Z72489) CP12 [Pisum sativum]
Seq. No.	223077
Seq. ID	LIB3165-038-Q1-K1-G9
Method	BLASTX
NCBI GI	g3914603
BLAST score	561
E value	5.0e-58
Match length	118
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]
Seq. No.	223078
Seq. ID	LIB3165-038-Q1-K1-H1
Method	BLASTX
NCBI GI	g1352821
BLAST score	503
E value	1.0e-60
Match length	124
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	223079
Seq. ID	LIB3165-038-Q1-K1-H2
Method	BLASTX
NCBI GI	g2275196
BLAST score	272
E value	3.0e-34
Match length	81

% identity	95
NCBI Description	(AC002337) water stress-induced protein, WSI76 isolog [Arabidopsis thaliana]

Seq. No.	223080
Seq. ID	LIB3165-038-Q1-K1-H3
Method	BLASTX
NCBI GI	g1352821
BLAST score	622
E value	5.0e-65
Match length	117
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223081
Seq. ID	LIB3165-038-Q1-K1-H7
Method	BLASTX
NCBI GI	g1352821
BLAST score	424
E value	6.0e-42
Match length	90
% identity	91
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223082
Seq. ID	LIB3165-038-Q1-K1-H8
Method	BLASTX
NCBI GI	g1439609
BLAST score	521
E value	3.0e-53
Match length	105
% identity	98
NCBI Description	(U62778) delta-tonoplast intrinsic protein [Gossypium hirsutum]

Seq. No.	223083
Seq. ID	LIB3165-038-Q1-K1-H9
Method	BLASTX
NCBI GI	g2924520
BLAST score	601
E value	1.0e-62
Match length	130
% identity	88
NCBI Description	(AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]

Seq. No.	223084
Seq. ID	LIB3165-039-Q1-K1-A1
Method	BLASTX

NCBI GI	g166702
BLAST score	516
E value	1.0e-52
Match length	140
% identity	75
NCBI Description	(M64114) glyceraldehyde 3-phosphate dehydrogenase A subunit [Arabidopsis thaliana]

Seq. No.	223085
Seq. ID	LIB3165-039-Q1-K1-A10
Method	BLASTX
NCBI GI	g3023752
BLAST score	334
E value	3.0e-31
Match length	113
% identity	62
NCBI Description	FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520) ferredoxin-I [Lycopersicon esculentum]

Seq. No.	223086
Seq. ID	LIB3165-039-Q1-K1-A11
Method	BLASTX
NCBI GI	g1352821
BLAST score	535
E value	1.0e-55
Match length	110
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223087
Seq. ID	LIB3165-039-Q1-K1-A3
Method	BLASTX
NCBI GI	g3688174
BLAST score	426
E value	5.0e-42
Match length	111
% identity	74
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	223088
Seq. ID	LIB3165-039-Q1-K1-A4
Method	BLASTX
NCBI GI	g1169494
BLAST score	234
E value	2.0e-19
Match length	81
% identity	59
NCBI Description	ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >gi_2119915_pir__S60659 EF-Tu protein precursor - soybean >gi_949873_emb_CAA61444_ (X89058) EF-Tu protein [Glycine max]

Seq. No.	223089

Seq. ID	LIB3165-039-Q1-K1-A7
Method	BLASTX
NCBI GI	g3036944
BLAST score	580
E value	4.0e-60
Match length	126
% identity	95
NCBI Description	(AB012637) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	223090
Seq. ID	LIB3165-039-Q1-K1-A8
Method	BLASTX
NCBI GI	g1352821
BLAST score	586
E value	8.0e-61
Match length	110
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223091
Seq. ID	LIB3165-039-Q1-K1-A9
Method	BLASTX
NCBI GI	g167367
BLAST score	547
E value	3.0e-56
Match length	136
% identity	79
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	223092
Seq. ID	LIB3165-039-Q1-K1-B1
Method	BLASTX
NCBI GI	g3913295
BLAST score	311
E value	1.0e-28
Match length	118
% identity	55
NCBI Description	CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_602588_emb_CAA58218_ (X83217) caffeic O-methyltransferase [Prunus dulcis]

Seq. No.	223093
Seq. ID	LIB3165-039-Q1-K1-B10
Method	BLASTX
NCBI GI	g1781348
BLAST score	483
E value	1.0e-48
Match length	97
% identity	94
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No.	223094
Seq. ID	LIB3165-039-Q1-K1-B11
Method	BLASTX
NCBI GI	g4406814
BLAST score	456
E value	1.0e-45
Match length	107
% identity	81
NCBI Description	(AC006201) putative peptidyl-prolyl isomerase [Arabidopsis thaliana]

Seq. No.	223095
Seq. ID	LIB3165-039-Q1-K1-B2
Method	BLASTX
NCBI GI	g1702986
BLAST score	302
E value	6.0e-32
Match length	97
% identity	85
NCBI Description	14-3-3-LIKE PROTEIN GF14 CHI >gi_1255987 (U09377) GF14chi isoform [Arabidopsis thaliana] >gi_1256534 (L09112) GF14 chi chain [Arabidopsis thaliana]

Seq. No.	223096
Seq. ID	LIB3165-039-Q1-K1-B3
Method	BLASTX
NCBI GI	g166834
BLAST score	296
E value	8.0e-31
Match length	104
% identity	68
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	223097
Seq. ID	LIB3165-039-Q1-K1-B5
Method	BLASTX
NCBI GI	g3914605
BLAST score	695
E value	1.0e-73
Match length	141
% identity	92
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase - apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica]

Seq. No.	223098
Seq. ID	LIB3165-039-Q1-K1-B6
Method	BLASTX
NCBI GI	g2129511
BLAST score	657
E value	4.0e-69

Match length	141
% identity	89
NCBI Description	glycerate dehydrogenase (EC 1.1.1.29) splice form HPR1, microbody - cucurbit >gi_1304042_dbj_BAA08410_ (D49432) hydroxypyruvate reductase [Cucurbita sp.]

Seq. No.	223099
Seq. ID	LIB3165-039-Q1-K1-B7
Method	BLASTX
NCBI GI	g4115357
BLAST score	363
E value	1.0e-34
Match length	134
% identity	51
NCBI Description	(AC005957) hypothetical protein [Arabidopsis thaliana]

Seq. No.	223100
Seq. ID	LIB3165-039-Q1-K1-B8
Method	BLASTX
NCBI GI	g3420052
BLAST score	350
E value	4.0e-33
Match length	118
% identity	62
NCBI Description	(AC004680) putative ubiqinone reductase [Arabidopsis thaliana]

Seq. No.	223101
Seq. ID	LIB3165-039-Q1-K1-B9
Method	BLASTX
NCBI GI	g4406530
BLAST score	361
E value	2.0e-34
Match length	98
% identity	76
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223102
Seq. ID	LIB3165-039-Q1-K1-C1
Method	BLASTX
NCBI GI	g4406530
BLAST score	453
E value	4.0e-45
Match length	122
% identity	77
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223103
Seq. ID	LIB3165-039-Q1-K1-C10
Method	BLASTX
NCBI GI	g4566614
BLAST score	414
E value	1.0e-40
Match length	108
% identity	74
NCBI Description	(AF112887) actin depolymerizing factor [Populus alba x Populus tremula]

Seq. No.	223104
Seq. ID	LIB3165-039-Q1-K1-C3
Method	BLASTX
NCBI GI	g266893
BLAST score	730
E value	1.0e-77
Match length	141
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__S28172 ribulose-bisphosphate carboxylase activase - cucumber >gi_18284_emb_CAA47906_ (X67674) rubisco activase [Cucumis sativus]

Seq. No.	223105
Seq. ID	LIB3165-039-Q1-K1-C5
Method	BLASTX
NCBI GI	g294060
BLAST score	174
E value	2.0e-12
Match length	128
% identity	33
NCBI Description	(L06467) major latex protein [Papaver somniferum]

Seq. No.	223106
Seq. ID	LIB3165-039-Q1-K1-C7
Method	BLASTX
NCBI GI	g2244924
BLAST score	334
E value	3.0e-31
Match length	93
% identity	65
NCBI Description	(Z97339) glutaredoxin [Arabidopsis thaliana]

Seq. No.	223107
Seq. ID	LIB3165-039-Q1-K1-C8
Method	BLASTX
NCBI GI	g2500378
BLAST score	423
E value	1.0e-41
Match length	87
% identity	89
NCBI Description	60S RIBOSOMAL PROTEIN L37

Seq. No.	223108
Seq. ID	LIB3165-039-Q1-K1-D1
Method	BLASTX
NCBI GI	g1352821
BLAST score	641
E value	3.0e-67
Match length	124
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223109
Seq. ID	LIB3165-039-Q1-K1-D5
Method	BLASTX
NCBI GI	g1408471
BLAST score	531
E value	2.0e-54
Match length	117
% identity	82
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	223110
Seq. ID	LIB3165-039-Q1-K1-D6
Method	BLASTX
NCBI GI	g68200
BLAST score	531
E value	2.0e-54
Match length	131
% identity	82
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	223111
Seq. ID	LIB3165-039-Q1-K1-D7
Method	BLASTX
NCBI GI	g4406530
BLAST score	361
E value	2.0e-34
Match length	98
% identity	76
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223112
Seq. ID	LIB3165-039-Q1-K1-D8
Method	BLASTX
NCBI GI	g4559292
BLAST score	370
E value	2.0e-35
Match length	109
% identity	63
NCBI Description	(AF124148) trehalase 1 GMTRE1 [Glycine max]

Seq. No.	223113
Seq. ID	LIB3165-039-Q1-K1-D9
Method	BLASTX
NCBI GI	g4454458
BLAST score	186
E value	6.0e-14
Match length	125
% identity	43
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 223114

Seq. ID	LIB3165-039-Q1-K1-E11
Method	BLASTX
NCBI GI	g2677828
BLAST score	484
E value	8.0e-49
Match length	135
% identity	68
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	223115
Seq. ID	LIB3165-039-Q1-K1-E12
Method	BLASTX
NCBI GI	g228403
BLAST score	542
E value	1.0e-55
Match length	121
% identity	87
NCBI Description	glycolate oxidase [Lens culinaris]

Seq. No.	223116
Seq. ID	LIB3165-039-Q1-K1-E2
Method	BLASTX
NCBI GI	g1061040
BLAST score	644
E value	1.0e-67
Match length	128
% identity	91
NCBI Description	(X89867) sterol-C-methyltransferase [Arabidopsis thaliana] >gi_1587694_prf__2207220A sterol C-methyltransferase [Arabidopsis thaliana]

Seq. No.	223117
Seq. ID	LIB3165-039-Q1-K1-E3
Method	BLASTX
NCBI GI	g3953473
BLAST score	451
E value	6.0e-45
Match length	141
% identity	72
NCBI Description	(AC002328) F22O2.18 [Arabidopsis thaliana]

Seq. No.	223118
Seq. ID	LIB3165-039-Q1-K1-E4
Method	BLASTX
NCBI GI	g1788965
BLAST score	187
E value	5.0e-14
Match length	124
% identity	37
NCBI Description	(AE000347) orf, hypothetical protein [Escherichia coli]

Seq. No.	223119
Seq. ID	LIB3165-039-Q1-K1-E5
Method	BLASTX
NCBI GI	g421843
BLAST score	327
E value	2.0e-30

Match length	131
% identity	57
NCBI Description	protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana >gi_217861_dbj_BAA01715_ (D10909) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	223120
Seq. ID	LIB3165-039-Q1-K1-E7
Method	BLASTX
NCBI GI	g3687652
BLAST score	639
E value	5.0e-67
Match length	133
% identity	94
NCBI Description	(AF047352) rubisco activase precursor [Datisca glomerata]

Seq. No.	223121
Seq. ID	LIB3165-039-Q1-K1-E9
Method	BLASTX
NCBI GI	g3023752
BLAST score	346
E value	1.0e-32
Match length	113
% identity	63
NCBI Description	FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520) ferredoxin-I [Lycopersicon esculentum]

Seq. No.	223122
Seq. ID	LIB3165-039-Q1-K1-F1
Method	BLASTX
NCBI GI	g3059131
BLAST score	226
E value	1.0e-18
Match length	69
% identity	62
NCBI Description	(AJ000478) cytochrome P450 [Helianthus tuberosus]

Seq. No.	223123
Seq. ID	LIB3165-039-Q1-K1-F11
Method	BLASTX
NCBI GI	g1168411
BLAST score	525
E value	1.0e-53
Match length	127
% identity	83
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	223124
Seq. ID	LIB3165-039-Q1-K1-F12
Method	BLASTX
NCBI GI	g1354515
BLAST score	317
E value	3.0e-29
Match length	139
% identity	50
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	223125
Seq. ID	LIB3165-039-Q1-K1-F3
Method	BLASTX
NCBI GI	g2499966
BLAST score	159
E value	1.0e-10
Match length	107
% identity	42
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E A) >gi_632722_bbs_151001 (S72356) photosystem I subunit PSI-E [Nicotiana sylvestris, leaves, Peptide Chloroplast, 141 aa] [Nicotiana sylvestris]

Seq. No.	223126
Seq. ID	LIB3165-039-Q1-K1-F4
Method	BLASTX
NCBI GI	g231688
BLAST score	672
E value	1.0e-70
Match length	134
% identity	100
NCBI Description	CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC 1.11.1.6) - upland cotton >gi_18488_emb_CAA39998_ (X56675) subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No.	223127
Seq. ID	LIB3165-039-Q1-K1-F5
Method	BLASTX
NCBI GI	g1168411
BLAST score	147
E value	2.0e-09
Match length	90
% identity	43
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	223128
Seq. ID	LIB3165-039-Q1-K1-F6
Method	BLASTX
NCBI GI	g1352821
BLAST score	495
E value	4.0e-50
Match length	95
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223129
Seq. ID	LIB3165-039-Q1-K1-F7
Method	BLASTX
NCBI GI	g1354515
BLAST score	310
E value	2.0e-28
Match length	139

% identity	53
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	223130
Seq. ID	LIB3165-039-Q1-K1-F8
Method	BLASTX
NCBI GI	g1352821
BLAST score	531
E value	2.0e-54
Match length	103
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223131
Seq. ID	LIB3165-039-Q1-K1-G1
Method	BLASTX
NCBI GI	g2905643
BLAST score	265
E value	4.0e-23
Match length	108
% identity	48
NCBI Description	(AF045244) ribitol kinase [Klebsiella pneumoniae]

Seq. No.	223132
Seq. ID	LIB3165-039-Q1-K1-G11
Method	BLASTX
NCBI GI	g4415908
BLAST score	163
E value	3.0e-11
Match length	48
% identity	54
NCBI Description	(AC006282) unknown protein [Arabidopsis thaliana]

Seq. No.	223133
Seq. ID	LIB3165-039-Q1-K1-G12
Method	BLASTX
NCBI GI	g4455208
BLAST score	305
E value	7.0e-28
Match length	100
% identity	65
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	223134
Seq. ID	LIB3165-039-Q1-K1-G3
Method	BLASTX
NCBI GI	g3885513
BLAST score	329
E value	1.0e-30
Match length	68
% identity	87
NCBI Description	(AF084201) similar to chloroplast 50S ribosomal protein L31

[Medicago sativa]

Seq. No.	223135
Seq. ID	LIB3165-039-Q1-K1-G6
Method	BLASTX
NCBI GI	g1352821
BLAST score	590
E value	3.0e-61
Match length	110
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223136
Seq. ID	LIB3165-039-Q1-K1-G7
Method	BLASTX
NCBI GI	g131167
BLAST score	447
E value	2.0e-44
Match length	138
% identity	67
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_100292_pir__S18348 photosystem I chain II precursor - wood tobacco >gi_19748_emb_CAA42623_ (X60008) PSI-D2 [Nicotiana sylvestris]

Seq. No.	223137
Seq. ID	LIB3165-039-Q1-K1-G8
Method	BLASTX
NCBI GI	g421826
BLAST score	426
E value	5.0e-42
Match length	125
% identity	66
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	223138
Seq. ID	LIB3165-039-Q1-K1-H1
Method	BLASTX
NCBI GI	g3913651
BLAST score	381
E value	9.0e-37
Match length	92
% identity	76
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR (FNR) >gi_2225993_emb_CAA74359_ (Y14032) ferredoxin--NADP(+) reductase [Nicotiana tabacum]

Seq. No.	223139
Seq. ID	LIB3165-039-Q1-K1-H10
Method	BLASTX

NCBI GI	g1332579
BLAST score	507
E value	1.0e-67
Match length	140
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	223140
Seq. ID	LIB3165-039-Q1-K1-H11
Method	BLASTX
NCBI GI	g3914605
BLAST score	171
E value	2.0e-12
Match length	97
% identity	42
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase - apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica]

Seq. No.	223141
Seq. ID	LIB3165-039-Q1-K1-H3
Method	BLASTX
NCBI GI	g3417451
BLAST score	417
E value	3.0e-41
Match length	89
% identity	89
NCBI Description	(AB013728) light-harvesting chlorophyll a/b-binding protein of photosystem II [Cryptomeria japonica]

Seq. No.	223142
Seq. ID	LIB3165-039-Q1-K1-H5
Method	BLASTX
NCBI GI	g1352821
BLAST score	375
E value	5.0e-36
Match length	67
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223143
Seq. ID	LIB3165-039-Q1-K1-H6
Method	BLASTX
NCBI GI	g1352821
BLAST score	627
E value	1.0e-65
Match length	124
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

09960.0004

	ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	223144
Seq. ID	LIB3165-039-Q1-K1-H7
Method	BLASTX
NCBI GI	g68200
BLAST score	512
E value	4.0e-52
Match length	125
% identity	83
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]
Seq. No.	223145
Seq. ID	LIB3165-039-Q1-K1-H8
Method	BLASTX
NCBI GI	g1168411
BLAST score	500
E value	1.0e-50
Match length	124
% identity	82
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
Seq. No.	223146
Seq. ID	LIB3165-039-Q1-K1-H9
Method	BLASTX
NCBI GI	g100200
BLAST score	488
E value	3.0e-49
Match length	123
% identity	76
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato
Seq. No.	223147
Seq. ID	LIB3165-040-Q1-K1-A1
Method	BLASTX
NCBI GI	g1352821
BLAST score	666
E value	3.0e-70
Match length	125
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	223148
Seq. ID	LIB3165-040-Q1-K1-A10
Method	BLASTX
NCBI GI	g2618721
BLAST score	169
E value	6.0e-12
Match length	77

% identity	56
NCBI Description	(U49072) IAA16 [Arabidopsis thaliana]

Seq. No.	223149
Seq. ID	LIB3165-040-Q1-K1-A11
Method	BLASTX
NCBI GI	g4103987
BLAST score	414
E value	1.0e-50
Match length	122
% identity	84
NCBI Description	(AF030516) 5,10-methylenetetrahydrofolate dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum]

Seq. No.	223150
Seq. ID	LIB3165-040-Q1-K1-A12
Method	BLASTX
NCBI GI	g3355480
BLAST score	312
E value	9.0e-29
Match length	101
% identity	58
NCBI Description	(AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No.	223151
Seq. ID	LIB3165-040-Q1-K1-A5
Method	BLASTX
NCBI GI	g68200
BLAST score	468
E value	5.0e-47
Match length	115
% identity	82
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	223152
Seq. ID	LIB3165-040-Q1-K1-A6
Method	BLASTX
NCBI GI	g3913414
BLAST score	507
E value	2.0e-51
Match length	135
% identity	76
NCBI Description	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME 2 (ADOMETDC 2) (SAMDC 2) (SAMDC16) >gi_1155242 (U38527) S-adenosylmethionine decarboxylase 2 [Dianthus caryophyllus]

Seq. No.	223153
Seq. ID	LIB3165-040-Q1-K1-A7
Method	BLASTX
NCBI GI	g82188
BLAST score	383
E value	5.0e-37

Match length	114
% identity	69
NCBI Description	photosystem II oxygen-evolving complex protein 2 precursor - common tobacco (fragment) >gi_19896_emb_CAA41713_ (X58910) photosystem II 23 kDa polypeptide [Nicotiana tabacum]

Seq. No.	223154
Seq. ID	LIB3165-040-Q1-K1-B1
Method	BLASTX
NCBI GI	g1170897
BLAST score	311
E value	1.0e-28
Match length	86
% identity	72
NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi_1076276_pir__S52039 NAD-malate dehydrogenase - cucumber >gi_695311 (L31900) glyoxysomal malate dehydrogenase [Cucumis sativus]

Seq. No.	223155
Seq. ID	LIB3165-040-Q1-K1-B10
Method	BLASTX
NCBI GI	g1532135
BLAST score	601
E value	1.0e-62
Match length	138
% identity	83
NCBI Description	(U49442) chloroplast mRNA-binding protein CSP41 precursor [Spinacia oleracea]

Seq. No.	223156
Seq. ID	LIB3165-040-Q1-K1-B11
Method	BLASTX
NCBI GI	g3928099
BLAST score	288
E value	7.0e-26
Match length	139
% identity	23
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	223157
Seq. ID	LIB3165-040-Q1-K1-B3
Method	BLASTX
NCBI GI	g2213590
BLAST score	203
E value	7.0e-16
Match length	106
% identity	40
NCBI Description	(AC000348) T7N9.10 [Arabidopsis thaliana]

Seq. No.	223158
Seq. ID	LIB3165-040-Q1-K1-B5
Method	BLASTX
NCBI GI	g1076708
BLAST score	552
E value	8.0e-57

Match length	126
% identity	25
NCBI Description	seed tetraubiquitin - common sunflower >gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max] >gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max] >gi_556688_emb_CAA84440_ (Z34988) seed tetraubiquitin [Helianthus annuus] >gi_994785_dbj_BAA05085_ (D26092) Ubiquitin [Glycine max] >gi_4263514_gb_AAD15340_ (AC004044) putative polyubiquitin [Arabidopsis thaliana] >gi_1096513_prf__2111434A tetraubiquitin [Helianthus annuus]
Seq. No.	223159
Seq. ID	LIB3165-040-Q1-K1-B7
Method	BLASTX
NCBI GI	g117822
BLAST score	653
E value	1.0e-68
Match length	137
% identity	90
NCBI Description	CYTOCHROME B6 >gi_65635_pir__CBNT6 plastoquinol--plastocyanin reductase (EC 1.10.99.1) cytochrome b6 - common tobacco chloroplast >gi_11858_emb_CAA77375_ (Z00044) cytochrome b6 [Nicotiana tabacum] >gi_225226_prf__1211235BH cytochrome b6 [Nicotiana tabacum]
Seq. No.	223160
Seq. ID	LIB3165-040-Q1-K1-B8
Method	BLASTX
NCBI GI	g1419090
BLAST score	365
E value	7.0e-35
Match length	104
% identity	70
NCBI Description	(X94968) 37kDa chloroplast inner envelope membrane polypeptide precursor [Nicotiana tabacum]
Seq. No.	223161
Seq. ID	LIB3165-040-Q1-K1-B9
Method	BLASTX
NCBI GI	g1170507
BLAST score	172
E value	3.0e-12
Match length	45
% identity	80
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3) >gi_100276_pir__S22579 translation initiation factor eIF-4A - curled-leaved tobacco >gi_19699_emb_CAA43514_ (X61206) nicotiana eukaryotic translation initiation factor 4A [Nicotiana plumbaginifolia]
Seq. No.	223162
Seq. ID	LIB3165-040-Q1-K1-C1
Method	BLASTX
NCBI GI	g1354515
BLAST score	255

E value	5.0e-22
Match length	103
% identity	55
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	223163
Seq. ID	LIB3165-040-Q1-K1-C2
Method	BLASTX
NCBI GI	g1814403
BLAST score	660
E value	2.0e-69
Match length	140
% identity	89
NCBI Description	(U84889) methionine synthase [Mesembryanthemum crystallinum]

Seq. No.	223164
Seq. ID	LIB3165-040-Q1-K1-C4
Method	BLASTX
NCBI GI	g4490297
BLAST score	291
E value	2.0e-42
Match length	127
% identity	64
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	223165
Seq. ID	LIB3165-040-Q1-K1-C5
Method	BLASTX
NCBI GI	g1352821
BLAST score	398
E value	9.0e-39
Match length	107
% identity	76
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223166
Seq. ID	LIB3165-040-Q1-K1-C6
Method	BLASTX
NCBI GI	g166702
BLAST score	250
E value	3.0e-26
Match length	68
% identity	91
NCBI Description	(M64114) glyceraldehyde 3-phosphate dehydrogenase A subunit [Arabidopsis thaliana]

Seq. No.	223167
Seq. ID	LIB3165-040-Q1-K1-C7
Method	BLASTX
NCBI GI	g4115357
BLAST score	261

E value	1.0e-22
Match length	137
% identity	43
NCBI Description	(AC005957) hypothetical protein [Arabidopsis thaliana]

Seq. No.	223168
Seq. ID	LIB3165-040-Q1-K1-C8
Method	BLASTX
NCBI GI	g20729
BLAST score	508
E value	1.0e-51
Match length	134
% identity	78
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	223169
Seq. ID	LIB3165-040-Q1-K1-D1
Method	BLASTX
NCBI GI	g3914605
BLAST score	440
E value	1.0e-43
Match length	138
% identity	64
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase - apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica]

Seq. No.	223170
Seq. ID	LIB3165-040-Q1-K1-D2
Method	BLASTX
NCBI GI	g1652745
BLAST score	260
E value	1.0e-22
Match length	112
% identity	43
NCBI Description	(D90908) hypothetical protein [Synechocystis sp.]

Seq. No.	223171
Seq. ID	LIB3165-040-Q1-K1-D3
Method	BLASTX
NCBI GI	g3928760
BLAST score	215
E value	3.0e-17
Match length	104
% identity	47
NCBI Description	(AB011797) homolog to plastid-lipid-associated protein [Citrus unshiu]

Seq. No.	223172
Seq. ID	LIB3165-040-Q1-K1-D4
Method	BLASTX
NCBI GI	g289920
BLAST score	697
E value	8.0e-74

Match length	131
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	223173
Seq. ID	LIB3165-040-Q1-K1-D5
Method	BLASTX
NCBI GI	g1396054
BLAST score	136
E value	1.0e-08
Match length	39
% identity	67
NCBI Description	(D86180) phosphoribosylanthranilate transferase [Pisum sativum]

Seq. No.	223174
Seq. ID	LIB3165-040-Q1-K1-D7
Method	BLASTX
NCBI GI	g1352821
BLAST score	584
E value	1.0e-60
Match length	110
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223175
Seq. ID	LIB3165-040-Q1-K1-D8
Method	BLASTX
NCBI GI	g1170711
BLAST score	183
E value	9.0e-14
Match length	65
% identity	60
NCBI Description	SHAGGY RELATED PROTEIN KINASE ASK-ALPHA >gi_541901_pir__S41596 protein kinase ASK-alpha (EC 2.7.1.-) - Arabidopsis thaliana >gi_460832_emb_CAA53181_ (X75432) shaggy related kinase [Arabidopsis thaliana] >gi_1769889_emb_CAA48538_ (X68525) serine /threonine protein kinase [Arabidopsis thaliana]

Seq. No.	223176
Seq. ID	LIB3165-040-Q1-K1-D9
Method	BLASTX
NCBI GI	g3660471
BLAST score	636
E value	1.0e-66
Match length	135
% identity	88
NCBI Description	(AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

Seq. No.	223177

Seq. ID	LIB3165-040-Q1-K1-E11
Method	BLASTX
NCBI GI	g2388577
BLAST score	415
E value	9.0e-41
Match length	136
% identity	56
NCBI Description	(AC000098) Similar to Arabidopsis putative ion-channel PID:g2262157 (gb_AC002329). [Arabidopsis thaliana]

Seq. No.	223178
Seq. ID	LIB3165-040-Q1-K1-E2
Method	BLASTX
NCBI GI	g1709651
BLAST score	411
E value	3.0e-40
Match length	130
% identity	62
NCBI Description	PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209 plastocyanin a precursor - black poplar >gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus nigra]

Seq. No.	223179
Seq. ID	LIB3165-040-Q1-K1-E3
Method	BLASTX
NCBI GI	g505482
BLAST score	669
E value	2.0e-70
Match length	136
% identity	93
NCBI Description	(X64349) 33 kDa polypeptide of water-oxidizing complex of photosystem II [Nicotiana tabacum]

Seq. No.	223180
Seq. ID	LIB3165-040-Q1-K1-E4
Method	BLASTX
NCBI GI	g729668
BLAST score	300
E value	3.0e-27
Match length	70
% identity	84
NCBI Description	HISTONE H1 >gi_2147479_pir__S65059 histone H1, drought-inducible - Lycopersicon pennellii >gi_436823 (U01890) Solanum pennellii histone H1 [Solanum pennellii]

Seq. No.	223181
Seq. ID	LIB3165-040-Q1-K1-E8
Method	BLASTX
NCBI GI	g231688
BLAST score	664
E value	5.0e-72
Match length	133
% identity	100
NCBI Description	CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC 1.11.1.6) - upland cotton >gi_18488_emb_CAA39998_ (X56675) subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No.	223182
Seq. ID	LIB3165-040-Q1-K1-F10
Method	BLASTX
NCBI GI	g1255954
BLAST score	534
E value	1.0e-54
Match length	118
% identity	83
NCBI Description	(Z70677) thioredoxin [Ricinus communis]

Seq. No.	223183
Seq. ID	LIB3165-040-Q1-K1-F11
Method	BLASTX
NCBI GI	g1352821
BLAST score	249
E value	1.0e-24
Match length	72
% identity	85
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223184
Seq. ID	LIB3165-040-Q1-K1-F2
Method	BLASTX
NCBI GI	g2529668
BLAST score	652
E value	1.0e-68
Match length	140
% identity	87
NCBI Description	(AC002535) putative photolyase/blue-light receptor [Arabidopsis thaliana] >gi_3319288 (AF053366) photolyase/blue light photoreceptor PHR2 [Arabidopsis thaliana]

Seq. No.	223185
Seq. ID	LIB3165-040-Q1-K1-F3
Method	BLASTX
NCBI GI	g4539316
BLAST score	301
E value	2.0e-33
Match length	101
% identity	81
NCBI Description	(AL035679) putative fructose-bisphosphate aldolase [Arabidopsis thaliana]

Seq. No.	223186
Seq. ID	LIB3165-040-Q1-K1-F8
Method	BLASTX
NCBI GI	g131385
BLAST score	516
E value	9.0e-55
Match length	135
% identity	85

NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN)

Seq. No.	223187
Seq. ID	LIB3165-040-Q1-K1-G1
Method	BLASTX
NCBI GI	g1352821
BLAST score	643
E value	2.0e-67
Match length	120
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223188
Seq. ID	LIB3165-040-Q1-K1-G10
Method	BLASTX
NCBI GI	g2129752
BLAST score	344
E value	2.0e-32
Match length	87
% identity	68
NCBI Description	thioredoxin - Arabidopsis thaliana >gi_992964_emb_CAA84612_ (Z35475) thioredoxin [Arabidopsis thaliana]

Seq. No.	223189
Seq. ID	LIB3165-040-Q1-K1-G2
Method	BLASTX
NCBI GI	g289920
BLAST score	711
E value	2.0e-75
Match length	134
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	223190
Seq. ID	LIB3165-040-Q1-K1-G3
Method	BLASTX
NCBI GI	g1946367
BLAST score	507
E value	2.0e-51
Match length	118
% identity	81
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	223191
Seq. ID	LIB3165-040-Q1-K1-G4
Method	BLASTX
NCBI GI	g1707017
BLAST score	464
E value	6.0e-61
Match length	136

% identity	85
NCBI Description	(U78721) RNA helicase isolog [Arabidopsis thaliana]
Seq. No.	223192
Seq. ID	LIB3165-040-Q1-K1-G7
Method	BLASTX
NCBI GI	g3334113
BLAST score	333
E value	4.0e-31
Match length	89
% identity	74
NCBI Description	ACYL-COA-BINDING PROTEIN (ACBP) >gi_1006831 (U35015) acyl-CoA-binding protein [Gossypium hirsutum]
Seq. No.	223193
Seq. ID	LIB3165-040-Q1-K1-G8
Method	BLASTX
NCBI GI	g3292831
BLAST score	143
E value	7.0e-09
Match length	124
% identity	35
NCBI Description	(AL031018) putative serine/threonine kinase [Arabidopsis thaliana]
Seq. No.	223194
Seq. ID	LIB3165-040-Q1-K1-H1
Method	BLASTX
NCBI GI	g403160
BLAST score	333
E value	2.0e-43
Match length	110
% identity	74
NCBI Description	(L24497) ribulose 1,5-bisphosphate carboxylase small subunit [Pyrus malus X domestica]
Seq. No.	223195
Seq. ID	LIB3165-040-Q1-K1-H10
Method	BLASTX
NCBI GI	g4206206
BLAST score	226
E value	1.0e-18
Match length	105
% identity	44
NCBI Description	(AF071527) putative M-type thioredoxin [Arabidopsis thaliana] >gi_4263039_gb_AAD15308_ (AC005142) putative M-type thioredoxin [Arabidopsis thaliana]
Seq. No.	223196
Seq. ID	LIB3165-040-Q1-K1-H12
Method	BLASTX
NCBI GI	g2864613
BLAST score	349
E value	5.0e-33
Match length	127
% identity	51
NCBI Description	(AL021811) S-receptor kinase -like protein [Arabidopsis

thaliana] >gi_4049333_emb_CAA22558_ (AL034567) S-receptor kinase-like protein [Arabidopsis thaliana]

Seq. No.	223197
Seq. ID	LIB3165-040-Q1-K1-H2
Method	BLASTX
NCBI GI	g231610
BLAST score	356
E value	7.0e-34
Match length	118
% identity	65
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]

Seq. No.	223198
Seq. ID	LIB3165-040-Q1-K1-H3
Method	BLASTX
NCBI GI	g3869088
BLAST score	583
E value	2.0e-60
Match length	115
% identity	97
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No.	223199
Seq. ID	LIB3165-040-Q1-K1-H5
Method	BLASTX
NCBI GI	g3885884
BLAST score	585
E value	1.0e-60
Match length	117
% identity	92
NCBI Description	(AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No.	223200
Seq. ID	LIB3165-040-Q1-K1-H8
Method	BLASTX
NCBI GI	g119748
BLAST score	529
E value	4.0e-54
Match length	114
% identity	91
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_67241_pir__PASPY fructose-bisphosphatase (EC 3.1.3.11), cytosolic - spinach >gi_21245_emb_CAA43860_ (X61690) fructose-bisphosphatase [Spinacia oleracea]

Seq. No.	223201
Seq. ID	LIB3165-040-Q1-K1-H9
Method	BLASTX
NCBI GI	g4454472
BLAST score	156
E value	1.0e-10

Match length	94
% identity	40
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	223202
Seq. ID	LIB3165-041-Q1-K1-A10
Method	BLASTX
NCBI GI	g4099835
BLAST score	416
E value	7.0e-41
Match length	112
% identity	63
NCBI Description	(U90266) bifunctional nuclease [Zinnia elegans]

Seq. No.	223203
Seq. ID	LIB3165-041-Q1-K1-A4
Method	BLASTX
NCBI GI	g1781348
BLAST score	291
E value	2.0e-26
Match length	64
% identity	86
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No.	223204
Seq. ID	LIB3165-041-Q1-K1-A7
Method	BLASTX
NCBI GI	g587564
BLAST score	315
E value	2.0e-29
Match length	83
% identity	73
NCBI Description	(X80235) mitochondrial processing peptidase [Solanum tuberosum]

Seq. No.	223205
Seq. ID	LIB3165-041-Q1-K1-A8
Method	BLASTX
NCBI GI	g417544
BLAST score	590
E value	3.0e-61
Match length	112
% identity	98
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD PROTEIN) (PSI-D) (PS I SUBUNIT 5) >gi_320209_pir__A60695 photosystem I chain II precursor - cucumber >gi_625966_pir__JQ2132 photosystem I complex 20K protein precursor - cucumber >gi_227772_prf__1710320A photosystem I 20kD protein [Cucumis sativus]

Seq. No.	223206
Seq. ID	LIB3165-041-Q1-K1-A9
Method	BLASTX
NCBI GI	g4127456
BLAST score	334
E value	3.0e-31

09034005.1001000

Match length 117
% identity 62
NCBI Description (AJ010818) Cpn21 protein [Arabidopsis thaliana]

Seq. No. 223207
Seq. ID LIB3165-041-Q1-K1-B10
Method BLASTX
NCBI GI g4091806
BLAST score 545
E value 5.0e-56
Match length 128
% identity 82
NCBI Description (AF052585) CONSTANS-like protein 2 [Malus domestica]

Seq. No. 223208
Seq. ID LIB3165-041-Q1-K1-B2
Method BLASTX
NCBI GI g4090943
BLAST score 305
E value 7.0e-28
Match length 123
% identity 46
NCBI Description (AF029984) COP1 homolog [Lycopersicon esculentum]

Seq. No. 223209
Seq. ID LIB3165-041-Q1-K1-B6
Method BLASTX
NCBI GI g3885884
BLAST score 523
E value 2.0e-53
Match length 105
% identity 90
NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No. 223210
Seq. ID LIB3165-041-Q1-K1-B7
Method BLASTX
NCBI GI g1353352
BLAST score 320
E value 1.0e-29
Match length 90
% identity 73
NCBI Description (U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No. 223211
Seq. ID LIB3165-041-Q1-K1-C10
Method BLASTX
NCBI GI g2980770
BLAST score 395
E value 1.0e-38
Match length 84
% identity 88
NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No. 223212
Seq. ID LIB3165-041-Q1-K1-C11

Method	BLASTX
NCBI GI	g2262164
BLAST score	168
E value	9.0e-12
Match length	64
% identity	59
NCBI Description	(AC002329) putative obtusifoliol 14-alpha demethylase [Arabidopsis thaliana]

Seq. No.	223213
Seq. ID	LIB3165-041-Q1-K1-C12
Method	BLASTX
NCBI GI	g2262164
BLAST score	157
E value	2.0e-10
Match length	64
% identity	58
NCBI Description	(AC002329) putative obtusifoliol 14-alpha demethylase [Arabidopsis thaliana]

Seq. No.	223214
Seq. ID	LIB3165-041-Q1-K1-C8
Method	BLASTX
NCBI GI	g3914603
BLAST score	665
E value	4.0e-70
Match length	132
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No.	223215
Seq. ID	LIB3165-041-Q1-K1-D10
Method	BLASTX
NCBI GI	g289920
BLAST score	743
E value	3.0e-79
Match length	140
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	223216
Seq. ID	LIB3165-041-Q1-K1-D11
Method	BLASTX
NCBI GI	g3980394
BLAST score	182
E value	2.0e-13
Match length	94
% identity	46
NCBI Description	(AC004561) putative zinc transporter [Arabidopsis thaliana]

Seq. No.	223217
Seq. ID	LIB3165-041-Q1-K1-D2
Method	BLASTX

NCBI GI	g289920
BLAST score	242
E value	4.0e-25
Match length	80
% identity	76
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	223218
Seq. ID	LIB3165-041-Q1-K1-D4
Method	BLASTX
NCBI GI	g115813
BLAST score	309
E value	1.0e-51
Match length	140
% identity	73
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE III PRECURSOR (CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	223219
Seq. ID	LIB3165-041-Q1-K1-D7
Method	BLASTX
NCBI GI	g3288821
BLAST score	318
E value	1.0e-29
Match length	99
% identity	64
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana]

Seq. No.	223220
Seq. ID	LIB3165-041-Q1-K1-D8
Method	BLASTX
NCBI GI	g4406530
BLAST score	369
E value	2.0e-35
Match length	123
% identity	64
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223221
Seq. ID	LIB3165-041-Q1-K1-E1
Method	BLASTX
NCBI GI	g126334
BLAST score	171
E value	4.0e-12
Match length	82
% identity	46
NCBI Description	LIPASE PRECURSOR (TRIACYLGLYCEROL LIPASE) >gi_79925_pir__A24075 lipase precursor - Staphylococcus hyicus >gi_47136_emb_CAA26602_ (X02844) precursor [Staphylococcus hyicus]

Seq. No.	223222
Seq. ID	LIB3165-041-Q1-K1-E10
Method	BLASTX

NCBI GI	g3165581
BLAST score	187
E value	5.0e-14
Match length	106
% identity	39
NCBI Description	(AF067942) similar to lysosomal acid lipases (SW:P38571) [Caenorhabditis elegans]

Seq. No.	223223
Seq. ID	LIB3165-041-Q1-K1-E2
Method	BLASTX
NCBI GI	g3660471
BLAST score	532
E value	1.0e-54
Match length	116
% identity	84
NCBI Description	(AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

Seq. No.	223224
Seq. ID	LIB3165-041-Q1-K1-E7
Method	BLASTX
NCBI GI	g1352821
BLAST score	585
E value	1.0e-60
Match length	109
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223225
Seq. ID	LIB3165-041-Q1-K1-E8
Method	BLASTX
NCBI GI	g4220477
BLAST score	281
E value	4.0e-25
Match length	113
% identity	56
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	223226
Seq. ID	LIB3165-041-Q1-K1-F1
Method	BLASTX
NCBI GI	g1708313
BLAST score	555
E value	4.0e-57
Match length	117
% identity	95
NCBI Description	HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi_999396_bbs_163637 (S77849) heat-shock Protein=HSP81-3 [Arabidopsis thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis thaliana]

Seq. No.	223227

Seq. ID	LIB3165-041-Q1-K1-F7
Method	BLASTX
NCBI GI	g1352821
BLAST score	630
E value	6.0e-66
Match length	116
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223228
Seq. ID	LIB3165-041-Q1-K1-F8
Method	BLASTX
NCBI GI	g1352821
BLAST score	554
E value	5.0e-57
Match length	107
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223229
Seq. ID	LIB3165-041-Q1-K1-G5
Method	BLASTX
NCBI GI	g2501568
BLAST score	163
E value	3.0e-11
Match length	54
% identity	52
NCBI Description	HYPOTHETICAL 28.8 KD PROTEIN SLL0506 >gi_1001342_dbj_BAA10829_ (D64006) hypothetical protein [Synechocystis sp.]

Seq. No.	223230
Seq. ID	LIB3165-041-Q1-K1-G8
Method	BLASTX
NCBI GI	g3292824
BLAST score	297
E value	6.0e-27
Match length	77
% identity	75
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	223231
Seq. ID	LIB3165-041-Q1-K1-G9
Method	BLASTX
NCBI GI	g289920
BLAST score	605
E value	4.0e-63
Match length	112
% identity	100

NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	223232
Seq. ID	LIB3165-041-Q1-K1-H10
Method	BLASTX
NCBI GI	g3426043
BLAST score	595
E value	8.0e-62
Match length	134
% identity	77
NCBI Description	(AC005168) putative choline kinase [Arabidopsis thaliana]

Seq. No.	223233
Seq. ID	LIB3165-041-Q1-K1-H5
Method	BLASTX
NCBI GI	g2995384
BLAST score	162
E value	1.0e-11
Match length	44
% identity	73
NCBI Description	(AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No.	223234
Seq. ID	LIB3165-041-Q1-K1-H7
Method	BLASTX
NCBI GI	g2088651
BLAST score	419
E value	3.0e-41
Match length	125
% identity	63
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	223235
Seq. ID	LIB3165-041-Q1-K1-H8
Method	BLASTX
NCBI GI	g2815246
BLAST score	225
E value	2.0e-18
Match length	55
% identity	73
NCBI Description	(X95709) class I type 2 metallothionein [Cicer arietinum]

Seq. No.	223236
Seq. ID	LIB3165-041-Q1-K1-H9
Method	BLASTX
NCBI GI	g2969887
BLAST score	454
E value	3.0e-45
Match length	138
% identity	65
NCBI Description	(Y16766) sucrose/H+ symporter [Daucus carota] >gi_2969889_emb_CAA76368_ (Y16767) sucrose/H+ symporter [Daucus carota]

Seq. No.	223237

Seq. ID	LIB3165-042-Q1-K1-A10
Method	BLASTX
NCBI GI	g1352821
BLAST score	342
E value	2.0e-32
Match length	67
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223238
Seq. ID	LIB3165-042-Q1-K1-A11
Method	BLASTX
NCBI GI	g2864617
BLAST score	141
E value	1.0e-08
Match length	110
% identity	36
NCBI Description	(AL021811) H+-transporting ATP synthase chain9 - like protein [Arabidopsis thaliana]

Seq. No.	223239
Seq. ID	LIB3165-042-Q1-K1-A12
Method	BLASTX
NCBI GI	g266893
BLAST score	699
E value	5.0e-74
Match length	134
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__S28172 ribulose-bisphosphate carboxylase activase - cucumber >gi_18284_emb_CAA47906_ (X67674) rubisco activase [Cucumis sativus]

Seq. No.	223240
Seq. ID	LIB3165-042-Q1-K1-A3
Method	BLASTX
NCBI GI	g1353352
BLAST score	167
E value	3.0e-12
Match length	71
% identity	52
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	223241
Seq. ID	LIB3165-042-Q1-K1-A4
Method	BLASTX
NCBI GI	g430947
BLAST score	507
E value	2.0e-51
Match length	128
% identity	80

NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]
Seq. No.	223242
Seq. ID	LIB3165-042-Q1-K1-A6
Method	BLASTX
NCBI GI	g131385
BLAST score	463
E value	2.0e-46
Match length	116
% identity	83
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN)
Seq. No.	223243
Seq. ID	LIB3165-042-Q1-K1-A8
Method	BLASTX
NCBI GI	g1354515
BLAST score	213
E value	2.0e-17
Match length	82
% identity	61
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]
Seq. No.	223244
Seq. ID	LIB3165-042-Q1-K1-B12
Method	BLASTX
NCBI GI	g4455177
BLAST score	271
E value	7.0e-24
Match length	102
% identity	53
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]
Seq. No.	223245
Seq. ID	LIB3165-042-Q1-K1-B2
Method	BLASTX
NCBI GI	g3413167
BLAST score	369
E value	2.0e-35
Match length	73
% identity	99
NCBI Description	(AJ010225) elongation factor 1-alpha [Cicer arietinum]
Seq. No.	223246
Seq. ID	LIB3165-042-Q1-K1-B3
Method	BLASTX
NCBI GI	g3386621
BLAST score	632
E value	3.0e-66
Match length	135
% identity	90
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]
Seq. No.	223247

Seq. ID	LIB3165-042-Q1-K1-B4
Method	BLASTX
NCBI GI	g1352821
BLAST score	570
E value	6.0e-59
Match length	108
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223248
Seq. ID	LIB3165-042-Q1-K1-B5
Method	BLASTX
NCBI GI	g416681
BLAST score	318
E value	2.0e-29
Match length	99
% identity	65
NCBI Description	ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR >gi_280404_pir__S26198 H+-transporting ATP synthase (EC 3.6.1.34) delta chain precursor, chloroplast - common tobacco >gi_19787_emb_CAA45153_ (X63607) chloroplast ATP synthase (delta subunit) [Nicotiana tabacum]

Seq. No.	223249
Seq. ID	LIB3165-042-Q1-K1-B6
Method	BLASTX
NCBI GI	g289920
BLAST score	586
E value	7.0e-61
Match length	114
% identity	96
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	223250
Seq. ID	LIB3165-042-Q1-K1-B7
Method	BLASTX
NCBI GI	g1352821
BLAST score	343
E value	2.0e-32
Match length	68
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223251
Seq. ID	LIB3165-042-Q1-K1-B8
Method	BLASTX
NCBI GI	g1168411
BLAST score	295

E value	2.0e-43
Match length	117
% identity	81
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	223252
Seq. ID	LIB3165-042-Q1-K1-C1
Method	BLASTX
NCBI GI	g2662343
BLAST score	602
E value	1.0e-62
Match length	115
% identity	100
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	223253
Seq. ID	LIB3165-042-Q1-K1-C12
Method	BLASTX
NCBI GI	g289920
BLAST score	577
E value	8.0e-60
Match length	110
% identity	97
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	223254
Seq. ID	LIB3165-042-Q1-K1-C2
Method	BLASTX
NCBI GI	g542020
BLAST score	479
E value	3.0e-48
Match length	117
% identity	77
NCBI Description	sucrose transport protein - castor bean >gi_468562_emb_CAA83436_ (Z31561) sucrose carrier [Ricinus communis]

Seq. No.	223255
Seq. ID	LIB3165-042-Q1-K1-C3
Method	BLASTX
NCBI GI	g100200
BLAST score	482
E value	1.0e-48
Match length	122
% identity	76
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	223256
Seq. ID	LIB3165-042-Q1-K1-C4
Method	BLASTX
NCBI GI	g417103
BLAST score	618
E value	2.0e-64
Match length	125
% identity	99
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone

H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	223257
Seq. ID	LIB3165-042-Q1-K1-C6
Method	BLASTX
NCBI GI	g505482
BLAST score	357
E value	3.0e-35
Match length	104
% identity	82
NCBI Description	(X64349) 33 kDa polypeptide of water-oxidizing complex of photosystem II [Nicotiana tabacum]

Seq. No.	223258
Seq. ID	LIB3165-042-Q1-K1-C7
Method	BLASTX
NCBI GI	g1352821
BLAST score	529
E value	4.0e-54
Match length	101
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223259
Seq. ID	LIB3165-042-Q1-K1-D5
Method	BLASTX
NCBI GI	g100200
BLAST score	263
E value	4.0e-32
Match length	105
% identity	71
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	223260
Seq. ID	LIB3165-042-Q1-K1-D9
Method	BLASTX

NCBI GI g1483218
BLAST score 229
E value 5.0e-19
Match length 105
% identity 50
NCBI Description (X99793) induced upon wounding stress [Arabidopsis thaliana]

Seq. No. 223261
Seq. ID LIB3165-042-Q1-K1-E1
Method BLASTX
NCBI GI g4234941
BLAST score 513
E value 3.0e-52
Match length 121
% identity 88
NCBI Description (AF097938) cytosolic phosphoglucomutase [Populus tremula x Populus tremuloides]

Seq. No. 223262
Seq. ID LIB3165-042-Q1-K1-E10
Method BLASTX
NCBI GI g430947
BLAST score 442
E value 7.0e-44
Match length 108
% identity 81
NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No. 223263
Seq. ID LIB3165-042-Q1-K1-E12
Method BLASTX
NCBI GI g3243234
BLAST score 270
E value 1.0e-23
Match length 123
% identity 44
NCBI Description (AF071477) isoflavone reductase related protein [Pyrus communis]

Seq. No. 223264
Seq. ID LIB3165-042-Q1-K1-E2
Method BLASTX
NCBI GI g1352821
BLAST score 614
E value 4.0e-64
Match length 114
% identity 100
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223265
Seq. ID LIB3165-042-Q1-K1-E3

Method	BLASTX
NCBI GI	g100616
BLAST score	232
E value	2.0e-19
Match length	57
% identity	81
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	223266
Seq. ID	LIB3165-042-Q1-K1-E7
Method	BLASTX
NCBI GI	g1363556
BLAST score	170
E value	4.0e-12
Match length	47
% identity	64
NCBI Description	hypothetical protein 58 - maize chloroplast >gi_902297_emb_CAA60361_ (X86563) ORF58 [Zea mays]

Seq. No.	223267
Seq. ID	LIB3165-042-Q1-K1-E8
Method	BLASTX
NCBI GI	g1352821
BLAST score	471
E value	2.0e-47
Match length	89
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223268
Seq. ID	LIB3165-042-Q1-K1-F10
Method	BLASTX
NCBI GI	g1352821
BLAST score	543
E value	1.0e-55
Match length	105
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223269
Seq. ID	LIB3165-042-Q1-K1-F11
Method	BLASTX
NCBI GI	g231573
BLAST score	164
E value	7.0e-23

Match length	99
% identity	64
NCBI Description	L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE) >gi_99970_pir__S24757 asparaginase (EC 3.5.1.1) - narrow-leaved blue lupine >gi_19135_emb_CAA43099_ (X60691) developing seed L-asparaginase [Lupinus angustifolius]
Seq. No.	223270
Seq. ID	LIB3165-042-Q1-K1-F12
Method	BLASTX
NCBI GI	g4115379
BLAST score	314
E value	6.0e-29
Match length	114
% identity	61
NCBI Description	(AC005967) putative carbonyl reductase [Arabidopsis thaliana]
Seq. No.	223271
Seq. ID	LIB3165-042-Q1-K1-F4
Method	BLASTX
NCBI GI	g1352821
BLAST score	594
E value	1.0e-61
Match length	111
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	223272
Seq. ID	LIB3165-042-Q1-K1-F5
Method	BLASTX
NCBI GI	g2213590
BLAST score	268
E value	2.0e-23
Match length	140
% identity	41
NCBI Description	(AC000348) T7N9.10 [Arabidopsis thaliana]
Seq. No.	223273
Seq. ID	LIB3165-042-Q1-K1-F6
Method	BLASTX
NCBI GI	g2190012
BLAST score	337
E value	1.0e-31
Match length	108
% identity	63
NCBI Description	(AB004242) din1 [Raphanus sativus]
Seq. No.	223274
Seq. ID	LIB3165-042-Q1-K1-F9
Method	BLASTX
NCBI GI	g1351270
BLAST score	418

E value	4.0e-41
Match length	118
% identity	69
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_478410_pir__JQ2255 triose-phosphate isomerase (EC 5.3.1.1) - rice >gi_169821 (M87064) triosephosphate isomerase [Oryza sativa]

Seq. No.	223275
Seq. ID	LIB3165-042-Q1-K1-G1
Method	BLASTX
NCBI GI	g4406530
BLAST score	305
E value	7.0e-28
Match length	87
% identity	74
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223276
Seq. ID	LIB3165-042-Q1-K1-G3
Method	BLASTX
NCBI GI	g1352821
BLAST score	546
E value	4.0e-56
Match length	105
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223277
Seq. ID	LIB3165-042-Q1-K1-G4
Method	BLASTX
NCBI GI	g481132
BLAST score	150
E value	1.0e-09
Match length	31
% identity	94
NCBI Description	sucrose transport protein SUC1 - Arabidopsis thaliana >gi_407094_emb_CAA53147_ (X75365) sucrose-proton symporter [Arabidopsis thaliana]

Seq. No.	223278
Seq. ID	LIB3165-042-Q1-K1-G6
Method	BLASTX
NCBI GI	g115471
BLAST score	479
E value	3.0e-48
Match length	139
% identity	67
NCBI Description	CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) >gi_100078_pir__S10200 carbonate dehydratase (EC 4.2.1.1) precursor - garden pea >gi_20673_emb_CAA36792_ (X52558) precursor peptide (AA -104 to 224) [Pisum sativum]

Seq. No.	223279
Seq. ID	LIB3165-042-Q1-K1-H12
Method	BLASTX
NCBI GI	g3158476
BLAST score	372
E value	7.0e-36
Match length	82
% identity	85
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	223280
Seq. ID	LIB3165-042-Q1-K1-H2
Method	BLASTX
NCBI GI	g1352821
BLAST score	569
E value	8.0e-59
Match length	107
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223281
Seq. ID	LIB3165-042-Q1-K1-H3
Method	BLASTX
NCBI GI	g3834388
BLAST score	222
E value	3.0e-18
Match length	118
% identity	45
NCBI Description	(AF038547) beta-1,4-mannanase [Bacillus stearothermophilus]

Seq. No.	223282
Seq. ID	LIB3165-042-Q1-K1-H4
Method	BLASTX
NCBI GI	g3702327
BLAST score	201
E value	1.0e-15
Match length	111
% identity	49
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	223283
Seq. ID	LIB3165-042-Q1-K1-H6
Method	BLASTX
NCBI GI	g2369714
BLAST score	577
E value	7.0e-60
Match length	116
% identity	94
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	223284
Seq. ID	LIB3165-042-Q1-K1-H7
Method	BLASTX

NCBI GI	g20729
BLAST score	331
E value	5.0e-31
Match length	101
% identity	68
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	223285
Seq. ID	LIB3165-042-Q1-K1-H8
Method	BLASTX
NCBI GI	g68064
BLAST score	155
E value	1.0e-10
Match length	56
% identity	62
NCBI Description	ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - rape >gi_17855_emb_CAA30290_ (X07367) rubisco ssu precursor [Brassica napus]

Seq. No.	223286
Seq. ID	LIB3165-043-Q1-K1-A10
Method	BLASTX
NCBI GI	g1778095
BLAST score	409
E value	5.0e-40
Match length	118
% identity	67
NCBI Description	(U64903) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris]

Seq. No.	223287
Seq. ID	LIB3165-043-Q1-K1-A11
Method	BLASTX
NCBI GI	g1168411
BLAST score	551
E value	1.0e-56
Match length	137
% identity	82
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	223288
Seq. ID	LIB3165-043-Q1-K1-A12
Method	BLASTX
NCBI GI	g100616
BLAST score	186
E value	4.0e-14
Match length	43
% identity	86
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	223289
Seq. ID	LIB3165-043-Q1-K1-A7

Method	BLASTX
NCBI GI	g2739375
BLAST score	225
E value	2.0e-18
Match length	126
% identity	45
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	223290
Seq. ID	LIB3165-043-Q1-K1-A9
Method	BLASTX
NCBI GI	g3334197
BLAST score	446
E value	2.0e-44
Match length	113
% identity	74
NCBI Description	AMINOMETHYLTRANSFERASE PRECURSOR (GLYCINE CLEAVAGE SYSTEM T PROTEIN) >gi_2894400_emb_CAA94902_ (Z71184) T-protein [Flaveria anomala]

Seq. No.	223291
Seq. ID	LIB3165-043-Q1-K1-B11
Method	BLASTX
NCBI GI	g1709651
BLAST score	229
E value	5.0e-28
Match length	124
% identity	62
NCBI Description	PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209 plastocyanin a precursor - black poplar >gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus nigra]

Seq. No.	223292
Seq. ID	LIB3165-043-Q1-K1-B12
Method	BLASTX
NCBI GI	g1168408
BLAST score	629
E value	8.0e-66
Match length	134
% identity	92
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1 >gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828) fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No.	223293
Seq. ID	LIB3165-043-Q1-K1-B2
Method	BLASTX
NCBI GI	g1173347
BLAST score	596
E value	6.0e-62
Match length	126
% identity	91
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC

3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No.	223294
Seq. ID	LIB3165-043-Q1-K1-B4
Method	BLASTX
NCBI GI	g231688
BLAST score	282
E value	9.0e-26
Match length	59
% identity	90
NCBI Description	CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC 1.11.1.6) - upland cotton >gi_18488_emb_CAA39998_ (X56675) subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No.	223295
Seq. ID	LIB3165-043-Q1-K1-B8
Method	BLASTX
NCBI GI	g3288821
BLAST score	519
E value	6.0e-53
Match length	123
% identity	80
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana]

Seq. No.	223296
Seq. ID	LIB3165-043-Q1-K1-C11
Method	BLASTX
NCBI GI	g1527219
BLAST score	347
E value	9.0e-33
Match length	76
% identity	83
NCBI Description	(U68218) ATP sulphurylase [Brassica napus]

Seq. No.	223297
Seq. ID	LIB3165-043-Q1-K1-C12
Method	BLASTX
NCBI GI	g1352821
BLAST score	762
E value	2.0e-81
Match length	145
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223298
Seq. ID	LIB3165-043-Q1-K1-C7
Method	BLASTX
NCBI GI	g3288821
BLAST score	488
E value	3.0e-49

Match length	117
% identity	79
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana]

Seq. No.	223299
Seq. ID	LIB3165-043-Q1-K1-C9
Method	BLASTX
NCBI GI	g120669
BLAST score	439
E value	1.0e-43
Match length	89
% identity	91
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	223300
Seq. ID	LIB3165-043-Q1-K1-D1
Method	BLASTX
NCBI GI	g3287270
BLAST score	175
E value	3.0e-13
Match length	50
% identity	72
NCBI Description	(Y09533) involved in starch metabalism [Solanum tuberosum]

Seq. No.	223301
Seq. ID	LIB3165-043-Q1-K1-D11
Method	BLASTX
NCBI GI	g1169494
BLAST score	147
E value	2.0e-09
Match length	30
% identity	97
NCBI Description	ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >gi_2119915_pir__S60659 EF-Tu protein precursor - soybean >gi_949873_emb_CAA61444_ (X89058) EF-Tu protein [Glycine max]

Seq. No.	223302
Seq. ID	LIB3165-043-Q1-K1-D6
Method	BLASTX
NCBI GI	g120663
BLAST score	279
E value	2.0e-50
Match length	139
% identity	76
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR, CHLOROPLAST >gi_66027_pir__DEPMNB glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast - garden pea >gi_309671 (M55147) glyceraldehyde-3-phosphate dehydrogenase B subunit [Pisum sativum]

Seq. No.	223303
Seq. ID	LIB3165-043-Q1-K1-D9
Method	BLASTX
NCBI GI	g1352821
BLAST score	593
E value	1.0e-61
Match length	111
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223304
Seq. ID	LIB3165-043-Q1-K1-E10
Method	BLASTX
NCBI GI	g1352821
BLAST score	612
E value	8.0e-64
Match length	114
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223305
Seq. ID	LIB3165-043-Q1-K1-E11
Method	BLASTX
NCBI GI	g1174162
BLAST score	638
E value	7.0e-67
Match length	121
% identity	93
NCBI Description	(U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi_3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No.	223306
Seq. ID	LIB3165-043-Q1-K1-E12
Method	BLASTX
NCBI GI	g3242702
BLAST score	333
E value	4.0e-31
Match length	137
% identity	48
NCBI Description	(AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No.	223307
Seq. ID	LIB3165-043-Q1-K1-E3
Method	BLASTX
NCBI GI	g3080428
BLAST score	239
E value	1.0e-20
Match length	62

% identity	81
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	223308
Seq. ID	LIB3165-043-Q1-K1-E4
Method	BLASTX
NCBI GI	g2632109
BLAST score	168
E value	2.0e-21
Match length	132
% identity	45
NCBI Description	(AJ000508) phospholipid glutathione peroxidase [Pisum sativum]

Seq. No.	223309
Seq. ID	LIB3165-043-Q1-K1-E6
Method	BLASTX
NCBI GI	g3334223
BLAST score	510
E value	7.0e-52
Match length	143
% identity	69
NCBI Description	4-HYDROXYPHENYLPYRUVATE DIOXYGENASE (4HPPD) (HPD) >gi_2145039 (AF000228) p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana] >gi_2392518 (U89267) p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana] >gi_3098559 (AF047834) 4-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana]

Seq. No.	223310
Seq. ID	LIB3165-043-Q1-K1-E7
Method	BLASTX
NCBI GI	g2605911
BLAST score	349
E value	2.0e-66
Match length	138
% identity	91
NCBI Description	(AF029258) plasma membrane H+-ATPase [Kosteletzkya virginica]

Seq. No.	223311
Seq. ID	LIB3165-043-Q1-K1-E9
Method	BLASTX
NCBI GI	g115705
BLAST score	395
E value	6.0e-66
Match length	128
% identity	94
NCBI Description	CATALASE >gi_279448_pir__CSPM catalase (EC 1.11.1.6) - garden pea >gi_20677_emb_CAA42736_ (X60169) catalase [Pisum sativum]

Seq. No.	223312
Seq. ID	LIB3165-043-Q1-K1-F10
Method	BLASTX
NCBI GI	g285739
BLAST score	392

E value	5.0e-38
Match length	125
% identity	57
NCBI Description	(D14605) AX110P [Daucus carota] >gi_740202_prf__2004427A embryogenesis-associated protein [Daucus carota]

Seq. No.	223313
Seq. ID	LIB3165-043-Q1-K1-F11
Method	BLASTX
NCBI GI	g166834
BLAST score	711
E value	2.0e-75
Match length	138
% identity	97
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	223314
Seq. ID	LIB3165-043-Q1-K1-F12
Method	BLASTX
NCBI GI	g1169384
BLAST score	490
E value	2.0e-49
Match length	101
% identity	87
NCBI Description	DNAJ PROTEIN HOMOLOG ANJ1 >gi_543510_pir__JQ2142 chaperone ANJ1 protein - Atriplex nummularia

Seq. No.	223315
Seq. ID	LIB3165-043-Q1-K1-F2
Method	BLASTX
NCBI GI	g3402705
BLAST score	184
E value	9.0e-14
Match length	104
% identity	43
NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No.	223316
Seq. ID	LIB3165-043-Q1-K1-F3
Method	BLASTX
NCBI GI	g479406
BLAST score	275
E value	4.0e-51
Match length	115
% identity	59
NCBI Description	chlorophyll a/b-binding protein - garden pea >gi_20671_emb_CAA49149_ (X69215) chlorophyll a/b-binding protein [Pisum sativum]

Seq. No.	223317
Seq. ID	LIB3165-043-Q1-K1-F4
Method	BLASTX
NCBI GI	g3426041
BLAST score	98
E value	2.0e-09

Match length	95
% identity	46
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	223318
Seq. ID	LIB3165-043-Q1-K1-F6
Method	BLASTX
NCBI GI	g1168408
BLAST score	633
E value	3.0e-66
Match length	136
% identity	91
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1 >gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828) fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No.	223319
Seq. ID	LIB3165-043-Q1-K1-F7
Method	BLASTX
NCBI GI	g1352821
BLAST score	590
E value	3.0e-61
Match length	110
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223320
Seq. ID	LIB3165-043-Q1-K1-G1
Method	BLASTX
NCBI GI	g1352821
BLAST score	350
E value	1.0e-33
Match length	74
% identity	82
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223321
Seq. ID	LIB3165-043-Q1-K1-G11
Method	BLASTX
NCBI GI	g3360289
BLAST score	129
E value	4.0e-09
Match length	51
% identity	63
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	223322

Seq. ID	LIB3165-043-Q1-K1-G12
Method	BLASTX
NCBI GI	g228403
BLAST score	511
E value	5.0e-52
Match length	119
% identity	83
NCBI Description	glycolate oxidase [Lens culinaris]

Seq. No.	223323
Seq. ID	LIB3165-043-Q1-K1-G3
Method	BLASTX
NCBI GI	g286122
BLAST score	367
E value	4.0e-39
Match length	92
% identity	84
NCBI Description	(D14576) glutamine synthetase [Zea mays]

Seq. No.	223324
Seq. ID	LIB3165-043-Q1-K1-G7
Method	BLASTX
NCBI GI	g4091806
BLAST score	578
E value	7.0e-60
Match length	137
% identity	80
NCBI Description	(AF052585) CONSTANS-like protein 2 [Malus domestica]

Seq. No.	223325
Seq. ID	LIB3165-043-Q1-K1-G8
Method	BLASTX
NCBI GI	g1181599
BLAST score	310
E value	2.0e-28
Match length	135
% identity	52
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.	223326
Seq. ID	LIB3165-043-Q1-K1-H2
Method	BLASTX
NCBI GI	g3913651
BLAST score	141
E value	7.0e-09
Match length	58
% identity	42
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR (FNR) >gi_2225993_emb_CAA74359_ (Y14032) ferredoxin--NADP(+) reductase [Nicotiana tabacum]

Seq. No.	223327
Seq. ID	LIB3165-043-Q1-K1-H3
Method	BLASTX
NCBI GI	g4210948
BLAST score	390
E value	7.0e-38

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Match length	96
% identity	80
NCBI Description	(AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No.	223328
Seq. ID	LIB3165-043-Q1-K1-H4
Method	BLASTX
NCBI GI	g120663
BLAST score	255
E value	3.0e-22
Match length	82
% identity	65
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR, CHLOROPLAST >gi_66027_pir__DEPMNB glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast - garden pea >gi_309671 (M55147) glyceraldehyde-3-phosphate dehydrogenase B subunit [Pisum sativum]

Seq. No.	223329
Seq. ID	LIB3165-043-Q1-K1-H7
Method	BLASTX
NCBI GI	g1352821
BLAST score	627
E value	1.0e-65
Match length	116
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223330
Seq. ID	LIB3165-043-Q1-K1-H8
Method	BLASTX
NCBI GI	g1352681
BLAST score	189
E value	3.0e-14
Match length	115
% identity	43
NCBI Description	PROTEIN PHOSPHATASE 2C (PP2C) >gi_1076391_pir__S55457 phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis thaliana >gi_633028_dbj_BAA07287_ (D38109) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	223331
Seq. ID	LIB3165-043-Q1-K1-H9
Method	BLASTX
NCBI GI	g1345698
BLAST score	652
E value	2.0e-68
Match length	135
% identity	90
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR (CAB-151) (LHCP) >gi_99601_pir__S20917 chlorophyll a/b-binding protein - upland cotton

	>gi_452314_emb_CAA38025_ (X54090) chlorophyll ab binding protein [Gossypium hirsutum]
Seq. No.	223332
Seq. ID	LIB3165-044-Q1-K1-A10
Method	BLASTX
NCBI GI	g226996
BLAST score	609
E value	2.0e-63
Match length	132
% identity	89
NCBI Description	petB2 gene [Pisum sativum]
Seq. No.	223333
Seq. ID	LIB3165-044-Q1-K1-A11
Method	BLASTX
NCBI GI	g4406530
BLAST score	347
E value	8.0e-33
Match length	118
% identity	63
NCBI Description	(AF126870) rubisco activase [Vigna radiata]
Seq. No.	223334
Seq. ID	LIB3165-044-Q1-K1-A4
Method	BLASTX
NCBI GI	g124224
BLAST score	483
E value	7.0e-49
Match length	97
% identity	94
NCBI Description	INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) >gi_100345_pir__S21060 translation initiation factor eIF-5A - common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]
Seq. No.	223335
Seq. ID	LIB3165-044-Q1-K1-A5
Method	BLASTX
NCBI GI	g2493129
BLAST score	243
E value	9.0e-21
Match length	69
% identity	74
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B SUBUNIT) >gi_459198 (U07052) vacuolar H+-ATPase subunit B [Gossypium hirsutum]
Seq. No.	223336
Seq. ID	LIB3165-044-Q1-K1-A8
Method	BLASTX
NCBI GI	g3023752
BLAST score	279
E value	8.0e-25
Match length	101
% identity	58
NCBI Description	FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520)

ferredoxin-I [Lycopersicon esculentum]

Seq. No.	223337
Seq. ID	LIB3165-044-Q1-K1-A9
Method	BLASTX
NCBI GI	g1352821
BLAST score	309
E value	1.0e-28
Match length	84
% identity	79
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223338
Seq. ID	LIB3165-044-Q1-K1-B10
Method	BLASTX
NCBI GI	g3832512
BLAST score	541
E value	2.0e-55
Match length	138
% identity	75
NCBI Description	(AF097922) granule-bound glycogen (starch) synthase [Astragalus membranaceus]

Seq. No.	223339
Seq. ID	LIB3165-044-Q1-K1-B11
Method	BLASTX
NCBI GI	g100616
BLAST score	272
E value	6.0e-46
Match length	129
% identity	77
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	223340
Seq. ID	LIB3165-044-Q1-K1-B12
Method	BLASTX
NCBI GI	g2494076
BLAST score	479
E value	3.0e-48
Match length	103
% identity	87
NCBI Description	NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi_1842115 (U87848) non-phosphorylating glyceraldehyde dehydrogenase [Nicotiana plumbaginifolia]

Seq. No.	223341

Seq. ID LIB3165-044-Q1-K1-B3
Method BLASTX
NCBI GI g470373
BLAST score 183
E value 2.0e-13
Match length 112
% identity 36
NCBI Description (U00047) ZK418.5 gene product [Caenorhabditis elegans]

Seq. No. 223342
Seq. ID LIB3165-044-Q1-K1-B6
Method BLASTX
NCBI GI g1928981
BLAST score 507
E value 1.0e-51
Match length 110
% identity 93
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No. 223343
Seq. ID LIB3165-044-Q1-K1-B8
Method BLASTX
NCBI GI g1856971
BLAST score 524
E value 2.0e-53
Match length 109
% identity 92
NCBI Description (D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No. 223344
Seq. ID LIB3165-044-Q1-K1-C1
Method BLASTX
NCBI GI g1352821
BLAST score 645
E value 1.0e-67
Match length 121
% identity 98
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223345
Seq. ID LIB3165-044-Q1-K1-C10
Method BLASTX
NCBI GI g3687652
BLAST score 410
E value 8.0e-63
Match length 135
% identity 88
NCBI Description (AF047352) rubisco activase precursor [Datisca glomerata]

Seq. No. 223346

Seq. ID	LIB3165-044-Q1-K1-C11
Method	BLASTX
NCBI GI	g3914603
BLAST score	582
E value	2.0e-60
Match length	134
% identity	80
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No.	223347
Seq. ID	LIB3165-044-Q1-K1-C12
Method	BLASTX
NCBI GI	g1354515
BLAST score	216
E value	2.0e-17
Match length	112
% identity	48
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	223348
Seq. ID	LIB3165-044-Q1-K1-C3
Method	BLASTX
NCBI GI	g4454458
BLAST score	307
E value	4.0e-28
Match length	136
% identity	55
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	223349
Seq. ID	LIB3165-044-Q1-K1-C4
Method	BLASTX
NCBI GI	g399082
BLAST score	210
E value	9.0e-17
Match length	134
% identity	40
NCBI Description	ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR >gi_322713_pir__S28171 H+-transporting ATP synthase (EC 3.6.1.34) delta chain, chloroplast - garden pea >gi_169045 (M94558) ATP synthase delta subunit [Pisum sativum]

Seq. No.	223350
Seq. ID	LIB3165-044-Q1-K1-C5
Method	BLASTX
NCBI GI	g4406530
BLAST score	233
E value	4.0e-31
Match length	104
% identity	68
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223351

Seq. ID	LIB3165-044-Q1-K1-C6
Method	BLASTX
NCBI GI	g1352821
BLAST score	595
E value	8.0e-62
Match length	114
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223352
Seq. ID	LIB3165-044-Q1-K1-C7
Method	BLASTX
NCBI GI	g2443751
BLAST score	447
E value	2.0e-44
Match length	103
% identity	84
NCBI Description	(AF020303) fumarase [Arabidopsis thaliana] >gi_2529676 (AC002535) putative fumarase [Arabidopsis thaliana]

Seq. No.	223353
Seq. ID	LIB3165-044-Q1-K1-D10
Method	BLASTX
NCBI GI	g231688
BLAST score	727
E value	2.0e-77
Match length	141
% identity	97
NCBI Description	CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC 1.11.1.6) - upland cotton >gi_18488_emb_CAA39998_ (X56675) subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No.	223354
Seq. ID	LIB3165-044-Q1-K1-D11
Method	BLASTX
NCBI GI	g115471
BLAST score	434
E value	6.0e-43
Match length	137
% identity	64
NCBI Description	CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) >gi_100078_pir__S10200 carbonate dehydratase (EC 4.2.1.1) precursor - garden pea >gi_20673_emb_CAA36792_ (X52558) precursor peptide (AA -104 to 224) [Pisum sativum]

Seq. No.	223355
Seq. ID	LIB3165-044-Q1-K1-D4
Method	BLASTX
NCBI GI	g1354515
BLAST score	290
E value	4.0e-26
Match length	137
% identity	50

NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]
Seq. No.	223356
Seq. ID	LIB3165-044-Q1-K1-D6
Method	BLASTX
NCBI GI	g4115934
BLAST score	443
E value	5.0e-44
Match length	116
% identity	74
NCBI Description	(AF118223) contains similarity to Methanobacterium thermoautotrophicum transcriptional regulator (GB:AE000850) [Arabidopsis thaliana]
Seq. No.	223357
Seq. ID	LIB3165-044-Q1-K1-D9
Method	BLASTX
NCBI GI	g3510256
BLAST score	157
E value	2.0e-10
Match length	90
% identity	41
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]
Seq. No.	223358
Seq. ID	LIB3165-044-Q1-K1-E1
Method	BLASTX
NCBI GI	g100488
BLAST score	160
E value	7.0e-11
Match length	123
% identity	35
NCBI Description	TNP2 protein - garden snapdragon
Seq. No.	223359
Seq. ID	LIB3165-044-Q1-K1-E10
Method	BLASTX
NCBI GI	g1352821
BLAST score	585
E value	1.0e-60
Match length	109
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	223360
Seq. ID	LIB3165-044-Q1-K1-E11
Method	BLASTX
NCBI GI	g4567227
BLAST score	395
E value	2.0e-38
Match length	135
% identity	53

NCBI Description	(AC007119) putative transport protein [Arabidopsis thaliana]
Seq. No.	223361
Seq. ID	LIB3165-044-Q1-K1-E12
Method	BLASTX
NCBI GI	g505482
BLAST score	508
E value	1.0e-56
Match length	128
% identity	89
NCBI Description	(X64349) 33 kDa polypeptide of water-oxidizing complex of photosystem II [Nicotiana tabacum]
Seq. No.	223362
Seq. ID	LIB3165-044-Q1-K1-E2
Method	BLASTX
NCBI GI	g2677828
BLAST score	456
E value	1.0e-45
Match length	118
% identity	70
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]
Seq. No.	223363
Seq. ID	LIB3165-044-Q1-K1-E5
Method	BLASTX
NCBI GI	g1346155
BLAST score	543
E value	8.0e-56
Match length	119
% identity	88
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_481942_pir__S40212 glycine hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei >gi_437995_emb_CAA81078_ (Z25859) glycine hydroxymethyltransferase [Flaveria pringlei]
Seq. No.	223364
Seq. ID	LIB3165-044-Q1-K1-E8
Method	BLASTX
NCBI GI	g3264759
BLAST score	534
E value	1.0e-54
Match length	126
% identity	83
NCBI Description	(AF071889) 40S ribosomal protein S8 [Prunus armeniaca]
Seq. No.	223365
Seq. ID	LIB3165-044-Q1-K1-F1
Method	BLASTX
NCBI GI	g4091806
BLAST score	484
E value	7.0e-49
Match length	96
% identity	90

NCBI Description	(AF052585) CONSTANS-like protein 2 [Malus domestica]

Seq. No.	223366
Seq. ID	LIB3165-044-Q1-K1-F12
Method	BLASTX
NCBI GI	g1172873
BLAST score	310
E value	4.0e-45
Match length	129
% identity	65
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	223367
Seq. ID	LIB3165-044-Q1-K1-F2
Method	BLASTX
NCBI GI	g1495366
BLAST score	404
E value	2.0e-39
Match length	124
% identity	61
NCBI Description	(Z69370) nitrite transporter [Cucumis sativus]

Seq. No.	223368
Seq. ID	LIB3165-044-Q1-K1-F4
Method	BLASTX
NCBI GI	g2651316
BLAST score	115
E value	1.0e-10
Match length	58
% identity	71
NCBI Description	(AC002336) unknown protein [Arabidopsis thaliana]

Seq. No.	223369
Seq. ID	LIB3165-044-Q1-K1-F7
Method	BLASTX
NCBI GI	g128405
BLAST score	318
E value	2.0e-29
Match length	112
% identity	60
NCBI Description	NODULIN 21 (N-21) >gi_99942_pir__S08632 nodulin-21 - soybean >gi_18694_emb_CAA34506_ (X16488) nodulin-21 (AA 1-201) [Glycine max]

Seq. No.	223370
Seq. ID	LIB3165-044-Q1-K1-F8
Method	BLASTX
NCBI GI	g20729
BLAST score	483
E value	8.0e-49
Match length	119
% identity	80
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	223371
Seq. ID	LIB3165-044-Q1-K1-F9
Method	BLASTX
NCBI GI	g3776005
BLAST score	290
E value	5.0e-38
Match length	92
% identity	92
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	223372
Seq. ID	LIB3165-044-Q1-K1-G1
Method	BLASTX
NCBI GI	g3763925
BLAST score	366
E value	4.0e-35
Match length	92
% identity	77
NCBI Description	(AC004450) putative Af10-protein [Arabidopsis thaliana]

Seq. No.	223373
Seq. ID	LIB3165-044-Q1-K1-G10
Method	BLASTX
NCBI GI	g4263711
BLAST score	431
E value	1.0e-42
Match length	95
% identity	80
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	223374
Seq. ID	LIB3165-044-Q1-K1-G3
Method	BLASTX
NCBI GI	g4033469
BLAST score	390
E value	8.0e-38
Match length	114
% identity	44
NCBI Description	ARGININE/SERINE-RICH SPLICING FACTOR RSP41 >gi_1707370_emb_CAA67799_ (X99436) splicing factor [Arabidopsis thaliana]

Seq. No.	223375
Seq. ID	LIB3165-044-Q1-K1-G4
Method	BLASTX
NCBI GI	g3183088
BLAST score	165
E value	9.0e-12
Match length	60
% identity	55
NCBI Description	PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer like protein [Vigna unguiculata]

Seq. No.	223376

Seq. ID	LIB3165-044-Q1-K1-G9
Method	BLASTX
NCBI GI	g1352821
BLAST score	585
E value	1.0e-60
Match length	109
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223377
Seq. ID	LIB3165-044-Q1-K1-H1
Method	BLASTX
NCBI GI	g1871577
BLAST score	192
E value	1.0e-14
Match length	98
% identity	43
NCBI Description	(Y11553) putative 21kD protein precursor [Medicago sativa]

Seq. No.	223378
Seq. ID	LIB3165-044-Q1-K1-H12
Method	BLASTX
NCBI GI	g1486472
BLAST score	233
E value	1.0e-19
Match length	53
% identity	85
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]

Seq. No.	223379
Seq. ID	LIB3165-044-Q1-K1-H3
Method	BLASTX
NCBI GI	g3023501
BLAST score	165
E value	2.0e-11
Match length	46
% identity	61
NCBI Description	PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP) >gi_2224431_dbj_BAA57915_ (AB001684) ATP-dependent Clp protease proteolytic subunit [Chlorella vulgaris]

Seq. No.	223380
Seq. ID	LIB3165-044-Q1-K1-H4
Method	BLASTX
NCBI GI	g1352821
BLAST score	370
E value	1.0e-35
Match length	75
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223381
Seq. ID	LIB3165-044-Q1-K1-H5
Method	BLASTX
NCBI GI	g3914472
BLAST score	279
E value	5.0e-25
Match length	68
% identity	78
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10) >gi_322764_pir__S32021 photosystem II 10K protein - common tobacco >gi_22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana tabacum]

Seq. No.	223382
Seq. ID	LIB3165-044-Q1-K1-H8
Method	BLASTX
NCBI GI	g4115357
BLAST score	323
E value	6.0e-30
Match length	132
% identity	52
NCBI Description	(AC005957) hypothetical protein [Arabidopsis thaliana]

Seq. No.	223383
Seq. ID	LIB3165-044-Q1-K1-H9
Method	BLASTX
NCBI GI	g3287696
BLAST score	201
E value	1.0e-15
Match length	78
% identity	56
NCBI Description	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]

Seq. No.	223384
Seq. ID	LIB3165-045-Q1-K1-A11
Method	BLASTX
NCBI GI	g131384
BLAST score	321
E value	9.0e-30
Match length	74
% identity	82
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_81934_pir__S04132 photosystem II oxygen-evolving complex protein 1 precursor - garden pea >gi_20621_emb_CAA33408_ (X15350) precursor (AA -81 to 248) [Pisum sativum] >gi_344004_dbj_BAA02554_ (D13297) precursor for 33-kDa protein of photosystem II [Pisum sativum] >gi_226937_prf__1611461A O2 evolving complex 33kD protein [Arachis hypogaea]

Seq. No.	223385
Seq. ID	LIB3165-045-Q1-K1-A12
Method	BLASTX
NCBI GI	g20729
BLAST score	466
E value	1.0e-46
Match length	125
% identity	76
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	223386
Seq. ID	LIB3165-045-Q1-K1-A5
Method	BLASTX
NCBI GI	g3023752
BLAST score	202
E value	8.0e-16
Match length	108
% identity	42
NCBI Description	FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520) ferredoxin-I [Lycopersicon esculentum]

Seq. No.	223387
Seq. ID	LIB3165-045-Q1-K1-A7
Method	BLASTX
NCBI GI	g1168411
BLAST score	506
E value	2.0e-51
Match length	126
% identity	82
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	223388
Seq. ID	LIB3165-045-Q1-K1-A8
Method	BLASTX
NCBI GI	g3298548
BLAST score	404
E value	2.0e-39
Match length	123
% identity	63
NCBI Description	(AC004681) putative spliceosomal protein [Arabidopsis thaliana]

Seq. No.	223389
Seq. ID	LIB3165-045-Q1-K1-B11
Method	BLASTX
NCBI GI	g1352821
BLAST score	167
E value	3.0e-17
Match length	49
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223390

Seq. ID	LIB3165-045-Q1-K1-B12
Method	BLASTX
NCBI GI	g1352821
BLAST score	467
E value	6.0e-47
Match length	91
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223391
Seq. ID	LIB3165-045-Q1-K1-B2
Method	BLASTX
NCBI GI	g2791834
BLAST score	206
E value	5.0e-34
Match length	85
% identity	80
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No.	223392
Seq. ID	LIB3165-045-Q1-K1-B7
Method	BLASTX
NCBI GI	g3158474
BLAST score	478
E value	3.0e-48
Match length	104
% identity	89
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]

Seq. No.	223393
Seq. ID	LIB3165-045-Q1-K1-B9
Method	BLASTX
NCBI GI	g2244847
BLAST score	286
E value	1.0e-25
Match length	93
% identity	59
NCBI Description	(Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No.	223394
Seq. ID	LIB3165-045-Q1-K1-C4
Method	BLASTX
NCBI GI	g505482
BLAST score	359
E value	1.0e-38
Match length	114
% identity	77
NCBI Description	(X64349) 33 kDa polypeptide of water-oxidizing complex of photosystem II [Nicotiana tabacum]

Seq. No.	223395
Seq. ID	LIB3165-045-Q1-K1-C7

Method	BLASTX
NCBI GI	g541951
BLAST score	426
E value	4.0e-42
Match length	107
% identity	79
NCBI Description	SPCP2 protein - soybean >gi_310578 (L12258) nodulin-26 [Glycine max]

Seq. No.	223396
Seq. ID	LIB3165-045-Q1-K1-C8
Method	BLASTX
NCBI GI	g3559814
BLAST score	495
E value	4.0e-50
Match length	139
% identity	70
NCBI Description	(Y15781) transketolase 1 [Capsicum annuum]

Seq. No.	223397
Seq. ID	LIB3165-045-Q1-K1-D10
Method	BLASTX
NCBI GI	g120663
BLAST score	326
E value	2.0e-35
Match length	108
% identity	72
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR, CHLOROPLAST >gi_66027_pir__DEPMNB glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast - garden pea >gi_309671 (M55147) glyceraldehyde-3-phosphate dehydrogenase B subunit [Pisum sativum]

Seq. No.	223398
Seq. ID	LIB3165-045-Q1-K1-D12
Method	BLASTX
NCBI GI	g3059095
BLAST score	656
E value	5.0e-69
Match length	141
% identity	91
NCBI Description	(AJ001091) magnesium chelatase subunit [Glycine max]

Seq. No.	223399
Seq. ID	LIB3165-045-Q1-K1-D7
Method	BLASTX
NCBI GI	g1352821
BLAST score	645
E value	1.0e-67
Match length	120
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223400
Seq. ID	LIB3165-045-Q1-K1-D8
Method	BLASTX
NCBI GI	g289920
BLAST score	709
E value	3.0e-75
Match length	136
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	223401
Seq. ID	LIB3165-045-Q1-K1-E10
Method	BLASTX
NCBI GI	g3914442
BLAST score	341
E value	4.0e-32
Match length	66
% identity	95
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No.	223402
Seq. ID	LIB3165-045-Q1-K1-E11
Method	BLASTX
NCBI GI	g1172664
BLAST score	257
E value	3.0e-22
Match length	55
% identity	91
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_419791_pir__S31165 photosystem I chain III precursor - Flaveria trinervia >gi_298482_bbs_127083 photosystem I reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem I subunit III [Flaveria trinervia]

Seq. No.	223403
Seq. ID	LIB3165-045-Q1-K1-E2
Method	BLASTX
NCBI GI	g1352821
BLAST score	192
E value	2.0e-26
Match length	119
% identity	31
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223404
Seq. ID	LIB3165-045-Q1-K1-E8
Method	BLASTX

NCBI GI	g2398679
BLAST score	608
E value	2.0e-63
Match length	127
% identity	88
NCBI Description	(Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Morinda citrifolia]

Seq. No.	223405
Seq. ID	LIB3165-045-Q1-K1-F12
Method	BLASTX
NCBI GI	g3885513
BLAST score	311
E value	1.0e-28
Match length	69
% identity	81
NCBI Description	(AF084201) similar to chloroplast 50S ribosomal protein L31 [Medicago sativa]

Seq. No.	223406
Seq. ID	LIB3165-045-Q1-K1-G10
Method	BLASTX
NCBI GI	g100200
BLAST score	358
E value	4.0e-34
Match length	99
% identity	71
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	223407
Seq. ID	LIB3165-045-Q1-K1-G11
Method	BLASTX
NCBI GI	g730850
BLAST score	141
E value	1.0e-08
Match length	123
% identity	28
NCBI Description	SUR2 PROTEIN (SYRINGOMYCIN RESPONSE PROTEIN 2) >gi_626942_pir__S48533 SUR2 protein - yeast (Saccharomyces cerevisiae) >gi_458718 (U07171) Sur2p [Saccharomyces cerevisiae] >gi_849215 (U28374) Sur2p: syringomycin response protein 2 [Saccharomyces cerevisiae] >gi_1786173 (U10427) Syr2p [Saccharomyces cerevisiae]

Seq. No.	223408
Seq. ID	LIB3165-045-Q1-K1-G12
Method	BLASTX
NCBI GI	g2136011
BLAST score	188
E value	4.0e-14
Match length	76
% identity	42
NCBI Description	protein DS 1; 24K - human >gi_1045059_emb_CAA57387_ (X81788) ICT1 protein [Homo sapiens] >gi_4557657_ref_NP_001536.1_pICT1_ immature colon carcinoma transcript

Seq. No.	223409
Seq. ID	LIB3165-045-Q1-K1-G6
Method	BLASTX
NCBI GI	g3850621
BLAST score	637
E value	8.0e-67
Match length	136
% identity	85
NCBI Description	(Y15382) putative RNA binding protein [Arabidopsis thaliana]

Seq. No.	223410
Seq. ID	LIB3165-045-Q1-K1-G7
Method	BLASTX
NCBI GI	g2191152
BLAST score	495
E value	3.0e-50
Match length	122
% identity	76
NCBI Description	(AF007269) A_IG002N01.31 gene product [Arabidopsis thaliana]

Seq. No.	223411
Seq. ID	LIB3165-045-Q1-K1-G8
Method	BLASTX
NCBI GI	g4538963
BLAST score	260
E value	6.0e-23
Match length	52
% identity	96
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana]

Seq. No.	223412
Seq. ID	LIB3165-045-Q1-K1-G9
Method	BLASTX
NCBI GI	g3668080
BLAST score	417
E value	5.0e-41
Match length	135
% identity	64
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	223413
Seq. ID	LIB3165-045-Q1-K1-H10
Method	BLASTX
NCBI GI	g2980770
BLAST score	656
E value	5.0e-69
Match length	135
% identity	90
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	223414
Seq. ID	LIB3165-045-Q1-K1-H12
Method	BLASTX
NCBI GI	g4249382

BLAST score	282
E value	2.0e-25
Match length	62
% identity	84
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	223415
Seq. ID	LIB3165-045-Q1-K1-H4
Method	BLASTX
NCBI GI	g136707
BLAST score	366
E value	5.0e-35
Match length	112
% identity	65
NCBI Description	CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_280397_pir__S26199 plastoquinol--plastocyanin reductase (EC 1.10.99.1) iron-sulfur protein precursor - garden pea >gi_20832_emb_CAA45151_ (X63605) chloroplast Rieske FeS protein [Pisum sativum]

Seq. No.	223416
Seq. ID	LIB3165-045-Q1-K1-H6
Method	BLASTX
NCBI GI	g2996407
BLAST score	215
E value	8.0e-26
Match length	84
% identity	82
NCBI Description	(AJ004940) heat shock cognate 70 [Gallus gallus]

Seq. No.	223417
Seq. ID	LIB3165-045-Q1-K1-H7
Method	BLASTX
NCBI GI	g3158476
BLAST score	511
E value	4.0e-52
Match length	112
% identity	86
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	223418
Seq. ID	LIB3165-045-Q1-K1-H8
Method	BLASTX
NCBI GI	g1352821
BLAST score	398
E value	6.0e-39
Match length	81
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223419
Seq. ID	LIB3165-045-Q1-K1-H9
Method	BLASTX
NCBI GI	g3914603
BLAST score	510
E value	3.0e-62
Match length	132
% identity	83
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No.	223420
Seq. ID	LIB3165-046-Q1-K1-A1
Method	BLASTX
NCBI GI	g166834
BLAST score	557
E value	2.0e-57
Match length	133
% identity	78
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	223421
Seq. ID	LIB3165-046-Q1-K1-A11
Method	BLASTX
NCBI GI	g1439609
BLAST score	589
E value	3.0e-61
Match length	119
% identity	99
NCBI Description	(U62778) delta-tonoplast intrinsic protein [Gossypium hirsutum]

Seq. No.	223422
Seq. ID	LIB3165-046-Q1-K1-A12
Method	BLASTX
NCBI GI	g289920
BLAST score	443
E value	3.0e-44
Match length	83
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	223423
Seq. ID	LIB3165-046-Q1-K1-A6
Method	BLASTX
NCBI GI	g4406530
BLAST score	364
E value	9.0e-35
Match length	98
% identity	76
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223424
Seq. ID	LIB3165-046-Q1-K1-A7
Method	BLASTX
NCBI GI	g1352821
BLAST score	618
E value	2.0e-64
Match length	128
% identity	93
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223425
Seq. ID	LIB3165-046-Q1-K1-B1
Method	BLASTX
NCBI GI	g4336436
BLAST score	382
E value	7.0e-37
Match length	103
% identity	70
NCBI Description	(AF092432) protein phosphatase type 2C [Lotus japonicus]

Seq. No.	223426
Seq. ID	LIB3165-046-Q1-K1-B10
Method	BLASTX
NCBI GI	g3023752
BLAST score	323
E value	5.0e-30
Match length	110
% identity	63
NCBI Description	FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520) ferredoxin-I [Lycopersicon esculentum]

Seq. No.	223427
Seq. ID	LIB3165-046-Q1-K1-B11
Method	BLASTX
NCBI GI	g20729
BLAST score	526
E value	8.0e-54
Match length	137
% identity	78
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	223428
Seq. ID	LIB3165-046-Q1-K1-B12
Method	BLASTX
NCBI GI	g266893
BLAST score	707
E value	5.0e-75
Match length	136
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__S28172 ribulose-bisphosphate carboxylase activase - cucumber >gi_18284_emb_CAA47906_ (X67674) rubisco activase [Cucumis

sativus]

Seq. No.	223429
Seq. ID	LIB3165-046-Q1-K1-B5
Method	BLASTX
NCBI GI	g2129740
BLAST score	328
E value	1.0e-30
Match length	123
% identity	56
NCBI Description	small nuclear ribonucleoprotein - Arabidopsis thaliana >gi_2129756_pir__S71411 U1 snRNP 70K protein - Arabidopsis thaliana >gi_1255711 (M93439) small nuclear ribonucleoprotein [Arabidopsis thaliana] >gi_1354469 (U52909) U1 snRNP 70K protein [Arabidopsis thaliana]

Seq. No.	223430
Seq. ID	LIB3165-046-Q1-K1-B6
Method	BLASTX
NCBI GI	g2982301
BLAST score	388
E value	1.0e-37
Match length	94
% identity	72
NCBI Description	(AF051235) YGL010w-like protein [Picea mariana]

Seq. No.	223431
Seq. ID	LIB3165-046-Q1-K1-B9
Method	BLASTX
NCBI GI	g1354515
BLAST score	243
E value	1.0e-20
Match length	127
% identity	46
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	223432
Seq. ID	LIB3165-046-Q1-K1-C1
Method	BLASTX
NCBI GI	g4510348
BLAST score	385
E value	3.0e-37
Match length	112
% identity	65
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	223433
Seq. ID	LIB3165-046-Q1-K1-C10
Method	BLASTX
NCBI GI	g1771160
BLAST score	472
E value	2.0e-47
Match length	131
% identity	68
NCBI Description	(X98929) SBT1 [Lycopersicon esculentum] >gi_3687305_emb_CAA06999_ (AJ006378) subtilisin-like

protease [Lycopersicon esculentum]

Seq. No.	223434
Seq. ID	LIB3165-046-Q1-K1-C12
Method	BLASTX
NCBI GI	g1352821
BLAST score	581
E value	3.0e-60
Match length	109
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223435
Seq. ID	LIB3165-046-Q1-K1-C3
Method	BLASTX
NCBI GI	g3914603
BLAST score	184
E value	9.0e-19
Match length	115
% identity	53
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No.	223436
Seq. ID	LIB3165-046-Q1-K1-C4
Method	BLASTX
NCBI GI	g4580460
BLAST score	454
E value	2.0e-45
Match length	117
% identity	79
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No.	223437
Seq. ID	LIB3165-046-Q1-K1-C5
Method	BLASTX
NCBI GI	g1781348
BLAST score	311
E value	8.0e-36
Match length	130
% identity	83
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No.	223438
Seq. ID	LIB3165-046-Q1-K1-C8
Method	BLASTX
NCBI GI	g1352821
BLAST score	522
E value	2.0e-53

Match length	100
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223439
Seq. ID	LIB3165-046-Q1-K1-D10
Method	BLASTX
NCBI GI	g131399
BLAST score	414
E value	9.0e-41
Match length	95
% identity	82
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi_82277_pir__S00411 photosystem II 10K protein precursor - potato >gi_21489_emb_CAA28450_ (X04753) ST-LS1 protein [Solanum tuberosum]

Seq. No.	223440
Seq. ID	LIB3165-046-Q1-K1-D11
Method	BLASTX
NCBI GI	g1881585
BLAST score	225
E value	1.0e-18
Match length	88
% identity	67
NCBI Description	(U72489) remorin [Solanum tuberosum]

Seq. No.	223441
Seq. ID	LIB3165-046-Q1-K1-D12
Method	BLASTX
NCBI GI	g131384
BLAST score	388
E value	1.0e-37
Match length	88
% identity	84
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_81934_pir__S04132 photosystem II oxygen-evolving complex protein 1 precursor - garden pea >gi_20621_emb_CAA33408_ (X15350) precursor (AA -81 to 248) [Pisum sativum] >gi_344004_dbj_BAA02554_ (D13297) precursor for 33-kDa protein of photosystem II [Pisum sativum] >gi_226937_prf__1611461A O2 evolving complex 33kD protein [Arachis hypogaea]

Seq. No.	223442
Seq. ID	LIB3165-046-Q1-K1-D5
Method	BLASTX
NCBI GI	g82188
BLAST score	468
E value	5.0e-47
Match length	134

% identity	71
NCBI Description	photosystem II oxygen-evolving complex protein 2 precursor - common tobacco (fragment) >gi_19896_emb_CAA41713_ (X58910) photosystem II 23 kDa polypeptide [Nicotiana tabacum]

Seq. No.	223443
Seq. ID	LIB3165-046-Q1-K1-D6
Method	BLASTX
NCBI GI	g231688
BLAST score	677
E value	2.0e-71
Match length	131
% identity	98
NCBI Description	CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC 1.11.1.6) - upland cotton >gi_18488_emb_CAA39998_ (X56675) subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No.	223444
Seq. ID	LIB3165-046-Q1-K1-D8
Method	BLASTX
NCBI GI	g100200
BLAST score	323
E value	5.0e-30
Match length	94
% identity	68
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	223445
Seq. ID	LIB3165-046-Q1-K1-E12
Method	BLASTX
NCBI GI	g508304
BLAST score	346
E value	1.0e-32
Match length	78
% identity	79
NCBI Description	(L22305) corC [Medicago sativa]

Seq. No.	223446
Seq. ID	LIB3165-046-Q1-K1-E2
Method	BLASTX
NCBI GI	g1168258
BLAST score	530
E value	2.0e-54
Match length	111
% identity	86
NCBI Description	ASPARTATE AMINOTRANSFERASE, CHLOROPLAST PRECURSOR (TRANSAMINASE A) >gi_693692 (U15034) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	223447
Seq. ID	LIB3165-046-Q1-K1-E6
Method	BLASTX
NCBI GI	g2827141
BLAST score	709
E value	3.0e-75
Match length	139

% identity	91
NCBI Description	(AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	223448
Seq. ID	LIB3165-046-Q1-K1-E7
Method	BLASTX
NCBI GI	g629597
BLAST score	314
E value	3.0e-29
Match length	114
% identity	63
NCBI Description	proline-rich protein - rape >gi_545029_bbs_142669 (S68113) proline-rich SAC51 [Brassica napus=oilseed rape, pods, Peptide, 147 aa] [Brassica napus]

Seq. No.	223449
Seq. ID	LIB3165-046-Q1-K1-E9
Method	BLASTX
NCBI GI	g125578
BLAST score	448
E value	1.0e-44
Match length	120
% identity	73
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_167266 (M73707) phosphoribulokinase [Mesembryanthemum crystallinum]

Seq. No.	223450
Seq. ID	LIB3165-046-Q1-K1-F1
Method	BLASTX
NCBI GI	g2501578
BLAST score	688
E value	9.0e-73
Match length	140
% identity	97
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No.	223451
Seq. ID	LIB3165-046-Q1-K1-F10
Method	BLASTX
NCBI GI	g1352821
BLAST score	138
E value	1.0e-08
Match length	47
% identity	64
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223452
Seq. ID	LIB3165-046-Q1-K1-F11

Method	BLASTX
NCBI GI	g100616
BLAST score	602
E value	1.0e-62
Match length	131
% identity	87
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	223453
Seq. ID	LIB3165-046-Q1-K1-F12
Method	BLASTX
NCBI GI	g1352821
BLAST score	586
E value	8.0e-61
Match length	110
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223454
Seq. ID	LIB3165-046-Q1-K1-F4
Method	BLASTX
NCBI GI	g4406530
BLAST score	600
E value	2.0e-62
Match length	139
% identity	83
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223455
Seq. ID	LIB3165-046-Q1-K1-F5
Method	BLASTX
NCBI GI	g231688
BLAST score	770
E value	2.0e-82
Match length	137
% identity	100
NCBI Description	CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC 1.11.1.6) - upland cotton >gi_18488_emb_CAA39998_ (X56675) subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No.	223456
Seq. ID	LIB3165-046-Q1-K1-F6
Method	BLASTX
NCBI GI	g2780194
BLAST score	287
E value	7.0e-26
Match length	59
% identity	97
NCBI Description	(AJ003197) adenine nucleotide translocator [Lupinus albus]

Seq. No.	223457
Seq. ID	LIB3165-046-Q1-K1-F7
Method	BLASTX
NCBI GI	g3044218
BLAST score	170
E value	8.0e-19
Match length	69
% identity	64
NCBI Description	(AF057144) signal peptidase [Arabidopsis thaliana]

Seq. No.	223458
Seq. ID	LIB3165-046-Q1-K1-G10
Method	BLASTX
NCBI GI	g1732411
BLAST score	211
E value	7.0e-17
Match length	126
% identity	27
NCBI Description	(U47924) isopeptidase T [Homo sapiens]

Seq. No.	223459
Seq. ID	LIB3165-046-Q1-K1-G2
Method	BLASTX
NCBI GI	g1168411
BLAST score	417
E value	5.0e-41
Match length	107
% identity	80
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	223460
Seq. ID	LIB3165-046-Q1-K1-G3
Method	BLASTX
NCBI GI	g1168411
BLAST score	434
E value	6.0e-43
Match length	111
% identity	80
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	223461
Seq. ID	LIB3165-046-Q1-K1-G4
Method	BLASTX
NCBI GI	g4572673
BLAST score	421
E value	2.0e-41
Match length	113
% identity	75
NCBI Description	(AC006954) putative sarcosine oxidase [Arabidopsis thaliana]

Seq. No.	223462
Seq. ID	LIB3165-046-Q1-K1-G5
Method	BLASTX
NCBI GI	g421826
BLAST score	334

E value	3.0e-31
Match length	105
% identity	62
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	223463
Seq. ID	LIB3165-046-Q1-K1-H1
Method	BLASTX
NCBI GI	g121344
BLAST score	627
E value	1.0e-65
Match length	139
% identity	83
NCBI Description	GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR (GLUTAMATE-AMMONIA LIGASE) (CHLOROPLAST GS2) >gi_68597_pir__AJPMQ2 glutamate--ammonia ligase (EC 6.3.1.2) delta precursor, chloroplast - garden pea >gi_169059 (M20664) glutamine synthetase (chloroplast GS2) (EC 6.3.1.2) [Pisum sativum]

Seq. No.	223464
Seq. ID	LIB3165-046-Q1-K1-H10
Method	BLASTX
NCBI GI	g1709651
BLAST score	151
E value	5.0e-10
Match length	73
% identity	47
NCBI Description	PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209 plastocyanin a precursor - black poplar >gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus nigra]

Seq. No.	223465
Seq. ID	LIB3165-046-Q1-K1-H11
Method	BLASTX
NCBI GI	g1352821
BLAST score	697
E value	8.0e-74
Match length	139
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223466
Seq. ID	LIB3165-046-Q1-K1-H2
Method	BLASTX
NCBI GI	g125578
BLAST score	679
E value	1.0e-71
Match length	140
% identity	93

NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_167266 (M73707) phosphoribulokinase [Mesembryanthemum crystallinum]
Seq. No.	223467
Seq. ID	LIB3165-046-Q1-K1-H4
Method	BLASTX
NCBI GI	g82080
BLAST score	585
E value	1.0e-60
Match length	134
% identity	81
NCBI Description	chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf__1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]
Seq. No.	223468
Seq. ID	LIB3165-046-Q1-K1-H8
Method	BLASTX
NCBI GI	g1168411
BLAST score	515
E value	2.0e-52
Match length	127
% identity	83
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
Seq. No.	223469
Seq. ID	LIB3165-046-Q1-K1-H9
Method	BLASTX
NCBI GI	g4406530
BLAST score	361
E value	2.0e-34
Match length	98
% identity	76
NCBI Description	(AF126870) rubisco activase [Vigna radiata]
Seq. No.	223470
Seq. ID	LIB3165-047-Q1-K1-A1
Method	BLASTX
NCBI GI	g2245107
BLAST score	357
E value	6.0e-34
Match length	133
% identity	38
NCBI Description	(Z97343) thioesterase homolog [Arabidopsis thaliana]
Seq. No.	223471
Seq. ID	LIB3165-047-Q1-K1-A10
Method	BLASTX
NCBI GI	g4406530
BLAST score	349
E value	5.0e-33
Match length	93
% identity	76
NCBI Description	(AF126870) rubisco activase [Vigna radiata]
Seq. No.	223472

Seq. ID	LIB3165-047-Q1-K1-A11
Method	BLASTX
NCBI GI	g100200
BLAST score	593
E value	1.0e-61
Match length	128
% identity	66
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	223473
Seq. ID	LIB3165-047-Q1-K1-A12
Method	BLASTX
NCBI GI	g1352821
BLAST score	594
E value	9.0e-62
Match length	112
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223474
Seq. ID	LIB3165-047-Q1-K1-A4
Method	BLASTX
NCBI GI	g20729
BLAST score	408
E value	7.0e-40
Match length	106
% identity	77
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	223475
Seq. ID	LIB3165-047-Q1-K1-A5
Method	BLASTX
NCBI GI	g3033389
BLAST score	160
E value	8.0e-11
Match length	86
% identity	4
NCBI Description	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]

Seq. No.	223476
Seq. ID	LIB3165-047-Q1-K1-A7
Method	BLASTX
NCBI GI	g1352821
BLAST score	574
E value	2.0e-59
Match length	108
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223477
Seq. ID	LIB3165-047-Q1-K1-A8
Method	BLASTX
NCBI GI	g1168408
BLAST score	410
E value	2.0e-40
Match length	89
% identity	92
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1 >gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828) fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No.	223478
Seq. ID	LIB3165-047-Q1-K1-A9
Method	BLASTX
NCBI GI	g3023752
BLAST score	291
E value	3.0e-26
Match length	111
% identity	56
NCBI Description	FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520) ferredoxin-I [Lycopersicon esculentum]

Seq. No.	223479
Seq. ID	LIB3165-047-Q1-K1-B1
Method	BLASTX
NCBI GI	g2290528
BLAST score	575
E value	2.0e-59
Match length	119
% identity	88
NCBI Description	(U94746) ATAN11 [Arabidopsis thaliana]

Seq. No.	223480
Seq. ID	LIB3165-047-Q1-K1-B2
Method	BLASTX
NCBI GI	g2662341
BLAST score	657
E value	4.0e-69
Match length	131
% identity	97
NCBI Description	(D63580) EF-1 alpha [Oryza sativa] >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza sativa] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha [Oryza sativa]

Seq. No.	223481
Seq. ID	LIB3165-047-Q1-K1-B3
Method	BLASTX
NCBI GI	g4512654
BLAST score	173
E value	2.0e-12
Match length	127
% identity	38
NCBI Description	(AC007048) unknown protein [Arabidopsis thaliana]

Seq. No.	223482
Seq. ID	LIB3165-047-Q1-K1-B4
Method	BLASTX
NCBI GI	g3559814
BLAST score	294
E value	1.0e-26
Match length	119
% identity	55
NCBI Description	(Y15781) transketolase 1 [Capsicum annuum]

Seq. No.	223483
Seq. ID	LIB3165-047-Q1-K1-B9
Method	BLASTX
NCBI GI	g1352821
BLAST score	540
E value	2.0e-55
Match length	104
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223484
Seq. ID	LIB3165-047-Q1-K1-C1
Method	BLASTX
NCBI GI	g100200
BLAST score	362
E value	1.0e-34
Match length	100
% identity	71
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	223485
Seq. ID	LIB3165-047-Q1-K1-C2
Method	BLASTX
NCBI GI	g1352821
BLAST score	596
E value	6.0e-62
Match length	118
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223486
Seq. ID	LIB3165-047-Q1-K1-C4
Method	BLASTX
NCBI GI	g1352821
BLAST score	590
E value	3.0e-61
Match length	110
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223487
Seq. ID	LIB3165-047-Q1-K1-C7
Method	BLASTX
NCBI GI	g1708312
BLAST score	273
E value	2.0e-24
Match length	58
% identity	97
NCBI Description	HEAT SHOCK PROTEIN 81-1 (HSP81-1) (HEAT SHOCK PROTEIN 83)

Seq. No.	223488
Seq. ID	LIB3165-047-Q1-K1-C8
Method	BLASTX
NCBI GI	g1332579
BLAST score	592
E value	1.0e-61
Match length	119
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	223489
Seq. ID	LIB3165-047-Q1-K1-D10
Method	BLASTX
NCBI GI	g2765081
BLAST score	364
E value	7.0e-35
Match length	107
% identity	68
NCBI Description	(Y10557) g5bf [Arabidopsis thaliana]

Seq. No.	223490
Seq. ID	LIB3165-047-Q1-K1-D12
Method	BLASTX
NCBI GI	g4406530
BLAST score	293
E value	2.0e-26
Match length	104
% identity	62
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223491
Seq. ID	LIB3165-047-Q1-K1-D4
Method	BLASTX
NCBI GI	g3023281
BLAST score	333
E value	5.0e-48
Match length	116
% identity	78
NCBI Description	HIGH AFFINITY AMMONIUM TRANSPORTER >gi_2065194_emb_CAA64475_ (X95098) ammonium transporter [Lycopersicon esculentum]

Seq. No.	223492
Seq. ID	LIB3165-047-Q1-K1-D6
Method	BLASTX
NCBI GI	g1346155
BLAST score	618
E value	1.0e-64
Match length	134
% identity	90
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_481942_pir__S40212 glycine hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei >gi_437995_emb_CAA81078_ (Z25859) glycine hydroxymethyltransferase [Flaveria pringlei]

Seq. No.	223493
Seq. ID	LIB3165-047-Q1-K1-D7
Method	BLASTX
NCBI GI	g3511223
BLAST score	162
E value	3.0e-11
Match length	102
% identity	41
NCBI Description	(AF069528) plant adhesion molecule 1 [Arabidopsis thaliana]

Seq. No.	223494
Seq. ID	LIB3165-047-Q1-K1-D8
Method	BLASTX
NCBI GI	g20733
BLAST score	560
E value	9.0e-58
Match length	115
% identity	88
NCBI Description	(X15188) precursor C-terminal fragment (AA -80 to 367) [Pisum sativum]

Seq. No.	223495
Seq. ID	LIB3165-047-Q1-K1-D9
Method	BLASTX
NCBI GI	g4406530
BLAST score	389
E value	1.0e-37
Match length	111
% identity	74
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223496
Seq. ID	LIB3165-047-Q1-K1-E1
Method	BLASTX
NCBI GI	g3869088
BLAST score	587
E value	6.0e-61
Match length	112
% identity	99
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No.	223497

Seq. ID	LIB3165-047-Q1-K1-E12
Method	BLASTX
NCBI GI	g2129921
BLAST score	185
E value	9.0e-14
Match length	51
% identity	73
NCBI Description	hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]

Seq. No.	223498
Seq. ID	LIB3165-047-Q1-K1-E2
Method	BLASTX
NCBI GI	g1168411
BLAST score	509
E value	9.0e-52
Match length	126
% identity	83
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	223499
Seq. ID	LIB3165-047-Q1-K1-E3
Method	BLASTX
NCBI GI	g4512018
BLAST score	157
E value	1.0e-10
Match length	96
% identity	45
NCBI Description	(AF106660) mRNA binding protein precursor [Lycopersicon esculentum]

Seq. No.	223500
Seq. ID	LIB3165-047-Q1-K1-E4
Method	BLASTX
NCBI GI	g126894
BLAST score	580
E value	4.0e-60
Match length	131
% identity	85
NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi_319832_pir__DEPUGW malate dehydrogenase (EC 1.1.1.37) precursor, glyoxysomal - watermelon >gi_167284 (M33148) glyoxysomal malate dehydrogenase precursor (EC 1.1.1.37) [Citrullus vulgaris]

Seq. No.	223501
Seq. ID	LIB3165-047-Q1-K1-E7
Method	BLASTX
NCBI GI	g289920
BLAST score	598
E value	3.0e-62
Match length	112
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	223502

Seq. ID	LIB3165-047-Q1-K1-E8
Method	BLASTX
NCBI GI	g3868853
BLAST score	141
E value	1.0e-08
Match length	50
% identity	62
NCBI Description	(AB013853) GPI-anchored protein [Vigna radiata]

Seq. No.	223503
Seq. ID	LIB3165-047-Q1-K1-F12
Method	BLASTX
NCBI GI	g131385
BLAST score	500
E value	1.0e-50
Match length	125
% identity	83
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN)

Seq. No.	223504
Seq. ID	LIB3165-047-Q1-K1-F2
Method	BLASTX
NCBI GI	g1352821
BLAST score	490
E value	1.0e-49
Match length	104
% identity	89
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223505
Seq. ID	LIB3165-047-Q1-K1-F6
Method	BLASTX
NCBI GI	g729882
BLAST score	268
E value	2.0e-23
Match length	97
% identity	57
NCBI Description	CASEIN KINASE II BETA' CHAIN (CK II) >gi_1076300_pir__S47968 casein kinase II (EC 2.7.1.-) beta chain CKB2 - Arabidopsis thaliana >gi_467975 (U03984) casein kinase II beta subunit CKB2 [Arabidopsis thaliana] >gi_2245122_emb_CAB10544_ (Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No.	223506
Seq. ID	LIB3165-047-Q1-K1-F7
Method	BLASTX
NCBI GI	g3286721
BLAST score	193
E value	4.0e-15
Match length	65

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% identity	66
NCBI Description	(AJ007449) trans-cinnamic 4-monooxygenase [Cicer arietinum]

Seq. No.	223507
Seq. ID	LIB3165-047-Q1-K1-F8
Method	BLASTX
NCBI GI	g3297815
BLAST score	176
E value	8.0e-13
Match length	42
% identity	76
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	223508
Seq. ID	LIB3165-047-Q1-K1-G1
Method	BLASTX
NCBI GI	g1352821
BLAST score	522
E value	3.0e-53
Match length	100
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223509
Seq. ID	LIB3165-047-Q1-K1-G12
Method	BLASTX
NCBI GI	g1354515
BLAST score	315
E value	5.0e-29
Match length	138
% identity	51
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	223510
Seq. ID	LIB3165-047-Q1-K1-G3
Method	BLASTX
NCBI GI	g1181599
BLAST score	332
E value	4.0e-31
Match length	111
% identity	63
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.	223511
Seq. ID	LIB3165-047-Q1-K1-G5
Method	BLASTX
NCBI GI	g231688
BLAST score	283
E value	1.0e-48
Match length	123
% identity	82
NCBI Description	CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC

	1.11.1.6) - upland cotton >gi_18488_emb_CAA39998_ (X56675) subunit 2 of cotton catalase [Gossypium hirsutum]
Seq. No.	223512
Seq. ID	LIB3165-047-Q1-K1-G6
Method	BLASTX
NCBI GI	g1352821
BLAST score	173
E value	1.0e-26
Match length	81
% identity	80
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	223513
Seq. ID	LIB3165-047-Q1-K1-G7
Method	BLASTX
NCBI GI	g2982458
BLAST score	196
E value	4.0e-15
Match length	45
% identity	87
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]
Seq. No.	223514
Seq. ID	LIB3165-047-Q1-K1-G8
Method	BLASTX
NCBI GI	g505482
BLAST score	399
E value	6.0e-39
Match length	104
% identity	81
NCBI Description	(X64349) 33 kDa polypeptide of water-oxidizing complex of photosystem II [Nicotiana tabacum]
Seq. No.	223515
Seq. ID	LIB3165-047-Q1-K1-H10
Method	BLASTX
NCBI GI	g1652798
BLAST score	259
E value	2.0e-22
Match length	96
% identity	58
NCBI Description	(D90908) GcpE [Synechocystis sp.]
Seq. No.	223516
Seq. ID	LIB3165-047-Q1-K1-H11
Method	BLASTX
NCBI GI	g1508783
BLAST score	253
E value	9.0e-22
Match length	123
% identity	48
NCBI Description	(Z54351) SecY [Spinacia oleracea]

Seq. No.	223517
Seq. ID	LIB3165-047-Q1-K1-H12
Method	BLASTX
NCBI GI	g1362005
BLAST score	231
E value	3.0e-19
Match length	110
% identity	49
NCBI Description	secY protein homolog precursor - Arabidopsis thaliana

Seq. No.	223518
Seq. ID	LIB3165-047-Q1-K1-H4
Method	BLASTX
NCBI GI	g131397
BLAST score	298
E value	5.0e-27
Match length	129
% identity	54
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_81480_pir__S00008 photosystem II oxygen-evolving complex protein 3 precursor - spinach >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi_225597_prf__1307179B luminal protein 16kD [Spinacia oleracea]

Seq. No.	223519
Seq. ID	LIB3165-047-Q1-K1-H5
Method	BLASTX
NCBI GI	g3269292
BLAST score	245
E value	7.0e-21
Match length	62
% identity	73
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	223520
Seq. ID	LIB3165-047-Q1-K1-H6
Method	BLASTX
NCBI GI	g3319921
BLAST score	147
E value	2.0e-11
Match length	89
% identity	47
NCBI Description	(AJ223388) Hev b 3 [Hevea brasiliensis] >gi_3319923_emb_CAA11304_ (AJ223389) Hev b 3 [Hevea brasiliensis] >gi_3319925_emb_CAA11305_ (AJ223390) Hev b 3 [Hevea brasiliensis] >gi_3818475 (AF051317) small rubber particle protein [Hevea brasiliensis]

Seq. No.	223521
Seq. ID	LIB3165-047-Q1-K1-H7
Method	BLASTX
NCBI GI	g1168408
BLAST score	390

E value	5.0e-38
Match length	98
% identity	82
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1 >gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828) fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No.	223522
Seq. ID	LIB3165-047-Q1-K1-H8
Method	BLASTX
NCBI GI	g3559814
BLAST score	147
E value	2.0e-09
Match length	48
% identity	69
NCBI Description	(Y15781) transketolase 1 [Capsicum annuum]

Seq. No.	223523
Seq. ID	LIB3165-047-Q1-K1-H9
Method	BLASTX
NCBI GI	g228403
BLAST score	439
E value	1.0e-43
Match length	93
% identity	90
NCBI Description	glycolate oxidase [Lens culinaris]

Seq. No.	223524
Seq. ID	LIB3165-048-Q1-K1-A1
Method	BLASTX
NCBI GI	g266936
BLAST score	455
E value	2.0e-45
Match length	125
% identity	76
NCBI Description	50S RIBOSOMAL PROTEIN L27, CHLOROPLAST PRECURSOR (CL27) >gi_282960_pir__A42840 ribosomal protein L27 - common tobacco >gi_170306 (M98473) ribosomal protein L27 [Nicotiana tabacum] >gi_170326 (M75731) ribosomal protein L27 [Nicotiana tabacum]

Seq. No.	223525
Seq. ID	LIB3165-048-Q1-K1-A10
Method	BLASTX
NCBI GI	g3236248
BLAST score	331
E value	5.0e-31
Match length	93
% identity	73
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	223526
Seq. ID	LIB3165-048-Q1-K1-A11
Method	BLASTX
NCBI GI	g2341045
BLAST score	313

E value	9.0e-29
Match length	136
% identity	45
NCBI Description	(AC000104) F19P19.16 [Arabidopsis thaliana]

Seq. No.	223527
Seq. ID	LIB3165-048-Q1-K1-A12
Method	BLASTX
NCBI GI	g4008159
BLAST score	698
E value	6.0e-74
Match length	137
% identity	93
NCBI Description	(AB015601) DnaJ homolog [Salix gilgiana]

Seq. No.	223528
Seq. ID	LIB3165-048-Q1-K1-A2
Method	BLASTX
NCBI GI	g4490313
BLAST score	411
E value	2.0e-40
Match length	111
% identity	72
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	223529
Seq. ID	LIB3165-048-Q1-K1-A4
Method	BLASTX
NCBI GI	g1352821
BLAST score	632
E value	4.0e-66
Match length	117
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223530
Seq. ID	LIB3165-048-Q1-K1-A5
Method	BLASTX
NCBI GI	g3980238
BLAST score	169
E value	7.0e-12
Match length	46
% identity	63
NCBI Description	(Z21677) ribosomal protein L18 [Thermotoga maritima]

Seq. No.	223531
Seq. ID	LIB3165-048-Q1-K1-A6
Method	BLASTX
NCBI GI	g1168408
BLAST score	634
E value	2.0e-66
Match length	135
% identity	92

NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1 >gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828) fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No.	223532
Seq. ID	LIB3165-048-Q1-K1-A8
Method	BLASTX
NCBI GI	g1170897
BLAST score	497
E value	2.0e-50
Match length	111
% identity	87
NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi_1076276_pir__S52039 NAD-malate dehydrogenase - cucumber >gi_695311 (L31900) glyoxysomal malate dehydrogenase [Cucumis sativus]

Seq. No.	223533
Seq. ID	LIB3165-048-Q1-K1-A9
Method	BLASTX
NCBI GI	g3738257
BLAST score	346
E value	6.0e-33
Match length	79
% identity	85
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	223534
Seq. ID	LIB3165-048-Q1-K1-B1
Method	BLASTX
NCBI GI	g2801536
BLAST score	266
E value	2.0e-23
Match length	75
% identity	69
NCBI Description	(AF039531) lysophospholipase homolog [Oryza sativa]

Seq. No.	223535
Seq. ID	LIB3165-048-Q1-K1-B10
Method	BLASTX
NCBI GI	g100200
BLAST score	649
E value	3.0e-68
Match length	141
% identity	69
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	223536
Seq. ID	LIB3165-048-Q1-K1-B11
Method	BLASTX
NCBI GI	g542157
BLAST score	626
E value	2.0e-65
Match length	144
% identity	82

NCBI Description	ribosomal 5S RNA-binding protein - Rice
Seq. No.	223537
Seq. ID	LIB3165-048-Q1-K1-B2
Method	BLASTX
NCBI GI	g430947
BLAST score	492
E value	9.0e-50
Match length	119
% identity	82
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]
Seq. No.	223538
Seq. ID	LIB3165-048-Q1-K1-B4
Method	BLASTX
NCBI GI	g400890
BLAST score	194
E value	4.0e-15
Match length	53
% identity	38
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_282837_pir__S26953 photosystem II 22K protein precursor - spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864) photosystem II 22 kda polypeptide [spinach, Peptide, 274 aa] [Spinacia oleracea]
Seq. No.	223539
Seq. ID	LIB3165-048-Q1-K1-B5
Method	BLASTX
NCBI GI	g2190992
BLAST score	378
E value	2.0e-36
Match length	142
% identity	54
NCBI Description	(AF004358) glutathione S-transferase TSI-1 [Aegilops tauschii]
Seq. No.	223540
Seq. ID	LIB3165-048-Q1-K1-B6
Method	BLASTX
NCBI GI	g1352821
BLAST score	464
E value	2.0e-46
Match length	102
% identity	89
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	223541
Seq. ID	LIB3165-048-Q1-K1-B8
Method	BLASTX
NCBI GI	g493636

BLAST score	382
E value	7.0e-37
Match length	96
% identity	44
NCBI Description	(D29684) predicted polypeptide for cytokinin-repressed mRNA [Cucumis sativus] >gi_746031_prf__2016504A cytokinin-repressed protein CR9 [Cucumis sativus]

Seq. No.	223542
Seq. ID	LIB3165-048-Q1-K1-B9
Method	BLASTX
NCBI GI	g4406530
BLAST score	358
E value	4.0e-34
Match length	104
% identity	73
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223543
Seq. ID	LIB3165-048-Q1-K1-C1
Method	BLASTX
NCBI GI	g121344
BLAST score	294
E value	1.0e-26
Match length	93
% identity	60
NCBI Description	GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR (GLUTAMATE-AMMONIA LIGASE) (CHLOROPLAST GS2) >gi_68597_pir__AJPMQ2 glutamate--ammonia ligase (EC 6.3.1.2) delta precursor, chloroplast - garden pea >gi_169059 (M20664) glutamine synthetase (chloroplast GS2) (EC 6.3.1.2) [Pisum sativum]

Seq. No.	223544
Seq. ID	LIB3165-048-Q1-K1-C10
Method	BLASTX
NCBI GI	g1332579
BLAST score	496
E value	2.0e-70
Match length	145
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	223545
Seq. ID	LIB3165-048-Q1-K1-C11
Method	BLASTX
NCBI GI	g2760320
BLAST score	360
E value	2.0e-34
Match length	109
% identity	68
NCBI Description	(AC002130) F1N21.4 [Arabidopsis thaliana]

Seq. No.	223546
Seq. ID	LIB3165-048-Q1-K1-C2
Method	BLASTX
NCBI GI	g4545262

BLAST score	165
E value	2.0e-11
Match length	44
% identity	66
NCBI Description	(AF118230) metallothionein-like protein [Gossypium hirsutum]

Seq. No.	223547
Seq. ID	LIB3165-048-Q1-K1-C4
Method	BLASTX
NCBI GI	g445116
BLAST score	577
E value	7.0e-60
Match length	120
% identity	88
NCBI Description	light-harvesting complex IIa protein; [Hordeum vulgare]

Seq. No.	223548
Seq. ID	LIB3165-048-Q1-K1-C6
Method	BLASTX
NCBI GI	g4469014
BLAST score	441
E value	9.0e-44
Match length	141
% identity	67
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	223549
Seq. ID	LIB3165-048-Q1-K1-C7
Method	BLASTX
NCBI GI	g3914603
BLAST score	646
E value	8.0e-68
Match length	137
% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No.	223550
Seq. ID	LIB3165-048-Q1-K1-C8
Method	BLASTX
NCBI GI	g1730502
BLAST score	251
E value	2.0e-21
Match length	91
% identity	51
NCBI Description	TRANSMEMBRANE PROTEIN PFT27 >gi_110903_pir__A31351 probable transmembrane protein FT27 - mouse >gi_535682 (M23568) transmembrane protein [Mus musculus]

Seq. No.	223551
Seq. ID	LIB3165-048-Q1-K1-C9
Method	BLASTX
NCBI GI	g1352821
BLAST score	543

E value	9.0e-56
Match length	103
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223552
Seq. ID	LIB3165-048-Q1-K1-D1
Method	BLASTX
NCBI GI	g625546
BLAST score	322
E value	6.0e-37
Match length	126
% identity	63
NCBI Description	photosystem II oxygen-evolving complex protein 2 precursor - common tobacco >gi_417604_emb_CAA45699_ (X64347) 23 kDa polypeptide of water-oxidizing complex of photosystem II [Nicotiana tabacum]

Seq. No.	223553
Seq. ID	LIB3165-048-Q1-K1-D10
Method	BLASTX
NCBI GI	g2924520
BLAST score	570
E value	6.0e-59
Match length	124
% identity	88
NCBI Description	(AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]

Seq. No.	223554
Seq. ID	LIB3165-048-Q1-K1-D11
Method	BLASTX
NCBI GI	g2894603
BLAST score	186
E value	7.0e-14
Match length	95
% identity	23
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	223555
Seq. ID	LIB3165-048-Q1-K1-D12
Method	BLASTX
NCBI GI	g2496789
BLAST score	583
E value	2.0e-60
Match length	139
% identity	79
NCBI Description	1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE (DXP REDUCTOISOMERASE) >gi_1001556_dbj_BAA10183_ (D64000) hypothetical protein [Synechocystis sp.]

Seq. No.	223556
Seq. ID	LIB3165-048-Q1-K1-D2

Method	BLASTX
NCBI GI	g4454010
BLAST score	442
E value	7.0e-44
Match length	142
% identity	60
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	223557
Seq. ID	LIB3165-048-Q1-K1-D3
Method	BLASTX
NCBI GI	g100454
BLAST score	620
E value	8.0e-65
Match length	144
% identity	87
NCBI Description	photosystem II oxygen-evolving complex protein 1 - potato >gi_809113_emb_CAA35601_ (X17578) 33kDa precursor protein of oxygen-evolving complex [Solanum tuberosum]

Seq. No.	223558
Seq. ID	LIB3165-048-Q1-K1-D5
Method	BLASTX
NCBI GI	g1168411
BLAST score	550
E value	1.0e-56
Match length	133
% identity	84
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	223559
Seq. ID	LIB3165-048-Q1-K1-D6
Method	BLASTX
NCBI GI	g3334245
BLAST score	446
E value	2.0e-44
Match length	104
% identity	80
NCBI Description	LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi_2909424_emb_CAA12028_ (AJ224520) Glyoxalase I [Cicer arietinum]

Seq. No.	223560
Seq. ID	LIB3165-048-Q1-K1-D8
Method	BLASTX
NCBI GI	g2832664
BLAST score	202
E value	9.0e-16
Match length	82
% identity	45
NCBI Description	(AL021710) pollen-specific protein - like [Arabidopsis thaliana]

Seq. No.	223561
Seq. ID	LIB3165-048-Q1-K1-D9

Method	BLASTX
NCBI GI	g282865
BLAST score	568
E value	1.0e-58
Match length	131
% identity	83
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	223562
Seq. ID	LIB3165-048-Q1-K1-E1
Method	BLASTX
NCBI GI	g421809
BLAST score	418
E value	4.0e-41
Match length	143
% identity	64
NCBI Description	dnaJ protein homolog DnaJ-1 - cucumber

Seq. No.	223563
Seq. ID	LIB3165-048-Q1-K1-E10
Method	BLASTX
NCBI GI	g2190012
BLAST score	281
E value	5.0e-25
Match length	90
% identity	63
NCBI Description	(AB004242) din1 [Raphanus sativus]

Seq. No.	223564
Seq. ID	LIB3165-048-Q1-K1-E12
Method	BLASTX
NCBI GI	g2347054
BLAST score	377
E value	2.0e-36
Match length	109
% identity	70
NCBI Description	(X96791) arginine decarboxylase [Vitis vinifera]

Seq. No.	223565
Seq. ID	LIB3165-048-Q1-K1-E2
Method	BLASTX
NCBI GI	g3341679
BLAST score	266
E value	2.0e-23
Match length	73
% identity	78
NCBI Description	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]

Seq. No.	223566
Seq. ID	LIB3165-048-Q1-K1-E3
Method	BLASTX
NCBI GI	g3298439
BLAST score	442

E value	7.0e-44
Match length	129
% identity	50
NCBI Description	(AB010878) chloroplast ribosomal protein L4 [Nicotiana tabacum]

Seq. No.	223567
Seq. ID	LIB3165-048-Q1-K1-E7
Method	BLASTX
NCBI GI	g2708749
BLAST score	351
E value	3.0e-33
Match length	111
% identity	59
NCBI Description	(AC003952) putative senescence-assoc. rhodanese-like protein [Arabidopsis thaliana]

Seq. No.	223568
Seq. ID	LIB3165-048-Q1-K1-E8
Method	BLASTX
NCBI GI	g421826
BLAST score	409
E value	5.0e-40
Match length	83
% identity	86
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	223569
Seq. ID	LIB3165-048-Q1-K1-E9
Method	BLASTX
NCBI GI	g1684716
BLAST score	363
E value	1.0e-34
Match length	110
% identity	60
NCBI Description	(Y09424) cytochrome P450 [Nepeta racemosa]

Seq. No.	223570
Seq. ID	LIB3165-048-Q1-K1-F1
Method	BLASTX
NCBI GI	g2497742
BLAST score	178
E value	4.0e-13
Match length	35
% identity	94
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) >gi_995907 (U15153) nonspecific lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	223571
Seq. ID	LIB3165-048-Q1-K1-F12
Method	BLASTX
NCBI GI	g3687243
BLAST score	178
E value	3.0e-14

Match length	60
% identity	75
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	223572
Seq. ID	LIB3165-048-Q1-K1-F2
Method	BLASTX
NCBI GI	g480450
BLAST score	422
E value	1.0e-41
Match length	109
% identity	77
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No.	223573
Seq. ID	LIB3165-048-Q1-K1-F3
Method	BLASTX
NCBI GI	g3702327
BLAST score	249
E value	3.0e-21
Match length	122
% identity	52
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	223574
Seq. ID	LIB3165-048-Q1-K1-F4
Method	BLASTX
NCBI GI	g1709651
BLAST score	148
E value	7.0e-10
Match length	54
% identity	54
NCBI Description	PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209 plastocyanin a precursor - black poplar >gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus nigra]

Seq. No.	223575
Seq. ID	LIB3165-048-Q1-K1-G1
Method	BLASTX
NCBI GI	g4510373
BLAST score	349
E value	5.0e-33
Match length	117
% identity	60
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]

Seq. No.	223576
Seq. ID	LIB3165-048-Q1-K1-G10
Method	BLASTX
NCBI GI	g3288821
BLAST score	640
E value	4.0e-67

Match length	130
% identity	92
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana]

Seq. No.	223577
Seq. ID	LIB3165-048-Q1-K1-G11
Method	BLASTX
NCBI GI	g1352821
BLAST score	706
E value	7.0e-75
Match length	129
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223578
Seq. ID	LIB3165-048-Q1-K1-G12
Method	BLASTX
NCBI GI	g1781348
BLAST score	540
E value	2.0e-55
Match length	118
% identity	89
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No.	223579
Seq. ID	LIB3165-048-Q1-K1-G4
Method	BLASTX
NCBI GI	g409756
BLAST score	261
E value	1.0e-22
Match length	122
% identity	45
NCBI Description	(L25643) ATP/GTP nucleotide-binding protein [Leishmania infantum]

Seq. No.	223580
Seq. ID	LIB3165-048-Q1-K1-G5
Method	BLASTX
NCBI GI	g289920
BLAST score	663
E value	8.0e-70
Match length	124
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	223581
Seq. ID	LIB3165-048-Q1-K1-G7
Method	BLASTX
NCBI GI	g68200
BLAST score	417

E value	6.0e-41
Match length	107
% identity	80
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	223582
Seq. ID	LIB3165-048-Q1-K1-G9
Method	BLASTX
NCBI GI	g2462762
BLAST score	266
E value	2.0e-23
Match length	100
% identity	56
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	223583
Seq. ID	LIB3165-048-Q1-K1-H1
Method	BLASTX
NCBI GI	g4056456
BLAST score	415
E value	8.0e-41
Match length	141
% identity	62
NCBI Description	(AC005990) Strong similarity to gb_U20808 auxin-induced protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF_00107. ESTs gb_T43674, gb_H77006 and gb_AA395179 come from this gene. [Arabidopsis thaliana]

Seq. No.	223584
Seq. ID	LIB3165-048-Q1-K1-H10
Method	BLASTX
NCBI GI	g1006610
BLAST score	344
E value	2.0e-32
Match length	126
% identity	52
NCBI Description	(D64005) hypothetical protein [Synechocystis sp.]

Seq. No.	223585
Seq. ID	LIB3165-048-Q1-K1-H12
Method	BLASTX
NCBI GI	g166835
BLAST score	252
E value	3.0e-22
Match length	65
% identity	74
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642170 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	223586
Seq. ID	LIB3165-048-Q1-K1-H2
Method	BLASTX
NCBI GI	g100203

BLAST score	261
E value	9.0e-23
Match length	91
% identity	60
NCBI Description	cysteine proteinase (EC 3.4.22.-) precursor - tomato >gi_19195_emb_CAA78403_ (Z14028) pre-pro-cysteine proteinase [Lycopersicon esculentum]

Seq. No.	223587
Seq. ID	LIB3165-048-Q1-K1-H4
Method	BLASTX
NCBI GI	g3800853
BLAST score	324
E value	3.0e-30
Match length	102
% identity	68
NCBI Description	(AF084478) ribulose-1,5-bisphosphate carboxylase/oxygenase activase precursor [Zea mays]

Seq. No.	223588
Seq. ID	LIB3165-048-Q1-K1-H7
Method	BLASTX
NCBI GI	g3928084
BLAST score	338
E value	9.0e-32
Match length	119
% identity	59
NCBI Description	(AC005770) retrotransposon-like protein [Arabidopsis thaliana]

Seq. No.	223589
Seq. ID	LIB3165-048-Q1-K1-H8
Method	BLASTX
NCBI GI	g4406049
BLAST score	373
E value	5.0e-36
Match length	113
% identity	58
NCBI Description	(AF067604) linalool synthase-like protein [Oenothera arizonica]

Seq. No.	223590
Seq. ID	LIB3165-049-Q1-K1-A10
Method	BLASTX
NCBI GI	g1170168
BLAST score	200
E value	1.0e-15
Match length	108
% identity	48
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT1 (HD-ZIP PROTEIN 1) >gi_549883 (U09332) homeobox protein [Arabidopsis thaliana] >gi_549884 (U09333) homeobox protein [Arabidopsis thaliana] >gi_2245105_emb_CAB10527_ (Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No.	223591
Seq. ID	LIB3165-049-Q1-K1-A11

Method	BLASTX
NCBI GI	g4128133
BLAST score	253
E value	9.0e-22
Match length	97
% identity	49
NCBI Description	(AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]

Seq. No.	223592
Seq. ID	LIB3165-049-Q1-K1-A12
Method	BLASTX
NCBI GI	g1814405
BLAST score	653
E value	1.0e-68
Match length	137
% identity	49
NCBI Description	(U84890) putative phosphate permease [Mesembryanthemum crystallinum]

Seq. No.	223593
Seq. ID	LIB3165-049-Q1-K1-A3
Method	BLASTX
NCBI GI	g430947
BLAST score	471
E value	2.0e-47
Match length	119
% identity	80
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	223594
Seq. ID	LIB3165-049-Q1-K1-A4
Method	BLASTX
NCBI GI	g4415908
BLAST score	154
E value	4.0e-10
Match length	74
% identity	46
NCBI Description	(AC006282) unknown protein [Arabidopsis thaliana]

Seq. No.	223595
Seq. ID	LIB3165-049-Q1-K1-A5
Method	BLASTX
NCBI GI	g4097547
BLAST score	233
E value	2.0e-19
Match length	49
% identity	46
NCBI Description	(U64906) ATFP3 [Arabidopsis thaliana]

Seq. No.	223596
Seq. ID	LIB3165-049-Q1-K1-A8
Method	BLASTX
NCBI GI	g1172664
BLAST score	264
E value	5.0e-23
Match length	56

% identity	91
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_419791_pir__S31165 photosystem I chain III precursor - Flaveria trinervia >gi_298482_bbs_127083 photosystem I reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem I subunit III [Flaveria trinervia]

Seq. No.	223597
Seq. ID	LIB3165-049-Q1-K1-B5
Method	BLASTX
NCBI GI	g2739375
BLAST score	195
E value	5.0e-15
Match length	102
% identity	47
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	223598
Seq. ID	LIB3165-049-Q1-K1-B6
Method	BLASTX
NCBI GI	g1352821
BLAST score	555
E value	4.0e-57
Match length	109
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223599
Seq. ID	LIB3165-049-Q1-K1-B7
Method	BLASTX
NCBI GI	g4335763
BLAST score	141
E value	1.0e-08
Match length	48
% identity	54
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	223600
Seq. ID	LIB3165-049-Q1-K1-B8
Method	BLASTX
NCBI GI	g1352821
BLAST score	574
E value	2.0e-59
Match length	110
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223601
Seq. ID	LIB3165-049-Q1-K1-C11
Method	BLASTX
NCBI GI	g2754849
BLAST score	492
E value	1.0e-51
Match length	117
% identity	81
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

Seq. No.	223602
Seq. ID	LIB3165-049-Q1-K1-C12
Method	BLASTX
NCBI GI	g131399
BLAST score	157
E value	5.0e-11
Match length	54
% identity	61
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi_82277_pir__S00411 photosystem II 10K protein precursor - potato >gi_21489_emb_CAA28450_ (X04753) ST-LS1 protein [Solanum tuberosum]

Seq. No.	223603
Seq. ID	LIB3165-049-Q1-K1-C2
Method	BLASTX
NCBI GI	g3786016
BLAST score	255
E value	5.0e-22
Match length	95
% identity	55
NCBI Description	(AC005499) putative elongation factor [Arabidopsis thaliana]

Seq. No.	223604
Seq. ID	LIB3165-049-Q1-K1-C4
Method	BLASTX
NCBI GI	g3249084
BLAST score	444
E value	4.0e-44
Match length	114
% identity	23
NCBI Description	(AC004473) Similar to red-1 (related to thioredoxin) gene gb_X92750 from Mus musculus. ESTs gb_AA712687 and gb_Z37223 come from this gene [Arabidopsis thaliana]

Seq. No.	223605
Seq. ID	LIB3165-049-Q1-K1-C8
Method	BLASTX
NCBI GI	g2499967
BLAST score	265
E value	4.0e-23
Match length	125
% identity	49
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV B PRECURSOR (PSI-E

B) >gi_632724_bbs_151002 (S72358) photosystem I subunit PSI-E [Nicotiana sylvestris, leaves, Peptide Chloroplast, 143 aa] [Nicotiana sylvestris]

Seq. No.	223606
Seq. ID	LIB3165-049-Q1-K1-D10
Method	BLASTX
NCBI GI	g505482
BLAST score	425
E value	6.0e-42
Match length	117
% identity	77
NCBI Description	(X64349) 33 kDa polypeptide of water-oxidizing complex of photosystem II [Nicotiana tabacum]

Seq. No.	223607
Seq. ID	LIB3165-049-Q1-K1-D12
Method	BLASTX
NCBI GI	g1055130
BLAST score	186
E value	7.0e-14
Match length	95
% identity	37
NCBI Description	(U39998) coded for by C. elegans cDNA yk92b11.3; coded for by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA yk78c2.3

Seq. No.	223608
Seq. ID	LIB3165-049-Q1-K1-D5
Method	BLASTX
NCBI GI	g2499945
BLAST score	521
E value	4.0e-53
Match length	138
% identity	69
NCBI Description	URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_1076363_pir__S46440 orotate phosphoribosyltransferase (EC 2.4.2.10) / orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842) pyrE-F [Arabidopsis thaliana]

Seq. No.	223609
Seq. ID	LIB3165-049-Q1-K1-D7
Method	BLASTX
NCBI GI	g1076315
BLAST score	370
E value	2.0e-35
Match length	83
% identity	81
NCBI Description	cytochrome P450 - Arabidopsis thaliana >gi_853719_emb_CAA60793_ (X87367) CYP90 protein [Arabidopsis thaliana] >gi_871988_emb_CAA60794_ (X87368) CYP90 protein [Arabidopsis thaliana]

Seq. No.	223610
Seq. ID	LIB3165-049-Q1-K1-D8
Method	BLASTX
NCBI GI	g1354515
BLAST score	289
E value	5.0e-26
Match length	111
% identity	57
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	223611
Seq. ID	LIB3165-049-Q1-K1-E1
Method	BLASTX
NCBI GI	g2160158
BLAST score	241
E value	2.0e-20
Match length	44
% identity	95
NCBI Description	(AC000132) Similar to elongation factor 1-gamma (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come from this gene. [Arabidopsis thaliana]

Seq. No.	223612
Seq. ID	LIB3165-049-Q1-K1-E10
Method	BLASTX
NCBI GI	g3201969
BLAST score	456
E value	1.0e-45
Match length	119
% identity	66
NCBI Description	(AF068332) submergence induced protein 2A [Oryza sativa]

Seq. No.	223613
Seq. ID	LIB3165-049-Q1-K1-E12
Method	BLASTX
NCBI GI	g2281633
BLAST score	440
E value	9.0e-44
Match length	119
% identity	71
NCBI Description	(AF003097) AP2 domain containing protein RAP2.4 [Arabidopsis thaliana]

Seq. No.	223614
Seq. ID	LIB3165-049-Q1-K1-E3
Method	BLASTX
NCBI GI	g131385
BLAST score	518
E value	8.0e-53
Match length	128
% identity	84
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN)

Seq. No.	223615
Seq. ID	LIB3165-049-Q1-K1-E4
Method	BLASTX
NCBI GI	g2462781
BLAST score	151
E value	9.0e-10
Match length	74
% identity	49
NCBI Description	(U73175) carbamoyl phosphate synthetase small subunit [Arabidopsis thaliana]

Seq. No.	223616
Seq. ID	LIB3165-049-Q1-K1-E9
Method	BLASTX
NCBI GI	g3288821
BLAST score	431
E value	1.0e-42
Match length	109
% identity	76
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana]

Seq. No.	223617
Seq. ID	LIB3165-049-Q1-K1-F10
Method	BLASTX
NCBI GI	g3023752
BLAST score	341
E value	4.0e-32
Match length	114
% identity	62
NCBI Description	FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520) ferredoxin-I [Lycopersicon esculentum]

Seq. No.	223618
Seq. ID	LIB3165-049-Q1-K1-F2
Method	BLASTX
NCBI GI	g100616
BLAST score	159
E value	8.0e-11
Match length	45
% identity	73
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	223619
Seq. ID	LIB3165-049-Q1-K1-F3
Method	BLASTX
NCBI GI	g4406530
BLAST score	352
E value	2.0e-33
Match length	119
% identity	63
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223620
Seq. ID	LIB3165-049-Q1-K1-F4
Method	BLASTX
NCBI GI	g2462929
BLAST score	164
E value	2.0e-11
Match length	44
% identity	64
NCBI Description	(Y12295) glutathione transferase [Arabidopsis thaliana]

Seq. No.	223621
Seq. ID	LIB3165-049-Q1-K1-F7
Method	BLASTX
NCBI GI	g549063
BLAST score	304
E value	8.0e-28
Match length	81
% identity	72
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]

Seq. No.	223622
Seq. ID	LIB3165-049-Q1-K1-F9
Method	BLASTX
NCBI GI	g1928981
BLAST score	572
E value	4.0e-59
Match length	126
% identity	90
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	223623
Seq. ID	LIB3165-049-Q1-K1-G11
Method	BLASTX
NCBI GI	g3800853
BLAST score	357
E value	4.0e-34
Match length	101
% identity	73
NCBI Description	(AF084478) ribulose-1,5-bisphosphate carboxylase/oxygenase activase precursor [Zea mays]

Seq. No.	223624
Seq. ID	LIB3165-049-Q1-K1-G2
Method	BLASTX
NCBI GI	g1352821
BLAST score	590
E value	3.0e-61
Match length	110
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223625
Seq. ID	LIB3165-049-Q1-K1-G4
Method	BLASTX
NCBI GI	g2828292
BLAST score	281
E value	4.0e-25
Match length	75
% identity	72
NCBI Description	(AL021687) neoxanthin cleavage enzyme-like protein [Arabidopsis thaliana]

Seq. No.	223626
Seq. ID	LIB3165-049-Q1-K1-G5
Method	BLASTX
NCBI GI	g2828292
BLAST score	381
E value	1.0e-36
Match length	93
% identity	76
NCBI Description	(AL021687) neoxanthin cleavage enzyme-like protein [Arabidopsis thaliana]

Seq. No.	223627
Seq. ID	LIB3165-049-Q1-K1-G8
Method	BLASTX
NCBI GI	g117290
BLAST score	251
E value	2.0e-21
Match length	119
% identity	47
NCBI Description	CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT) (P36) (E30) >gi_100071_pir__S23774 triose phosphate/3-phosphoglycerate/phosphate translocator precursor - garden pea >gi_20691_emb_CAA38451_ (X54639) chloroplast import receptor p36 [Pisum sativum] >gi_20853_emb_CAA48210_ (X68077) phosphate translocator [Pisum sativum] >gi_228551_prf__1805409A phosphate translocator [Pisum sativum]

Seq. No.	223628
Seq. ID	LIB3165-049-Q1-K1-G9
Method	BLASTX
NCBI GI	g1352821
BLAST score	525
E value	1.0e-53
Match length	111
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223629
Seq. ID	LIB3165-050-Q1-K1-A1

Method	BLASTX
NCBI GI	g1841870
BLAST score	322
E value	8.0e-30
Match length	81
% identity	77
NCBI Description	(U87222) elongation factor 1-beta [Pimpinella brachycarpa]

Seq. No.	223630
Seq. ID	LIB3165-050-Q1-K1-A11
Method	BLASTX
NCBI GI	g4406530
BLAST score	359
E value	3.0e-34
Match length	118
% identity	64
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223631
Seq. ID	LIB3165-050-Q1-K1-A12
Method	BLASTX
NCBI GI	g1352821
BLAST score	619
E value	1.0e-64
Match length	116
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223632
Seq. ID	LIB3165-050-Q1-K1-A3
Method	BLASTX
NCBI GI	g1168411
BLAST score	248
E value	1.0e-21
Match length	70
% identity	76
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	223633
Seq. ID	LIB3165-050-Q1-K1-A4
Method	BLASTX
NCBI GI	g3023752
BLAST score	261
E value	9.0e-23
Match length	81
% identity	64
NCBI Description	FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520) ferredoxin-I [Lycopersicon esculentum]

Seq. No.	223634
Seq. ID	LIB3165-050-Q1-K1-B2
Method	BLASTX
NCBI GI	g1168411

BLAST score	565
E value	3.0e-58
Match length	136
% identity	84
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	223635
Seq. ID	LIB3165-050-Q1-K1-B3
Method	BLASTX
NCBI GI	g2493146
BLAST score	535
E value	8.0e-55
Match length	142
% identity	58
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_755148 (U13669) vacuolar H+-ATPase proteolipid (16 kDa) subunit [Gossypium hirsutum] >gi_4519415_dbj_BAA75542.1_ (AB024275) vacuolar H+-ATPase c subunit [Citrus unshiu]

Seq. No.	223636
Seq. ID	LIB3165-050-Q1-K1-B8
Method	BLASTX
NCBI GI	g3860308
BLAST score	172
E value	3.0e-12
Match length	58
% identity	64
NCBI Description	(AJ012681) hypothetical protein [Cicer arietinum]

Seq. No.	223637
Seq. ID	LIB3165-050-Q1-K1-B9
Method	BLASTX
NCBI GI	g4204267
BLAST score	269
E value	1.0e-23
Match length	146
% identity	47
NCBI Description	(AC005223) 55585 [Arabidopsis thaliana]

Seq. No.	223638
Seq. ID	LIB3165-050-Q1-K1-C10
Method	BLASTX
NCBI GI	g1181599
BLAST score	503
E value	5.0e-51
Match length	129
% identity	77
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.	223639
Seq. ID	LIB3165-050-Q1-K1-C11
Method	BLASTX
NCBI GI	g3242704
BLAST score	173
E value	2.0e-12
Match length	51
% identity	61

NCBI Description (AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No. 223640
Seq. ID LIB3165-050-Q1-K1-C12
Method BLASTX
NCBI GI g1168411
BLAST score 529
E value 4.0e-54
Match length 130
% identity 83
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No. 223641
Seq. ID LIB3165-050-Q1-K1-C2
Method BLASTX
NCBI GI g1363479
BLAST score 271
E value 2.0e-24
Match length 78
% identity 69
NCBI Description photosystem I protein psaL - cucumber >gi_801740_dbj_BAA09047_ (D50456) PsaL [Cucumis sativus]

Seq. No. 223642
Seq. ID LIB3165-050-Q1-K1-C3
Method BLASTX
NCBI GI g1709825
BLAST score 449
E value 1.0e-44
Match length 112
% identity 75
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No. 223643
Seq. ID LIB3165-050-Q1-K1-C4
Method BLASTX
NCBI GI g231610
BLAST score 376
E value 4.0e-36
Match length 124
% identity 65
NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]

Seq. No. 223644
Seq. ID LIB3165-050-Q1-K1-C5
Method BLASTX
NCBI GI g1363479
BLAST score 325
E value 3.0e-30
Match length 88
% identity 72
NCBI Description photosystem I protein psaL - cucumber

>gi_801740_dbj_BAA09047_ (D50456) PsaL [Cucumis sativus]

Seq. No.	223645
Seq. ID	LIB3165-050-Q1-K1-C6
Method	BLASTX
NCBI GI	g1753085
BLAST score	157
E value	1.0e-10
Match length	40
% identity	78
NCBI Description	(U25283) leucine zipper protein [Oryza sativa]

Seq. No.	223646
Seq. ID	LIB3165-050-Q1-K1-C7
Method	BLASTX
NCBI GI	g2501578
BLAST score	433
E value	5.0e-43
Match length	93
% identity	95
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No.	223647
Seq. ID	LIB3165-050-Q1-K1-C8
Method	BLASTX
NCBI GI	g2262176
BLAST score	178
E value	5.0e-13
Match length	106
% identity	37
NCBI Description	(AC002329) putative RING zinc-finger protein [Arabidopsis thaliana] >gi_3790573 (AF078824) RING-H2 finger protein RHA3a [Arabidopsis thaliana]

Seq. No.	223648
Seq. ID	LIB3165-050-Q1-K1-C9
Method	BLASTX
NCBI GI	g1170567
BLAST score	329
E value	6.0e-31
Match length	67
% identity	88
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1085960_pir__S52648 INO1 protein - Citrus paradisi >gi_602565_emb_CAA83565_ (Z32632) INO1 [Citrus x paradisi]

Seq. No.	223649
Seq. ID	LIB3165-050-Q1-K1-D1
Method	BLASTX
NCBI GI	g1352821
BLAST score	408
E value	4.0e-40
Match length	81
% identity	95

NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	223650
Seq. ID	LIB3165-050-Q1-K1-D10
Method	BLASTX
NCBI GI	g1351271
BLAST score	386
E value	2.0e-37
Match length	131
% identity	63
NCBI Description	TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) >gi_1084309_pir__S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi_806312 (L36387) triosephosphate isomerase, chloroplast isozyme [Spinacia oleracea]
Seq. No.	223651
Seq. ID	LIB3165-050-Q1-K1-D11
Method	BLASTX
NCBI GI	g131399
BLAST score	506
E value	2.0e-51
Match length	125
% identity	77
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi_82277_pir__S00411 photosystem II 10K protein precursor - potato >gi_21489_emb_CAA28450_ (X04753) ST-LS1 protein [Solanum tuberosum]
Seq. No.	223652
Seq. ID	LIB3165-050-Q1-K1-D12
Method	BLASTX
NCBI GI	g1706261
BLAST score	348
E value	1.0e-36
Match length	83
% identity	84
NCBI Description	CYSTEINE PROTEINASE 2 PRECURSOR >gi_2118129_pir__S59598 cysteine proteinase 2 precursor - maize >gi_644490_dbj_BAA08245_ (D45403) cysteine proteinase [Zea mays]
Seq. No.	223653
Seq. ID	LIB3165-050-Q1-K1-D2
Method	BLASTX
NCBI GI	g3914442
BLAST score	412
E value	1.0e-40
Match length	94
% identity	83
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)

>gi_1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No.	223654
Seq. ID	LIB3165-050-Q1-K1-D4
Method	BLASTX
NCBI GI	g3288821
BLAST score	322
E value	8.0e-30
Match length	112
% identity	61
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana]

Seq. No.	223655
Seq. ID	LIB3165-050-Q1-K1-D6
Method	BLASTX
NCBI GI	g1352821
BLAST score	638
E value	7.0e-67
Match length	118
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223656
Seq. ID	LIB3165-050-Q1-K1-E10
Method	BLASTX
NCBI GI	g1352821
BLAST score	571
E value	5.0e-59
Match length	113
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223657
Seq. ID	LIB3165-050-Q1-K1-E11
Method	BLASTX
NCBI GI	g3914605
BLAST score	592
E value	2.0e-61
Match length	135
% identity	83
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase - apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica]

Seq. No. 223658

Seq. ID	LIB3165-050-Q1-K1-E4
Method	BLASTX
NCBI GI	g1352821
BLAST score	434
E value	6.0e-43
Match length	136
% identity	68
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223659
Seq. ID	LIB3165-050-Q1-K1-E5
Method	BLASTX
NCBI GI	g1352821
BLAST score	606
E value	4.0e-63
Match length	114
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223660
Seq. ID	LIB3165-050-Q1-K1-F10
Method	BLASTX
NCBI GI	g266972
BLAST score	204
E value	4.0e-16
Match length	54
% identity	65
NCBI Description	40S RIBOSOMAL PROTEIN S29 >gi_631884_pir__S30298 ribosomal protein S29 - rat >gi_1362934_pir__S55919 ribosomal protein S29 - human >gi_57133_emb_CAA41778_ (X59051) ribosomal protein S29 [Rattus norvegicus] >gi_550027 (U14973) ribosomal protein S29 [Homo sapiens] >gi_1220361 (L31610) homologous to antisense sequence of krev-1, anti oncogene [Homo sapiens] >gi_1220418 (L31609) S29 ribosomal protein [Mus musculus] >gi_1513230 (U66372) ribosomal protein S29 [Bos taurus] >gi_1096945_prf__2113200H ribosomal protein S29 [Homo sapiens] >gi_4506717_ref_NP_001023.1_pRPS29_ ribosomal protein S29

Seq. No.	223661
Seq. ID	LIB3165-050-Q1-K1-F7
Method	BLASTX
NCBI GI	g228403
BLAST score	447
E value	2.0e-44
Match length	93
% identity	92
NCBI Description	glycolate oxidase [Lens culinaris]

Seq. No.	223662
Seq. ID	LIB3165-050-Q1-K1-F8
Method	BLASTX
NCBI GI	g1172977
BLAST score	587
E value	6.0e-61
Match length	135
% identity	85
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	223663
Seq. ID	LIB3165-050-Q1-K1-G10
Method	BLASTX
NCBI GI	g4510372
BLAST score	152
E value	5.0e-10
Match length	57
% identity	53
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]

Seq. No.	223664
Seq. ID	LIB3165-050-Q1-K1-G12
Method	BLASTX
NCBI GI	g131276
BLAST score	637
E value	8.0e-67
Match length	125
% identity	98
NCBI Description	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi_72704_pir__QJNT6A photosystem II chlorophyll a-binding protein psbB - common tobacco chloroplast >gi_11856_emb_CAA77373_ (Z00044) PSII 47kD protein [Nicotiana tabacum] >gi_225224_prf__1211235BF photosystem II P680 apoprotein [Nicotiana tabacum]

Seq. No.	223665
Seq. ID	LIB3165-050-Q1-K1-G2
Method	BLASTX
NCBI GI	g1885326
BLAST score	341
E value	1.0e-32
Match length	67
% identity	91
NCBI Description	(Y11248) phosphoribulokinase [Pisum sativum]

Seq. No.	223666
Seq. ID	LIB3165-050-Q1-K1-G3
Method	BLASTX
NCBI GI	g1352821
BLAST score	618
E value	2.0e-64
Match length	115
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

	ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	223667
Seq. ID	LIB3165-050-Q1-K1-G5
Method	BLASTX
NCBI GI	g4193388
BLAST score	540
E value	2.0e-55
Match length	124
% identity	84
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]
Seq. No.	223668
Seq. ID	LIB3165-050-Q1-K1-G9
Method	BLASTX
NCBI GI	g3242704
BLAST score	352
E value	2.0e-33
Match length	133
% identity	52
NCBI Description	(AC003040) hypothetical protein [Arabidopsis thaliana]
Seq. No.	223669
Seq. ID	LIB3165-050-Q1-K1-H10
Method	BLASTX
NCBI GI	g131276
BLAST score	226
E value	9.0e-43
Match length	120
% identity	83
NCBI Description	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi_72704_pir__QJNT6A photosystem II chlorophyll a-binding protein psbB - common tobacco chloroplast >gi_11856_emb_CAA77373_ (Z00044) PSII 47kD protein [Nicotiana tabacum] >gi_225224_prf__1211235BF photosystem II P680 apoprotein [Nicotiana tabacum]
Seq. No.	223670
Seq. ID	LIB3165-050-Q1-K1-H11
Method	BLASTX
NCBI GI	g2501572
BLAST score	249
E value	3.0e-21
Match length	96
% identity	60
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi_1350545 (L47118) EMB8 gene product [Picea glauca]
Seq. No.	223671
Seq. ID	LIB3165-050-Q1-K1-H3
Method	BLASTX
NCBI GI	g1332579
BLAST score	357
E value	4.0e-68

Match length	140
% identity	9
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	223672
Seq. ID	LIB3165-050-Q1-K1-H4
Method	BLASTX
NCBI GI	g131270
BLAST score	335
E value	2.0e-31
Match length	130
% identity	72
NCBI Description	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi_100129_pir__S12132 photosystem II chlorophyll a-binding protein psbB - Hooker's evening primrose chloroplast >gi_485417_pir__S12129 photosystem II chlorophyll a-binding protein psbB - Appalachian evening primrose chloroplast >gi_11207_emb_CAA39388_ (X55899) psbB product, chlorophyll a-binding apoprotein (AA 1-508) [Oenothera argillicola]

Seq. No.	223673
Seq. ID	LIB3165-050-Q1-K1-H5
Method	BLASTX
NCBI GI	g2583134
BLAST score	177
E value	6.0e-13
Match length	80
% identity	51
NCBI Description	(AC002387) putative proline-rich protein [Arabidopsis thaliana]

Seq. No.	223674
Seq. ID	LIB3165-050-Q1-K1-H9
Method	BLASTX
NCBI GI	g4321096
BLAST score	143
E value	7.0e-09
Match length	92
% identity	37
NCBI Description	(M84135) flavonol 3-sulfotransferase [Flaveria chloraefolia]

Seq. No.	223675
Seq. ID	LIB3165-051-Q1-K1-A10
Method	BLASTX
NCBI GI	g4406530
BLAST score	213
E value	1.0e-23
Match length	86
% identity	67
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223676
Seq. ID	LIB3165-051-Q1-K1-A11
Method	BLASTX
NCBI GI	g3135543

BLAST score	282
E value	2.0e-38
Match length	113
% identity	62
NCBI Description	(AF062393) aquaporin [Oryza sativa]

Seq. No.	223677
Seq. ID	LIB3165-051-Q1-K1-A3
Method	BLASTX
NCBI GI	g1352821
BLAST score	569
E value	8.0e-59
Match length	107
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223678
Seq. ID	LIB3165-051-Q1-K1-A4
Method	BLASTX
NCBI GI	g4455246
BLAST score	148
E value	2.0e-09
Match length	60
% identity	44
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	223679
Seq. ID	LIB3165-051-Q1-K1-A5
Method	BLASTX
NCBI GI	g4115377
BLAST score	210
E value	7.0e-17
Match length	45
% identity	87
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	223680
Seq. ID	LIB3165-051-Q1-K1-A8
Method	BLASTX
NCBI GI	g1352821
BLAST score	118
E value	8.0e-09
Match length	68
% identity	57
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223681
Seq. ID	LIB3165-051-Q1-K1-B1
Method	BLASTX

NCBI GI	g464621
BLAST score	230
E value	2.0e-19
Match length	69
% identity	61
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	223682
Seq. ID	LIB3165-051-Q1-K1-B2
Method	BLASTX
NCBI GI	g4091806
BLAST score	524
E value	1.0e-53
Match length	120
% identity	82
NCBI Description	(AF052585) CONSTANS-like protein 2 [Malus domestica]

Seq. No.	223683
Seq. ID	LIB3165-051-Q1-K1-B4
Method	BLASTX
NCBI GI	g166878
BLAST score	343
E value	2.0e-32
Match length	121
% identity	58
NCBI Description	(M95796) St12p protein [Arabidopsis thaliana]

Seq. No.	223684
Seq. ID	LIB3165-051-Q1-K1-B6
Method	BLASTX
NCBI GI	g1352821
BLAST score	189
E value	1.0e-14
Match length	69
% identity	59
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223685
Seq. ID	LIB3165-051-Q1-K1-B8
Method	BLASTX
NCBI GI	g2129511
BLAST score	513
E value	2.0e-52
Match length	113
% identity	84
NCBI Description	glycerate dehydrogenase (EC 1.1.1.29) splice form HPR1, microbody - cucurbit >gi_1304042_dbj_BAA08410_ (D49432) hydroxypyruvate reductase [Cucurbita sp.]

Seq. No.	223686

Seq. ID	LIB3165-051-Q1-K1-B9
Method	BLASTX
NCBI GI	g4406530
BLAST score	339
E value	7.0e-32
Match length	94
% identity	74
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223687
Seq. ID	LIB3165-051-Q1-K1-C1
Method	BLASTX
NCBI GI	g3913651
BLAST score	512
E value	4.0e-52
Match length	122
% identity	80
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR (FNR) >gi_2225993_emb_CAA74359_ (Y14032) ferredoxin--NADP(+) reductase [Nicotiana tabacum]

Seq. No.	223688
Seq. ID	LIB3165-051-Q1-K1-C11
Method	BLASTX
NCBI GI	g400890
BLAST score	296
E value	8.0e-27
Match length	124
% identity	45
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_282837_pir__S26953 photosystem II 22K protein precursor - spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864) photosystem II 22 kda polypeptide [spinach, Peptide, 274 aa] [Spinacia oleracea]

Seq. No.	223689
Seq. ID	LIB3165-051-Q1-K1-C3
Method	BLASTX
NCBI GI	g2708741
BLAST score	304
E value	6.0e-28
Match length	99
% identity	60
NCBI Description	(AC003952) hypothetical protein [Arabidopsis thaliana]

Seq. No.	223690
Seq. ID	LIB3165-051-Q1-K1-C6
Method	BLASTX
NCBI GI	g1352821
BLAST score	519
E value	5.0e-53
Match length	104
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223691
Seq. ID	LIB3165-051-Q1-K1-C8
Method	BLASTX
NCBI GI	g289920
BLAST score	723
E value	7.0e-77
Match length	135
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	223692
Seq. ID	LIB3165-051-Q1-K1-C9
Method	BLASTX
NCBI GI	g1352821
BLAST score	586
E value	8.0e-61
Match length	110
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223693
Seq. ID	LIB3165-051-Q1-K1-D11
Method	BLASTX
NCBI GI	g100490
BLAST score	608
E value	2.0e-63
Match length	124
% identity	25
NCBI Description	polyubiquitin - garden snapdragon (fragment) >gi_16071_emb_CAA48140_ (X67957) ubiquitin [Antirrhinum majus]

Seq. No.	223694
Seq. ID	LIB3165-051-Q1-K1-D12
Method	BLASTX
NCBI GI	g452357
BLAST score	447
E value	2.0e-44
Match length	91
% identity	97
NCBI Description	(Z29591) guanine nucleotide regulatory protein [Vicia faba] >gi_1098294_prf__2115367B small GTP-binding protein [Vicia faba]

Seq. No.	223695
Seq. ID	LIB3165-051-Q1-K1-D3
Method	BLASTX
NCBI GI	g100200
BLAST score	380

E value	1.0e-36
Match length	103
% identity	71
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	223696
Seq. ID	LIB3165-051-Q1-K1-D4
Method	BLASTX
NCBI GI	g119905
BLAST score	316
E value	1.0e-29
Match length	74
% identity	81
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR) >gi_81898_pir__S04030 ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - garden pea >gi_20722_emb_CAA30978_ (X12446) ferredoxin-NADH+ reductase preprotein (AA -52 to 308) [Pisum sativum] >gi_226545_prf__1601517A ferredoxin NADP reductase [Arachis hypogaea]

Seq. No.	223697
Seq. ID	LIB3165-051-Q1-K1-D6
Method	BLASTX
NCBI GI	g3335341
BLAST score	158
E value	1.0e-10
Match length	35
% identity	89
NCBI Description	(AC004512) T8F5.10 [Arabidopsis thaliana]

Seq. No.	223698
Seq. ID	LIB3165-051-Q1-K1-D7
Method	BLASTX
NCBI GI	g289920
BLAST score	190
E value	9.0e-15
Match length	84
% identity	54
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	223699
Seq. ID	LIB3165-051-Q1-K1-D8
Method	BLASTX
NCBI GI	g3913018
BLAST score	684
E value	3.0e-72
Match length	139
% identity	92
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No.	223700
Seq. ID	LIB3165-051-Q1-K1-D9
Method	BLASTX
NCBI GI	g1928981

BLAST score	141
E value	9.0e-16
Match length	82
% identity	65
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	223701
Seq. ID	LIB3165-051-Q1-K1-E11
Method	BLASTX
NCBI GI	g4539545
BLAST score	226
E value	2.0e-28
Match length	96
% identity	61
NCBI Description	(Y16644) PRCI [Nicotiana tabacum]

Seq. No.	223702
Seq. ID	LIB3165-051-Q1-K1-E12
Method	BLASTX
NCBI GI	g3914437
BLAST score	196
E value	3.0e-27
Match length	73
% identity	69
NCBI Description	PROFILIN >gi_3183706_emb_CAA75312_ (Y15042) profilin [Hevea brasiliensis]

Seq. No.	223703
Seq. ID	LIB3165-051-Q1-K1-E3
Method	BLASTX
NCBI GI	g625509
BLAST score	626
E value	2.0e-65
Match length	126
% identity	25
NCBI Description	ubiquitin precursor - Arabidopsis thaliana (fragment)

Seq. No.	223704
Seq. ID	LIB3165-051-Q1-K1-E7
Method	BLASTX
NCBI GI	g20729
BLAST score	514
E value	2.0e-52
Match length	135
% identity	78
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	223705
Seq. ID	LIB3165-051-Q1-K1-E8
Method	BLASTX
NCBI GI	g166834
BLAST score	677
E value	2.0e-71
Match length	140
% identity	91
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase

activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	223706
Seq. ID	LIB3165-051-Q1-K1-E9
Method	BLASTX
NCBI GI	g3650033
BLAST score	150
E value	1.0e-09
Match length	74
% identity	45
NCBI Description	(AC005396) unknown protein [Arabidopsis thaliana]

Seq. No.	223707
Seq. ID	LIB3165-051-Q1-K1-F11
Method	BLASTX
NCBI GI	g3832512
BLAST score	361
E value	2.0e-34
Match length	123
% identity	59
NCBI Description	(AF097922) granule-bound glycogen (starch) synthase [Astragalus membranaceus]

Seq. No.	223708
Seq. ID	LIB3165-051-Q1-K1-F12
Method	BLASTX
NCBI GI	g3328122
BLAST score	663
E value	7.0e-70
Match length	135
% identity	99
NCBI Description	(AF073473) phosphoglycerate kinase precursor [Solanum tuberosum]

Seq. No.	223709
Seq. ID	LIB3165-051-Q1-K1-F2
Method	BLASTX
NCBI GI	g131393
BLAST score	340
E value	5.0e-32
Match length	104
% identity	72
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_100360_pir__S15005 photosystem II oxygen-evolving complex protein 2 - common tobacco >gi_19911_emb_CAA39039.1_ (X55354) photosystem II 23kDa polypeptide [Nicotiana tabacum]

Seq. No.	223710
Seq. ID	LIB3165-051-Q1-K1-F3
Method	BLASTX
NCBI GI	g231610
BLAST score	347
E value	8.0e-33
Match length	126

% identity	59
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]
Seq. No.	223711
Seq. ID	LIB3165-051-Q1-K1-F4
Method	BLASTX
NCBI GI	g3150404
BLAST score	418
E value	4.0e-41
Match length	136
% identity	62
NCBI Description	(AC004165) putative mitochondrial carrier protein [Arabidopsis thaliana]
Seq. No.	223712
Seq. ID	LIB3165-051-Q1-K1-F5
Method	BLASTX
NCBI GI	g1168411
BLAST score	549
E value	2.0e-56
Match length	132
% identity	84
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
Seq. No.	223713
Seq. ID	LIB3165-051-Q1-K1-F6
Method	BLASTX
NCBI GI	g1168411
BLAST score	139
E value	8.0e-12
Match length	91
% identity	53
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
Seq. No.	223714
Seq. ID	LIB3165-051-Q1-K1-F7
Method	BLASTX
NCBI GI	g3885511
BLAST score	252
E value	1.0e-21
Match length	104
% identity	51
NCBI Description	(AF084200) similar to PSI-K subunit of photosystem I from barley [Medicago sativa]
Seq. No.	223715
Seq. ID	LIB3165-051-Q1-K1-F8
Method	BLASTX
NCBI GI	g4490321
BLAST score	455
E value	2.0e-45
Match length	116
% identity	78

NCBI Description	(AJ011604) nitrate transporter [Arabidopsis thaliana]

Seq. No.	223716
Seq. ID	LIB3165-051-Q1-K1-G4
Method	BLASTX
NCBI GI	g400890
BLAST score	240
E value	3.0e-20
Match length	110
% identity	44
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_282837_pir__S26953 photosystem II 22K protein precursor - spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864) photosystem II 22 kda polypeptide [spinach, Peptide, 274 aa] [Spinacia oleracea]

Seq. No.	223717
Seq. ID	LIB3165-051-Q1-K1-G7
Method	BLASTX
NCBI GI	g2920666
BLAST score	203
E value	3.0e-30
Match length	86
% identity	78
NCBI Description	(AF048978) 2,4-D inducible glutathione S-transferase [Glycine max]

Seq. No.	223718
Seq. ID	LIB3165-051-Q1-K1-H1
Method	BLASTX
NCBI GI	g20733
BLAST score	408
E value	6.0e-40
Match length	81
% identity	90
NCBI Description	(X15188) precursor C-terminal fragment (AA -80 to 367) [Pisum sativum]

Seq. No.	223719
Seq. ID	LIB3165-051-Q1-K1-H10
Method	BLASTX
NCBI GI	g2492515
BLAST score	412
E value	2.0e-40
Match length	100
% identity	84
NCBI Description	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR >gi_2129924_pir__S58298 ATPase - pepper (fragment) >gi_929013_emb_CAA62084_ (X90472) ATPase [Capsicum annuum]

Seq. No.	223720
Seq. ID	LIB3165-051-Q1-K1-H11
Method	BLASTX
NCBI GI	g1545805
BLAST score	180
E value	1.0e-13

Match length	45
% identity	78
NCBI Description	(D64052) cytochrome P450 like_TBP [Nicotiana tabacum]

Seq. No.	223721
Seq. ID	LIB3165-051-Q1-K1-H2
Method	BLASTX
NCBI GI	g1168411
BLAST score	376
E value	3.0e-36
Match length	102
% identity	77
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	223722
Seq. ID	LIB3165-051-Q1-K1-H4
Method	BLASTX
NCBI GI	g20733
BLAST score	359
E value	3.0e-34
Match length	124
% identity	62
NCBI Description	(X15188) precursor C-terminal fragment (AA -80 to 367) [Pisum sativum]

Seq. No.	223723
Seq. ID	LIB3165-051-Q1-K1-H6
Method	BLASTX
NCBI GI	g2895188
BLAST score	153
E value	5.0e-10
Match length	69
% identity	27
NCBI Description	(AF016011) CONSTANS homolog [Brassica napus]

Seq. No.	223724
Seq. ID	LIB3165-051-Q1-K1-H8
Method	BLASTX
NCBI GI	g1352821
BLAST score	661
E value	1.0e-69
Match length	139
% identity	89
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223725
Seq. ID	LIB3165-051-Q1-K1-H9
Method	BLASTX
NCBI GI	g1730910
BLAST score	149
E value	2.0e-09
Match length	137
% identity	35

NCBI Description	HYPOTHETICAL 23.1 KD PROTEIN IN BSAA-ILVD INTERGENIC REGION >gi_1256633 (L77246) putative [Bacillus subtilis] >gi_2634609_emb_CAB14107_ (Z99115) similar to hypothetical proteins [Bacillus subtilis]
Seq. No.	223726
Seq. ID	LIB3165-052-Q1-K1-A1
Method	BLASTX
NCBI GI	g115473
BLAST score	199
E value	1.0e-15
Match length	89
% identity	52
NCBI Description	CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) >gi_170219 (M94135) chloroplast carbonic anhydrase [Nicotiana tabacum] >gi_445610_prf__1909357A carbonic anhydrase [Nicotiana tabacum]
Seq. No.	223727
Seq. ID	LIB3165-052-Q1-K1-A12
Method	BLASTX
NCBI GI	g3334200
BLAST score	571
E value	5.0e-59
Match length	131
% identity	83
NCBI Description	GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) >gi_2894362_emb_CAB16918_ (Z99770) P-Protein precursor [Solanum tuberosum]
Seq. No.	223728
Seq. ID	LIB3165-052-Q1-K1-A2
Method	BLASTX
NCBI GI	g282833
BLAST score	287
E value	1.0e-25
Match length	69
% identity	86
NCBI Description	phosphoglycerate kinase (EC 2.7.2.3) - spinach (fragment)
Seq. No.	223729
Seq. ID	LIB3165-052-Q1-K1-A3
Method	BLASTX
NCBI GI	g4406530
BLAST score	353
E value	2.0e-33
Match length	97
% identity	75
NCBI Description	(AF126870) rubisco activase [Vigna radiata]
Seq. No.	223730
Seq. ID	LIB3165-052-Q1-K1-A5
Method	BLASTX
NCBI GI	g2984709
BLAST score	461
E value	4.0e-46

Match length 95
% identity 89
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 223731
Seq. ID LIB3165-052-Q1-K1-A6
Method BLASTX
NCBI GI g3023752
BLAST score 360
E value 3.0e-34
Match length 121
% identity 62
NCBI Description FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520) ferredoxin-I [Lycopersicon esculentum]

Seq. No. 223732
Seq. ID LIB3165-052-Q1-K1-A8
Method BLASTX
NCBI GI g1350930
BLAST score 696
E value 1.0e-73
Match length 146
% identity 93
NCBI Description 40S RIBOSOMAL PROTEIN S13

Seq. No. 223733
Seq. ID LIB3165-052-Q1-K1-A9
Method BLASTX
NCBI GI g4467098
BLAST score 326
E value 3.0e-30
Match length 134
% identity 56
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 223734
Seq. ID LIB3165-052-Q1-K1-B12
Method BLASTX
NCBI GI g1352821
BLAST score 744
E value 3.0e-79
Match length 146
% identity 96
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223735
Seq. ID LIB3165-052-Q1-K1-B2
Method BLASTX
NCBI GI g1354515
BLAST score 302
E value 2.0e-27
Match length 137
% identity 49

NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]
Seq. No.	223736
Seq. ID	LIB3165-052-Q1-K1-B3
Method	BLASTX
NCBI GI	g2191138
BLAST score	334
E value	3.0e-31
Match length	120
% identity	62
NCBI Description	(AF007269) A_IG002N01.18 gene product [Arabidopsis thaliana]
Seq. No.	223737
Seq. ID	LIB3165-052-Q1-K1-B6
Method	BLASTX
NCBI GI	g1173345
BLAST score	412
E value	2.0e-40
Match length	133
% identity	63
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_1076403_pir__S51838 sedoheptulose-1,7-biphosphatase - Arabidopsis thaliana >gi_786466_bbs_159034 (S74719) sedoheptulose-1,7-bisphosphatase, SBPase {EC 3.1.3.37} [Arabidopsis thaliana, C24, Peptide Chloroplast, 393 aa] [Arabidopsis thaliana]
Seq. No.	223738
Seq. ID	LIB3165-052-Q1-K1-B8
Method	BLASTX
NCBI GI	g2677828
BLAST score	395
E value	2.0e-38
Match length	109
% identity	68
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]
Seq. No.	223739
Seq. ID	LIB3165-052-Q1-K1-B9
Method	BLASTX
NCBI GI	g3023752
BLAST score	352
E value	2.0e-33
Match length	128
% identity	59
NCBI Description	FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520) ferredoxin-I [Lycopersicon esculentum]
Seq. No.	223740
Seq. ID	LIB3165-052-Q1-K1-C11
Method	BLASTX
NCBI GI	g1352821
BLAST score	706
E value	8.0e-75

Match length	136
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223741
Seq. ID	LIB3165-052-Q1-K1-C12
Method	BLASTX
NCBI GI	g4406530
BLAST score	348
E value	7.0e-33
Match length	98
% identity	73
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223742
Seq. ID	LIB3165-052-Q1-K1-C2
Method	BLASTX
NCBI GI	g4262239
BLAST score	245
E value	8.0e-21
Match length	115
% identity	45
NCBI Description	(AC006200) putative membrane transporter [Arabidopsis thaliana]

Seq. No.	223743
Seq. ID	LIB3165-052-Q1-K1-C7
Method	BLASTX
NCBI GI	g4210948
BLAST score	497
E value	2.0e-50
Match length	98
% identity	96
NCBI Description	(AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No.	223744
Seq. ID	LIB3165-052-Q1-K1-C8
Method	BLASTX
NCBI GI	g1352821
BLAST score	535
E value	8.0e-55
Match length	101
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223745
Seq. ID	LIB3165-052-Q1-K1-C9
Method	BLASTX
NCBI GI	g100616

BLAST score	276
E value	2.0e-24
Match length	77
% identity	71
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	223746
Seq. ID	LIB3165-052-Q1-K1-D10
Method	BLASTX
NCBI GI	g2088651
BLAST score	368
E value	3.0e-35
Match length	133
% identity	56
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	223747
Seq. ID	LIB3165-052-Q1-K1-D11
Method	BLASTX
NCBI GI	g4406809
BLAST score	180
E value	4.0e-13
Match length	48
% identity	69
NCBI Description	(AC006201) unknown protein [Arabidopsis thaliana]

Seq. No.	223748
Seq. ID	LIB3165-052-Q1-K1-D12
Method	BLASTX
NCBI GI	g2765081
BLAST score	525
E value	1.0e-53
Match length	138
% identity	75
NCBI Description	(Y10557) g5bf [Arabidopsis thaliana]

Seq. No.	223749
Seq. ID	LIB3165-052-Q1-K1-D3
Method	BLASTX
NCBI GI	g1352821
BLAST score	574
E value	2.0e-59
Match length	108
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223750
Seq. ID	LIB3165-052-Q1-K1-D7

Method	BLASTX
NCBI GI	g2982453
BLAST score	681
E value	6.0e-72
Match length	143
% identity	92
NCBI Description	(AL022223) fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]

Seq. No.	223751
Seq. ID	LIB3165-052-Q1-K1-D8
Method	BLASTX
NCBI GI	g1168411
BLAST score	557
E value	2.0e-57
Match length	134
% identity	84
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	223752
Seq. ID	LIB3165-052-Q1-K1-D9
Method	BLASTX
NCBI GI	g289920
BLAST score	560
E value	8.0e-58
Match length	121
% identity	87
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	223753
Seq. ID	LIB3165-052-Q1-K1-E1
Method	BLASTX
NCBI GI	g2501572
BLAST score	149
E value	1.0e-09
Match length	74
% identity	51
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi_1350545 (L47118) EMB8 gene product [Picea glauca]

Seq. No.	223754
Seq. ID	LIB3165-052-Q1-K1-E10
Method	BLASTX
NCBI GI	g4406530
BLAST score	388
E value	1.0e-37
Match length	110
% identity	74
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223755
Seq. ID	LIB3165-052-Q1-K1-E11
Method	BLASTX
NCBI GI	g231688
BLAST score	619
E value	1.0e-64

Match length	117
% identity	100
NCBI Description	CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC 1.11.1.6) - upland cotton >gi_18488_emb_CAA39998_ (X56675) subunit 2 of cotton catalase [Gossypium hirsutum]
Seq. No.	223756
Seq. ID	LIB3165-052-Q1-K1-E12
Method	BLASTX
NCBI GI	g131399
BLAST score	465
E value	1.0e-46
Match length	109
% identity	82
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi_82277_pir__S00411 photosystem II 10K protein precursor - potato >gi_21489_emb_CAA28450_ (X04753) ST-LS1 protein [Solanum tuberosum]
Seq. No.	223757
Seq. ID	LIB3165-052-Q1-K1-E2
Method	BLASTX
NCBI GI	g2739004
BLAST score	258
E value	3.0e-22
Match length	81
% identity	54
NCBI Description	(AF022461) CYP82C1p [Glycine max]
Seq. No.	223758
Seq. ID	LIB3165-052-Q1-K1-E4
Method	BLASTX
NCBI GI	g1352821
BLAST score	374
E value	5.0e-36
Match length	76
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	223759
Seq. ID	LIB3165-052-Q1-K1-E5
Method	BLASTX
NCBI GI	g3885341
BLAST score	474
E value	1.0e-47
Match length	107
% identity	76
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]
Seq. No.	223760
Seq. ID	LIB3165-052-Q1-K1-E8
Method	BLASTX

NCBI GI	g2791834
BLAST score	623
E value	4.0e-65
Match length	120
% identity	99
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No.	223761
Seq. ID	LIB3165-052-Q1-K1-F1
Method	BLASTX
NCBI GI	g3395429
BLAST score	177
E value	7.0e-13
Match length	61
% identity	52
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No.	223762
Seq. ID	LIB3165-052-Q1-K1-F2
Method	BLASTX
NCBI GI	g2055273
BLAST score	634
E value	2.0e-66
Match length	135
% identity	88
NCBI Description	(D85339) hydroxypyruvate reductase [Arabidopsis thaliana]

Seq. No.	223763
Seq. ID	LIB3165-052-Q1-K1-F6
Method	BLASTX
NCBI GI	g2982463
BLAST score	491
E value	1.0e-49
Match length	145
% identity	70
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	223764
Seq. ID	LIB3165-052-Q1-K1-F7
Method	BLASTX
NCBI GI	g2632109
BLAST score	238
E value	5.0e-20
Match length	121
% identity	48
NCBI Description	(AJ000508) phospholipid glutathione peroxidase [Pisum sativum]

Seq. No.	223765
Seq. ID	LIB3165-052-Q1-K1-F8
Method	BLASTX
NCBI GI	g3540196
BLAST score	266
E value	3.0e-23
Match length	118
% identity	47
NCBI Description	(AC004260) Putative amp-binding protein [Arabidopsis

thaliana]

Seq. No.	223766
Seq. ID	LIB3165-052-Q1-K1-G1
Method	BLASTX
NCBI GI	g2765081
BLAST score	506
E value	2.0e-51
Match length	139
% identity	72
NCBI Description	(Y10557) g5bf [Arabidopsis thaliana]

Seq. No.	223767
Seq. ID	LIB3165-052-Q1-K1-G2
Method	BLASTX
NCBI GI	g3043428
BLAST score	524
E value	2.0e-53
Match length	111
% identity	87
NCBI Description	(AJ005346) 40S ribosomal protein S5 [Cicer arietinum]

Seq. No.	223768
Seq. ID	LIB3165-052-Q1-K1-G3
Method	BLASTX
NCBI GI	g4455208
BLAST score	562
E value	6.0e-58
Match length	139
% identity	78
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	223769
Seq. ID	LIB3165-052-Q1-K1-G5
Method	BLASTX
NCBI GI	g1352821
BLAST score	113
E value	2.0e-09
Match length	89
% identity	43
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223770
Seq. ID	LIB3165-052-Q1-K1-G7
Method	BLASTX
NCBI GI	g68200
BLAST score	565
E value	2.0e-58
Match length	139
% identity	83
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	223771
Seq. ID	LIB3165-052-Q1-K1-G8
Method	BLASTX
NCBI GI	g3688123
BLAST score	369
E value	2.0e-35
Match length	128
% identity	63
NCBI Description	(AJ006293) granule-bound starch synthase [Antirrhinum majus]

Seq. No.	223772
Seq. ID	LIB3165-052-Q1-K1-G9
Method	BLASTX
NCBI GI	g2582822
BLAST score	253
E value	1.0e-21
Match length	124
% identity	51
NCBI Description	(Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]

Seq. No.	223773
Seq. ID	LIB3165-052-Q1-K1-H10
Method	BLASTX
NCBI GI	g3885511
BLAST score	374
E value	6.0e-36
Match length	106
% identity	71
NCBI Description	(AF084200) similar to PSI-K subunit of photosystem I from barley [Medicago sativa]

Seq. No.	223774
Seq. ID	LIB3165-052-Q1-K1-H11
Method	BLASTX
NCBI GI	g1352821
BLAST score	518
E value	6.0e-53
Match length	100
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223775
Seq. ID	LIB3165-052-Q1-K1-H12
Method	BLASTX
NCBI GI	g1345698
BLAST score	672
E value	7.0e-71
Match length	132
% identity	95
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR

	(CAB-151) (LHCP) >gi_99601_pir__S20917 chlorophyll a/b-binding protein - upland cotton >gi_452314_emb_CAA38025_ (X54090) chlorophyll ab binding protein [Gossypium hirsutum]
Seq. No.	223776
Seq. ID	LIB3165-052-Q1-K1-H2
Method	BLASTX
NCBI GI	g267082
BLAST score	634
E value	2.0e-66
Match length	122
% identity	95
NCBI Description	TUBULIN BETA-8 CHAIN >gi_320189_pir__JQ1592 tubulin beta-8 chain - Arabidopsis thaliana >gi_166908 (M84705) beta-8 tubulin [Arabidopsis thaliana]
Seq. No.	223777
Seq. ID	LIB3165-052-Q1-K1-H3
Method	BLASTX
NCBI GI	g2388689
BLAST score	214
E value	3.0e-17
Match length	90
% identity	52
NCBI Description	(AF016633) GH1 protein [Glycine max]
Seq. No.	223778
Seq. ID	LIB3165-052-Q1-K1-H4
Method	BLASTX
NCBI GI	g4406530
BLAST score	393
E value	4.0e-38
Match length	109
% identity	75
NCBI Description	(AF126870) rubisco activase [Vigna radiata]
Seq. No.	223779
Seq. ID	LIB3165-052-Q1-K1-H5
Method	BLASTX
NCBI GI	g3126967
BLAST score	333
E value	2.0e-31
Match length	99
% identity	15
NCBI Description	(AF061807) polyubiquitin [Elaeagnus umbellata]
Seq. No.	223780
Seq. ID	LIB3165-052-Q1-K1-H7
Method	BLASTX
NCBI GI	g1354515
BLAST score	282
E value	4.0e-25
Match length	140
% identity	46
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	223781
Seq. ID	LIB3165-052-Q1-K1-H8
Method	BLASTX
NCBI GI	g2088647
BLAST score	223
E value	3.0e-18
Match length	78
% identity	53
NCBI Description	(AF002109) hypothetical protein [Arabidopsis thaliana] >gi_3158394 (AF036340) LRR-containing F-box protein [Arabidopsis thaliana]

Seq. No.	223782
Seq. ID	LIB3165-053-Q1-K1-A1
Method	BLASTX
NCBI GI	g1421730
BLAST score	494
E value	5.0e-50
Match length	118
% identity	77
NCBI Description	(U43082) RF2 [Zea mays]

Seq. No.	223783
Seq. ID	LIB3165-053-Q1-K1-A11
Method	BLASTX
NCBI GI	g3269292
BLAST score	183
E value	9.0e-14
Match length	62
% identity	56
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	223784
Seq. ID	LIB3165-053-Q1-K1-A12
Method	BLASTX
NCBI GI	g1652892
BLAST score	127
E value	1.0e-12
Match length	113
% identity	47
NCBI Description	(D90909) ABC transporter [Synechocystis sp.]

Seq. No.	223785
Seq. ID	LIB3165-053-Q1-K1-A2
Method	BLASTX
NCBI GI	g2501568
BLAST score	173
E value	2.0e-12
Match length	54
% identity	54
NCBI Description	HYPOTHETICAL 28.8 KD PROTEIN SLL0506 >gi_1001342_dbj_BAA10829_ (D64006) hypothetical protein [Synechocystis sp.]

Seq. No.	223786
Seq. ID	LIB3165-053-Q1-K1-A4

Method	BLASTX
NCBI GI	g3860264
BLAST score	418
E value	4.0e-41
Match length	86
% identity	88
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	223787
Seq. ID	LIB3165-053-Q1-K1-A5
Method	BLASTX
NCBI GI	g1778093
BLAST score	419
E value	5.0e-43
Match length	139
% identity	68
NCBI Description	(U64902) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris]

Seq. No.	223788
Seq. ID	LIB3165-053-Q1-K1-A7
Method	BLASTX
NCBI GI	g3559807
BLAST score	292
E value	1.0e-26
Match length	92
% identity	63
NCBI Description	(Y15628) HCF136 protein [Arabidopsis thaliana]

Seq. No.	223789
Seq. ID	LIB3165-053-Q1-K1-B1
Method	BLASTX
NCBI GI	g3080401
BLAST score	385
E value	3.0e-37
Match length	100
% identity	72
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana] >gi_4455265_emb_CAB36801.1_ (AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	223790
Seq. ID	LIB3165-053-Q1-K1-B12
Method	BLASTX
NCBI GI	g1170567
BLAST score	675
E value	3.0e-71
Match length	139
% identity	91
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1085960_pir__S52648 INO1 protein - Citrus paradisi >gi_602565_emb_CAA83565_ (Z32632) INO1 [Citrus x paradisi]

Seq. No.	223791
Seq. ID	LIB3165-053-Q1-K1-B2
Method	BLASTX

NCBI GI	g1363526
BLAST score	681
E value	6.0e-72
Match length	138
% identity	92
NCBI Description	plastoquinol--plastocyanin reductase (EC 1.10.99.1) cytochrome b6 - maize chloroplast >gi_902251_emb_CAA60315_ (X86563) cytochrome B6 [Zea mays]

Seq. No.	223792
Seq. ID	LIB3165-053-Q1-K1-B3
Method	BLASTX
NCBI GI	g3023281
BLAST score	457
E value	1.0e-45
Match length	141
% identity	64
NCBI Description	HIGH AFFINITY AMMONIUM TRANSPORTER >gi_2065194_emb_CAA64475_ (X95098) ammonium transporter [Lycopersicon esculentum]

Seq. No.	223793
Seq. ID	LIB3165-053-Q1-K1-B4
Method	BLASTX
NCBI GI	g2739375
BLAST score	243
E value	1.0e-20
Match length	107
% identity	50
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	223794
Seq. ID	LIB3165-053-Q1-K1-B5
Method	BLASTX
NCBI GI	g2129452
BLAST score	481
E value	2.0e-48
Match length	106
% identity	16
NCBI Description	polyubiquitin - red alga (Gracilaria verrucosa)

Seq. No.	223795
Seq. ID	LIB3165-053-Q1-K1-B6
Method	BLASTX
NCBI GI	g289920
BLAST score	206
E value	6.0e-29
Match length	90
% identity	80
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	223796
Seq. ID	LIB3165-053-Q1-K1-C10
Method	BLASTX
NCBI GI	g2494175
BLAST score	208

E value	2.0e-16
Match length	101
% identity	49
NCBI Description	GLUTAMATE DECARBOXYLASE 2 (GAD 2) >gi_1184960 (U46665) glutamate decarboxylase 2 [Arabidopsis thaliana] >gi_1236619 (U49937) glutamate decarboxylase [Arabidopsis thaliana]

Seq. No.	223797
Seq. ID	LIB3165-053-Q1-K1-C11
Method	BLASTX
NCBI GI	g131773
BLAST score	200
E value	8.0e-16
Match length	78
% identity	65
NCBI Description	40S RIBOSOMAL PROTEIN S14 (CLONE MCH2) >gi_82724_pir__B30097 ribosomal protein S14 (clone MCH2) - maize

Seq. No.	223798
Seq. ID	LIB3165-053-Q1-K1-C12
Method	BLASTX
NCBI GI	g1709825
BLAST score	338
E value	7.0e-32
Match length	124
% identity	65
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No.	223799
Seq. ID	LIB3165-053-Q1-K1-C2
Method	BLASTX
NCBI GI	g2114046
BLAST score	642
E value	2.0e-67
Match length	137
% identity	91
NCBI Description	(AB002147) water channel protein [Nicotiana excelsior]

Seq. No.	223800
Seq. ID	LIB3165-053-Q1-K1-C3
Method	BLASTX
NCBI GI	g3252807
BLAST score	159
E value	1.0e-12
Match length	107
% identity	44
NCBI Description	(AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No.	223801
Seq. ID	LIB3165-053-Q1-K1-C6
Method	BLASTX
NCBI GI	g1352821
BLAST score	268
E value	6.0e-25

Match length	78
% identity	79
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223802
Seq. ID	LIB3165-053-Q1-K1-D11
Method	BLASTX
NCBI GI	g3258571
BLAST score	463
E value	2.0e-46
Match length	117
% identity	80
NCBI Description	(U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	223803
Seq. ID	LIB3165-053-Q1-K1-D3
Method	BLASTX
NCBI GI	g1168411
BLAST score	547
E value	3.0e-56
Match length	137
% identity	82
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	223804
Seq. ID	LIB3165-053-Q1-K1-D4
Method	BLASTX
NCBI GI	g3023752
BLAST score	322
E value	7.0e-30
Match length	114
% identity	61
NCBI Description	FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520) ferredoxin-I [Lycopersicon esculentum]

Seq. No.	223805
Seq. ID	LIB3165-053-Q1-K1-D8
Method	BLASTX
NCBI GI	g1352821
BLAST score	386
E value	2.0e-37
Match length	73
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223806
Seq. ID	LIB3165-053-Q1-K1-E1
Method	BLASTX
NCBI GI	g4455208

BLAST score	531
E value	2.0e-54
Match length	141
% identity	73
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	223807
Seq. ID	LIB3165-053-Q1-K1-E11
Method	BLASTX
NCBI GI	g4006872
BLAST score	280
E value	6.0e-25
Match length	75
% identity	76
NCBI Description	(Z99707) methionyl aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	223808
Seq. ID	LIB3165-053-Q1-K1-E12
Method	BLASTX
NCBI GI	g231688
BLAST score	613
E value	5.0e-64
Match length	123
% identity	94
NCBI Description	CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC 1.11.1.6) - upland cotton >gi_18488_emb_CAA39998_ (X56675) subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No.	223809
Seq. ID	LIB3165-053-Q1-K1-E2
Method	BLASTX
NCBI GI	g2582822
BLAST score	203
E value	7.0e-16
Match length	115
% identity	48
NCBI Description	(Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]

Seq. No.	223810
Seq. ID	LIB3165-053-Q1-K1-E4
Method	BLASTX
NCBI GI	g2494076
BLAST score	442
E value	3.0e-55
Match length	124
% identity	84
NCBI Description	NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi_1842115 (U87848) non-phosphorylating glyceraldehyde dehydrogenase [Nicotiana plumbaginifolia]

Seq. No.	223811
Seq. ID	LIB3165-053-Q1-K1-E5

Method	BLASTX
NCBI GI	g1181599
BLAST score	414
E value	1.0e-40
Match length	111
% identity	74
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.	223812
Seq. ID	LIB3165-053-Q1-K1-E7
Method	BLASTX
NCBI GI	g1172664
BLAST score	330
E value	8.0e-31
Match length	70
% identity	91
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_419791_pir__S31165 photosystem I chain III precursor - Flaveria trinervia >gi_298482_bbs_127083 photosystem I reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem I subunit III [Flaveria trinervia]

Seq. No.	223813
Seq. ID	LIB3165-053-Q1-K1-F1
Method	BLASTX
NCBI GI	g1352821
BLAST score	482
E value	6.0e-49
Match length	89
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223814
Seq. ID	LIB3165-053-Q1-K1-F10
Method	BLASTX
NCBI GI	g125578
BLAST score	214
E value	5.0e-21
Match length	75
% identity	73
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_167266 (M73707) phosphoribulokinase [Mesembryanthemum crystallinum]

Seq. No.	223815
Seq. ID	LIB3165-053-Q1-K1-F12
Method	BLASTX
NCBI GI	g1346155
BLAST score	459
E value	6.0e-46
Match length	104

% identity	87
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_481942_pir__S40212 glycine hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei >gi_437995_emb_CAA81078_ (Z25859) glycine hydroxymethyltransferase [Flaveria pringlei]

Seq. No.	223816
Seq. ID	LIB3165-053-Q1-K1-F2
Method	BLASTX
NCBI GI	g2979550
BLAST score	203
E value	4.0e-16
Match length	95
% identity	48
NCBI Description	(AC003680) putative 7-ethoxycoumarin O-deethylase [Arabidopsis thaliana]

Seq. No.	223817
Seq. ID	LIB3165-053-Q1-K1-F4
Method	BLASTX
NCBI GI	g1352821
BLAST score	627
E value	1.0e-65
Match length	116
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223818
Seq. ID	LIB3165-053-Q1-K1-F5
Method	BLASTX
NCBI GI	g1709651
BLAST score	437
E value	2.0e-43
Match length	138
% identity	62
NCBI Description	PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209 plastocyanin a precursor - black poplar >gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus nigra]

Seq. No.	223819
Seq. ID	LIB3165-053-Q1-K1-F6
Method	BLASTX
NCBI GI	g1352821
BLAST score	557
E value	1.0e-57
Match length	105
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223820
Seq. ID	LIB3165-053-Q1-K1-G1
Method	BLASTX
NCBI GI	g232031
BLAST score	236
E value	1.0e-19
Match length	73
% identity	58
NCBI Description	ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224 translation elongation factor eEF-1 beta' chain - rice >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta' [Oryza sativa]

Seq. No.	223821
Seq. ID	LIB3165-053-Q1-K1-G2
Method	BLASTX
NCBI GI	g2661021
BLAST score	667
E value	3.0e-70
Match length	126
% identity	98
NCBI Description	(AF035255) catalase [Glycine max]

Seq. No.	223822
Seq. ID	LIB3165-053-Q1-K1-G3
Method	BLASTX
NCBI GI	g1352821
BLAST score	261
E value	1.0e-22
Match length	52
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223823
Seq. ID	LIB3165-053-Q1-K1-G4
Method	BLASTX
NCBI GI	g231503
BLAST score	166
E value	2.0e-21
Match length	80
% identity	67
NCBI Description	ACTIN 97 >gi_100417_pir__S20098 actin - potato >gi_21544_emb_CAA39280_ (X55751) actin [Solanum tuberosum]

Seq. No.	223824
Seq. ID	LIB3165-053-Q1-K1-G8
Method	BLASTX
NCBI GI	g3800853
BLAST score	642
E value	3.0e-71

Match length	140
% identity	96
NCBI Description	(AF084478) ribulose-1,5-bisphosphate carboxylase/oxygenase activase precursor [Zea mays]

Seq. No.	223825
Seq. ID	LIB3165-053-Q1-K1-H12
Method	BLASTX
NCBI GI	g2191136
BLAST score	323
E value	5.0e-51
Match length	140
% identity	70
NCBI Description	(AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290 [Arabidopsis thaliana]

Seq. No.	223826
Seq. ID	LIB3165-053-Q1-K1-H2
Method	BLASTX
NCBI GI	g3075400
BLAST score	289
E value	4.0e-26
Match length	73
% identity	71
NCBI Description	(AC004484) putative thromboxane-A synthase [Arabidopsis thaliana] >gi_3413720 (AC004747) putative thromboxin-A synthase [Arabidopsis thaliana]

Seq. No.	223827
Seq. ID	LIB3165-053-Q1-K1-H4
Method	BLASTX
NCBI GI	g1352821
BLAST score	412
E value	2.0e-40
Match length	137
% identity	64
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223828
Seq. ID	LIB3165-053-Q1-K1-H5
Method	BLASTX
NCBI GI	g1352821
BLAST score	178
E value	3.0e-15
Match length	56
% identity	80
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223829
Seq. ID	LIB3165-055-P1-K1-A1
Method	BLASTX
NCBI GI	g445116
BLAST score	558
E value	1.0e-57
Match length	116
% identity	91
NCBI Description	light-harvesting complex IIa protein; [Hordeum vulgare]

Seq. No.	223830
Seq. ID	LIB3165-055-P1-K1-A10
Method	BLASTX
NCBI GI	g100203
BLAST score	291
E value	2.0e-26
Match length	77
% identity	73
NCBI Description	cysteine proteinase (EC 3.4.22.-) precursor - tomato >gi_19195_emb_CAA78403_ (Z14028) pre-pro-cysteine proteinase [Lycopersicon esculentum]

Seq. No.	223831
Seq. ID	LIB3165-055-P1-K1-A11
Method	BLASTX
NCBI GI	g2673914
BLAST score	538
E value	3.0e-55
Match length	117
% identity	80
NCBI Description	(AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No.	223832
Seq. ID	LIB3165-055-P1-K1-A12
Method	BLASTX
NCBI GI	g4056507
BLAST score	189
E value	2.0e-14
Match length	55
% identity	65
NCBI Description	(AC005896) putative RNA binding protein [Arabidopsis thaliana]

Seq. No.	223833
Seq. ID	LIB3165-055-P1-K1-A5
Method	BLASTX
NCBI GI	g4406530
BLAST score	312
E value	9.0e-29
Match length	109
% identity	62
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223834
Seq. ID	LIB3165-055-P1-K1-A6
Method	BLASTX

NCBI GI	g266893
BLAST score	586
E value	6.0e-61
Match length	119
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__S28172 ribulose-bisphosphate carboxylase activase - cucumber >gi_18284_emb_CAA47906_ (X67674) rubisco activase [Cucumis sativus]

Seq. No.	223835
Seq. ID	LIB3165-055-P1-K1-B10
Method	BLASTX
NCBI GI	g2864617
BLAST score	239
E value	3.0e-20
Match length	108
% identity	50
NCBI Description	(AL021811) H+-transporting ATP synthase chain9 - like protein [Arabidopsis thaliana]

Seq. No.	223836
Seq. ID	LIB3165-055-P1-K1-B8
Method	BLASTX
NCBI GI	g3869088
BLAST score	511
E value	4.0e-52
Match length	97
% identity	100
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No.	223837
Seq. ID	LIB3165-055-P1-K1-B9
Method	BLASTX
NCBI GI	g70644
BLAST score	545
E value	4.0e-56
Match length	114
% identity	18
NCBI Description	ubiquitin precursor - common sunflower (fragment)

Seq. No.	223838
Seq. ID	LIB3165-055-P1-K1-C1
Method	BLASTX
NCBI GI	g4406759
BLAST score	204
E value	4.0e-16
Match length	92
% identity	47
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.	223839
Seq. ID	LIB3165-055-P1-K1-C11
Method	BLASTX
NCBI GI	g2499945
BLAST score	430

E value	1.0e-42
Match length	118
% identity	67
NCBI Description	URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_1076363_pir__S46440 orotate phosphoribosyltransferase (EC 2.4.2.10) / orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842) pyrE-F [Arabidopsis thaliana]

Seq. No.	223840
Seq. ID	LIB3165-055-P1-K1-C12
Method	BLASTX
NCBI GI	g2959643
BLAST score	137
E value	3.0e-13
Match length	102
% identity	22
NCBI Description	(AF001945) rim ABC transporter [Homo sapiens]

Seq. No.	223841
Seq. ID	LIB3165-055-P1-K1-C4
Method	BLASTX
NCBI GI	g1354515
BLAST score	203
E value	5.0e-16
Match length	97
% identity	51
NCBI Description	(U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No.	223842
Seq. ID	LIB3165-055-P1-K1-C5
Method	BLASTX
NCBI GI	g1362086
BLAST score	496
E value	2.0e-50
Match length	103
% identity	91
NCBI Description	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir__S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]

Seq. No.	223843
Seq. ID	LIB3165-055-P1-K1-C6
Method	BLASTX
NCBI GI	g4433048
BLAST score	325
E value	3.0e-30
Match length	92
% identity	75
NCBI Description	(D26578) DNA-binding protein [Daucus carota]

Seq. No.	223844
Seq. ID	LIB3165-055-P1-K1-C7
Method	BLASTX
NCBI GI	g1709825
BLAST score	277
E value	1.0e-24
Match length	112
% identity	62
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No.	223845
Seq. ID	LIB3165-055-P1-K1-C8
Method	BLASTX
NCBI GI	g1439609
BLAST score	566
E value	1.0e-58
Match length	113
% identity	54
NCBI Description	(U62778) delta-tonoplast intrinsic protein [Gossypium hirsutum]

Seq. No.	223846
Seq. ID	LIB3165-055-P1-K1-C9
Method	BLASTX
NCBI GI	g1352821
BLAST score	364
E value	7.0e-35
Match length	71
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223847
Seq. ID	LIB3165-055-P1-K1-D10
Method	BLASTX
NCBI GI	g3158474
BLAST score	324
E value	3.0e-30
Match length	85
% identity	76
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]

Seq. No.	223848
Seq. ID	LIB3165-055-P1-K1-D11
Method	BLASTX
NCBI GI	g167367
BLAST score	420
E value	2.0e-41
Match length	109
% identity	75
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	223849
Seq. ID	LIB3165-055-P1-K1-D3
Method	BLASTX
NCBI GI	g3122232
BLAST score	228
E value	6.0e-19
Match length	95
% identity	55
NCBI Description	MITOCHONDRIAL HEAT SHOCK 22 KD PROTEIN PRECURSOR >gi_1669866 (U72958) AtHSP23.6-mito [Arabidopsis thaliana] >gi_4454008_emb_CAA23061_ (AL035396) Arabidopsis mitochondrion-localized small heat shock protein (AtHSP23.6-mito) [Arabidopsis thaliana]

Seq. No.	223850
Seq. ID	LIB3165-055-P1-K1-D4
Method	BLASTX
NCBI GI	g1352821
BLAST score	505
E value	2.0e-51
Match length	104
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223851
Seq. ID	LIB3165-055-P1-K1-D6
Method	BLASTX
NCBI GI	g118564
BLAST score	562
E value	4.0e-58
Match length	113
% identity	92
NCBI Description	GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE REDUCTASE) (HPR) (GDH) >gi_65955_pir__DEKVG glycerate dehydrogenase (EC 1.1.1.29) - cucumber >gi_18264_emb_CAA41434_ (X58542) NADH-dependent hydroxypyruvate reductase [Cucumis sativus] >gi_18275_emb_CAA32764_ (X14609) NAPH-dependent hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

Seq. No.	223852
Seq. ID	LIB3165-055-P1-K1-D8
Method	BLASTX
NCBI GI	g4406530
BLAST score	292
E value	2.0e-26
Match length	80
% identity	75
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223853
Seq. ID	LIB3165-055-P1-K1-D9
Method	BLASTX

NCBI GI	g100196
BLAST score	441
E value	6.0e-44
Match length	98
% identity	83
NCBI Description	chlorophyll a/b-binding protein (cab-11) - tomato

Seq. No.	223854
Seq. ID	LIB3165-055-P1-K1-E12
Method	BLASTX
NCBI GI	g4164408
BLAST score	461
E value	3.0e-46
Match length	97
% identity	88
NCBI Description	(AJ132228) amino acid carrier [Ricinus communis]

Seq. No.	223855
Seq. ID	LIB3165-055-P1-K1-E8
Method	BLASTX
NCBI GI	g3510254
BLAST score	362
E value	1.0e-34
Match length	104
% identity	72
NCBI Description	(AC005310) putative zinc transporter [Arabidopsis thaliana]

Seq. No.	223856
Seq. ID	LIB3165-055-P1-K1-E9
Method	BLASTX
NCBI GI	g2765817
BLAST score	149
E value	1.0e-09
Match length	57
% identity	54
NCBI Description	(Z95352) AtMlo-h1 [Arabidopsis thaliana] >gi_3892049_gb_AAC78258.1_AAC78258 (AC002330) AtMlo-h1 [Arabidopsis thaliana]

Seq. No.	223857
Seq. ID	LIB3165-055-P1-K1-F10
Method	BLASTX
NCBI GI	g289920
BLAST score	571
E value	4.0e-59
Match length	108
% identity	97
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	223858
Seq. ID	LIB3165-055-P1-K1-F11
Method	BLASTX
NCBI GI	g4406530
BLAST score	278
E value	7.0e-25
Match length	79

% identity	73
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223859
Seq. ID	LIB3165-055-P1-K1-F12
Method	BLASTX
NCBI GI	g477280
BLAST score	427
E value	3.0e-42
Match length	110
% identity	73
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) 55K protein precursor - potato >gi_410633 [illegible]740 cytochrome c reductase-processing peptidase subunit 1, subunit I, P55 [potatoes, var. Marfona, tuber, Peptide Mi[illegible]chondrial, 534 aa]

Seq. No.	223860
Seq. ID	LIB3165-055-P1-K1-F2
Method	BLASTX
NCBI GI	g1737492
BLAST score	142
E value	7.0e-09
Match length	110
% identity	33
NCBI Description	(U81318) poly(A)-binding protein [Triticum aestivum]

Seq. No.	223861
Seq. ID	LIB3165-055-P1-K1-F3
Method	BLASTX
NCBI GI	g100602
BLAST score	337
E value	1.0e-31
Match length	97
% identity	65
NCBI Description	infection-related protein - barley

Seq. No.	223862
Seq. ID	LIB3165-055-P1-K1-F5
Method	BLASTX
NCBI GI	g729252
BLAST score	199
E value	2.0e-29
Match length	104
% identity	59
NCBI Description	CYTOCHROME B5 >gi_167140 (M87514) cytochrome b-5 [Brassica oleracea] >gi_384338_prf__1905426A cytochrome b5 [Brassica oleracea]

Seq. No.	223863
Seq. ID	LIB3165-055-P1-K1-F8
Method	BLASTX
NCBI GI	g289920
BLAST score	578
E value	6.0e-60
Match length	110
% identity	97

NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]
Seq. No.	223864
Seq. ID	LIB3165-055-P1-K1-F9
Method	BLASTX
NCBI GI	g2511693
BLAST score	376
E value	3.0e-36
Match length	100
% identity	73
NCBI Description	(Z99954) cysteine proteinase precursor [Phaseolus vulgaris]
Seq. No.	223865
Seq. ID	LIB3165-055-P1-K1-G1
Method	BLASTX
NCBI GI	g3914435
BLAST score	450
E value	6.0e-45
Match length	93
% identity	88
NCBI Description	PROFILIN 1 >gi_3021375_emb_CAA11756_ (AJ223982) profilin [Glycine max]
Seq. No.	223866
Seq. ID	LIB3165-055-P1-K1-G2
Method	BLASTX
NCBI GI	g1352821
BLAST score	486
E value	3.0e-49
Match length	99
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	223867
Seq. ID	LIB3165-055-P1-K1-G3
Method	BLASTX
NCBI GI	g2499931
BLAST score	268
E value	1.0e-23
Match length	65
% identity	80
NCBI Description	ADENINE PHOSPHORIBOSYLTRANSFERASE 2 (APRT) >gi_2129534_pir__S71272 adenine phosphoribosyltransferase (EC 2.4.2.7) - Arabidopsis thaliana >gi_1321681_emb_CAA65609_ (X96866) adenine phosphoribosyltransferase [Arabidopsis thaliana]
Seq. No.	223868
Seq. ID	LIB3165-055-P1-K1-G4
Method	BLASTX
NCBI GI	g3688125
BLAST score	274

E value	2.0e-24
Match length	97
% identity	64
NCBI Description	(AJ006294) granule-bound starch synthase [Antirrhinum majus]

Seq. No.	223869
Seq. ID	LIB3165-055-P1-K1-G5
Method	BLASTX
NCBI GI	g1352821
BLAST score	517
E value	8.0e-53
Match length	108
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223870
Seq. ID	LIB3165-055-P1-K1-G7
Method	BLASTX
NCBI GI	g1703292
BLAST score	312
E value	8.0e-29
Match length	98
% identity	69
NCBI Description	HIGH AFFINITY AMMONIUM TRANSPORTER >gi_551219_emb_CAA53473_ (X75879) amt1 [Arabidopsis thaliana]

Seq. No.	223871
Seq. ID	LIB3165-055-P1-K1-H1
Method	BLASTX
NCBI GI	g68200
BLAST score	285
E value	1.0e-25
Match length	78
% identity	77
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	223872
Seq. ID	LIB3165-055-P1-K1-H10
Method	BLASTX
NCBI GI	g4239845
BLAST score	190
E value	2.0e-14
Match length	118
% identity	40
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	223873
Seq. ID	LIB3165-055-P1-K1-H11
Method	BLASTX
NCBI GI	g1172664

BLAST score	186
E value	5.0e-14
Match length	39
% identity	92
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_419791_pir__S31165 photosystem I chain III precursor - Flaveria trinervia >gi_298482_bbs_127083 photosystem I reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem I subunit III [Flaveria trinervia]

Seq. No.	223874
Seq. ID	LIB3165-055-P1-K1-H12
Method	BLASTX
NCBI GI	g100616
BLAST score	396
E value	1.0e-38
Match length	108
% identity	69
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	223875
Seq. ID	LIB3165-055-P1-K1-H2
Method	BLASTX
NCBI GI	g1168408
BLAST score	518
E value	6.0e-53
Match length	113
% identity	91
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1 >gi_2118268_pir__S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828) fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No.	223876
Seq. ID	LIB3165-055-P1-K1-H3
Method	BLASTX
NCBI GI	g421826
BLAST score	308
E value	3.0e-28
Match length	98
% identity	62
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	223877
Seq. ID	LIB3165-055-P1-K1-H5
Method	BLASTX
NCBI GI	g2492782
BLAST score	284
E value	2.0e-25

Match length	59
% identity	78
NCBI Description	ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE) (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) >gi_504489 (L27992) alpha-galactosidase [Coffea arabica]

Seq. No.	223878
Seq. ID	LIB3165-055-P1-K1-H6
Method	BLASTX
NCBI GI	g3292814
BLAST score	173
E value	2.0e-12
Match length	100
% identity	46
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	223879
Seq. ID	LIB3165-055-P1-K1-H8
Method	BLASTX
NCBI GI	g2435517
BLAST score	312
E value	8.0e-29
Match length	107
% identity	55
NCBI Description	(AF024504) contains similarity to peptidase family A1 [Arabidopsis thaliana]

Seq. No.	223880
Seq. ID	LIB3165-055-P1-K1-H9
Method	BLASTX
NCBI GI	g1684851
BLAST score	262
E value	6.0e-23
Match length	81
% identity	64
NCBI Description	(U77935) DnaJ-like protein [Phaseolus vulgaris]

Seq. No.	223881
Seq. ID	LIB3165-056-P1-K1-A12
Method	BLASTX
NCBI GI	g1076748
BLAST score	178
E value	2.0e-13
Match length	59
% identity	59
NCBI Description	major intrinsic protein - rice >gi_440869_dbj_BAA04257_ (D17443) major intrinsic protein [Oryza sativa]

Seq. No.	223882
Seq. ID	LIB3165-056-P1-K1-A3
Method	BLASTX
NCBI GI	g1168411
BLAST score	403
E value	2.0e-39
Match length	106
% identity	80
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	223883
Seq. ID	LIB3165-056-P1-K1-B1
Method	BLASTX
NCBI GI	g2554675
BLAST score	202
E value	4.0e-16
Match length	66
% identity	68
NCBI Description	Three-Dimensional Structure Of Glycolate Oxidase With Bound Active-Site Inhibitors >gi_2624594_pdb_1AL7_ Three-Dimensional Structures Of Glycolate Oxidase With Bound Active-Site Inhibitors

Seq. No.	223884
Seq. ID	LIB3165-056-P1-K1-B10
Method	BLASTX
NCBI GI	g3023752
BLAST score	238
E value	4.0e-20
Match length	93
% identity	56
NCBI Description	FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520) ferredoxin-I [Lycopersicon esculentum]

Seq. No.	223885
Seq. ID	LIB3165-056-P1-K1-B12
Method	BLASTX
NCBI GI	g1352821
BLAST score	457
E value	8.0e-46
Match length	93
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223886
Seq. ID	LIB3165-056-P1-K1-B2
Method	BLASTX
NCBI GI	g131393
BLAST score	144
E value	2.0e-09
Match length	66
% identity	56
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_100360_pir__S15005 photosystem II oxygen-evolving complex protein 2 - common tobacco >gi_19911_emb_CAA39039.1_ (X55354) photosystem II 23kDa polypeptide [Nicotiana tabacum]

Seq. No.	223887
Seq. ID	LIB3165-056-P1-K1-C12
Method	BLASTX

NCBI GI	g2754849
BLAST score	312
E value	3.0e-29
Match length	77
% identity	86
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

Seq. No.	223888
Seq. ID	LIB3165-056-P1-K1-D10
Method	BLASTX
NCBI GI	g121344
BLAST score	165
E value	1.0e-11
Match length	68
% identity	53
NCBI Description	GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR (GLUTAMATE-AMMONIA LIGASE) (CHLOROPLAST GS2) >gi_68597_pir__AJPMQ2 glutamate--ammonia ligase (EC 6.3.1.2) delta precursor, chloroplast - garden pea >gi_169059 (M20664) glutamine synthetase (chloroplast GS2) (EC 6.3.1.2) [Pisum sativum]

Seq. No.	223889
Seq. ID	LIB3165-056-P1-K1-D12
Method	BLASTX
NCBI GI	g115813
BLAST score	565
E value	2.0e-58
Match length	114
% identity	89
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE III PRECURSOR (CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No.	223890
Seq. ID	LIB3165-056-P1-K1-E12
Method	BLASTX
NCBI GI	g1565225
BLAST score	151
E value	2.0e-13
Match length	66
% identity	39
NCBI Description	(X95572) salt-tolerance protein [Arabidopsis thaliana]

Seq. No.	223891
Seq. ID	LIB3165-056-P1-K1-F1
Method	BLASTX
NCBI GI	g4455235
BLAST score	181
E value	3.0e-16
Match length	63
% identity	78
NCBI Description	(AL035523) PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT-like [Arabidopsis thaliana]

Seq. No.	223892

Seq. ID	LIB3165-056-P1-K1-F11
Method	BLASTX
NCBI GI	g1169528
BLAST score	164
E value	4.0e-13
Match length	57
% identity	81
NCBI Description	ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi_602253 (U17973) enolase [Zea mays]

Seq. No.	223893
Seq. ID	LIB3165-056-P1-K1-F12
Method	BLASTX
NCBI GI	g1711355
BLAST score	232
E value	2.0e-19
Match length	90
% identity	59
NCBI Description	SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE >gi_421786_pir__S34678 short-chain alcohol dehydrogenase - Norway spruce >gi_395223_emb_CAA52213_ (X74115) short-chain alcohol dehydrogenase [Picea abies]

Seq. No.	223894
Seq. ID	LIB3165-056-P1-K1-H12
Method	BLASTX
NCBI GI	g2760537
BLAST score	137
E value	9.0e-09
Match length	34
% identity	79
NCBI Description	(Y16088) cytosolic form of cyclophilin [Lupinus luteus]

Seq. No.	223895
Seq. ID	LIB3165-057-P1-K1-A11
Method	BLASTX
NCBI GI	g3282092
BLAST score	160
E value	6.0e-11
Match length	106
% identity	38
NCBI Description	(AJ007446) hypothetical protein [Thermotoga neapolitana]

Seq. No.	223896
Seq. ID	LIB3165-057-P1-K1-A4
Method	BLASTX
NCBI GI	g4220518
BLAST score	232
E value	2.0e-19
Match length	111
% identity	47
NCBI Description	(AL035356) hypothetical protein [Arabidopsis thaliana]

Seq. No.	223897
Seq. ID	LIB3165-057-P1-K1-B10
Method	BLASTX

NCBI GI	g1352821
BLAST score	577
E value	8.0e-60
Match length	118
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223898
Seq. ID	LIB3165-057-P1-K1-B11
Method	BLASTX
NCBI GI	g2829916
BLAST score	167
E value	1.0e-11
Match length	48
% identity	75
NCBI Description	(AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No.	223899
Seq. ID	LIB3165-057-P1-K1-B4
Method	BLASTX
NCBI GI	g1352821
BLAST score	541
E value	2.0e-55
Match length	115
% identity	92
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223900
Seq. ID	LIB3165-057-P1-K1-B6
Method	BLASTX
NCBI GI	g3660471
BLAST score	379
E value	9.0e-37
Match length	91
% identity	82
NCBI Description	(AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

Seq. No.	223901
Seq. ID	LIB3165-057-P1-K1-C1
Method	BLASTX
NCBI GI	g430947
BLAST score	338
E value	1.0e-32
Match length	97
% identity	76
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	223902
Seq. ID	LIB3165-057-P1-K1-C2
Method	BLASTX
NCBI GI	g320622
BLAST score	593
E value	1.0e-61
Match length	123
% identity	89
NCBI Description	probable protein kinase - maize (fragment) >gi_168618 (M62985) protein kinase [Zea mays]

Seq. No.	223903
Seq. ID	LIB3165-057-P1-K1-D10
Method	BLASTX
NCBI GI	g1931640
BLAST score	325
E value	3.0e-30
Match length	90
% identity	64
NCBI Description	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]

Seq. No.	223904
Seq. ID	LIB3165-057-P1-K1-E12
Method	BLASTX
NCBI GI	g1168411
BLAST score	301
E value	1.0e-27
Match length	96
% identity	72
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	223905
Seq. ID	LIB3165-057-P1-K1-E4
Method	BLASTX
NCBI GI	g134892
BLAST score	223
E value	3.0e-19
Match length	114
% identity	55
NCBI Description	SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT (SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA) >gi_88607_pir__A29440 signal recognition particle receptor - human >gi_30866_emb_CAA29608_ (X06272) docking protein [Homo sapiens] >gi_4507223_ref_NP_003130.1_pSRPR_ signal recognition particle receptor ('docking protein')

Seq. No.	223906
Seq. ID	LIB3165-057-P1-K1-G11
Method	BLASTX
NCBI GI	g1352821
BLAST score	432
E value	8.0e-43
Match length	101
% identity	89
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU

	ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	223907
Seq. ID	LIB3165-057-P1-K1-H11
Method	BLASTX
NCBI GI	g4056493
BLAST score	202
E value	7.0e-16
Match length	97
% identity	40
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]
Seq. No.	223908
Seq. ID	LIB3165-058-P1-K1-A8
Method	BLASTX
NCBI GI	g3914603
BLAST score	188
E value	1.0e-14
Match length	58
% identity	62
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]
Seq. No.	223909
Seq. ID	LIB3165-058-P1-K1-B1
Method	BLASTX
NCBI GI	g3747111
BLAST score	267
E value	2.0e-23
Match length	67
% identity	72
NCBI Description	(AF095641) MTN3 homolog [Arabidopsis thaliana]
Seq. No.	223910
Seq. ID	LIB3165-058-P1-K1-B11
Method	BLASTX
NCBI GI	g1488043
BLAST score	171
E value	3.0e-12
Match length	56
% identity	66
NCBI Description	(U63784) PAPS-reductase-like protein [Catharanthus roseus]
Seq. No.	223911
Seq. ID	LIB3165-058-P1-K1-B2
Method	BLASTX
NCBI GI	g115765
BLAST score	258
E value	7.0e-37
Match length	107
% identity	73
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding

protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	223912
Seq. ID	LIB3165-058-P1-K1-B3
Method	BLASTX
NCBI GI	g231610
BLAST score	182
E value	1.0e-13
Match length	48
% identity	79
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]

Seq. No.	223913
Seq. ID	LIB3165-058-P1-K1-B8
Method	BLASTX
NCBI GI	g3953473
BLAST score	300
E value	2.0e-27
Match length	113
% identity	66
NCBI Description	(AC002328) F22O2.18 [Arabidopsis thaliana]

Seq. No.	223914
Seq. ID	LIB3165-058-P1-K1-C3
Method	BLASTX
NCBI GI	g2501578
BLAST score	339
E value	5.0e-32
Match length	73
% identity	90
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No.	223915
Seq. ID	LIB3165-058-P1-K1-C8
Method	BLASTX
NCBI GI	g4510376
BLAST score	186
E value	5.0e-14
Match length	69
% identity	54
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	223916
Seq. ID	LIB3165-058-P1-K1-C9
Method	BLASTX

NCBI GI	g3914605
BLAST score	166
E value	6.0e-12
Match length	77
% identity	52
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase - apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica]

Seq. No.	223917
Seq. ID	LIB3165-058-P1-K1-F3
Method	BLASTX
NCBI GI	g2879811
BLAST score	149
E value	1.0e-21
Match length	62
% identity	74
NCBI Description	(AJ223316) ribosomal protein L30 [Lupinus luteus]

Seq. No.	223918
Seq. ID	LIB3165-058-P1-K1-G1
Method	BLASTX
NCBI GI	g2501578
BLAST score	575
E value	2.0e-59
Match length	122
% identity	96
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No.	223919
Seq. ID	LIB3165-058-P1-K1-G10
Method	BLASTX
NCBI GI	g542087
BLAST score	196
E value	4.0e-32
Match length	112
% identity	67
NCBI Description	sucrose transport protein - potato >gi_439294_emb_CAA48915_ (X69165) sucrose transport protein [Solanum tuberosum]

Seq. No.	223920
Seq. ID	LIB3165-058-P1-K1-G12
Method	BLASTX
NCBI GI	g1181599
BLAST score	122
E value	5.0e-10
Match length	74
% identity	57
NCBI Description	(D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.	223921

Seq. ID	LIB3165-058-P1-K1-H12
Method	BLASTX
NCBI GI	g1352821
BLAST score	308
E value	9.0e-29
Match length	63
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223922
Seq. ID	LIB3165-058-P1-K1-H9
Method	BLASTX
NCBI GI	g2655098
BLAST score	202
E value	6.0e-16
Match length	82
% identity	44
NCBI Description	(AF023472) peptide transporter [Hordeum vulgare]

Seq. No.	223923
Seq. ID	LIB3165-059-P1-K1-A11
Method	BLASTX
NCBI GI	g121080
BLAST score	143
E value	3.0e-09
Match length	64
% identity	56
NCBI Description	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_1070638_pir__GCPMH glycine cleavage system protein H precursor - garden pea >gi_20737_emb_CAA45978_ (X64726) H protein [Pisum sativum] >gi_169093 (J05164) H-protein of glycine decarboxylase precursor (EC 2.1.2.10) [Pisum sativum] >gi_287815_emb_CAA37704_ (X53656) H-protein [Pisum sativum]

Seq. No.	223924
Seq. ID	LIB3165-059-P1-K1-A8
Method	BLASTX
NCBI GI	g4406530
BLAST score	250
E value	2.0e-21
Match length	85
% identity	64
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223925
Seq. ID	LIB3165-059-P1-K1-B12
Method	BLASTX
NCBI GI	g1684851
BLAST score	191
E value	1.0e-14
Match length	55
% identity	69

NCBI Description	(U77935) DnaJ-like protein [Phaseolus vulgaris]

Seq. No.	223926
Seq. ID	LIB3165-059-P1-K1-B4
Method	BLASTX
NCBI GI	g1352821
BLAST score	140
E value	5.0e-09
Match length	41
% identity	71
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223927
Seq. ID	LIB3165-059-P1-K1-C11
Method	BLASTX
NCBI GI	g541951
BLAST score	123
E value	1.0e-13
Match length	68
% identity	58
NCBI Description	SPCP2 protein - soybean >gi_310578 (L12258) nodulin-26 [Glycine max]

Seq. No.	223928
Seq. ID	LIB3165-059-P1-K1-D11
Method	BLASTX
NCBI GI	g2565305
BLAST score	366
E value	3.0e-35
Match length	99
% identity	73
NCBI Description	(AF024589) glycine decarboxylase P subunit [Hordeum sp. x Triticum sp.]

Seq. No.	223929
Seq. ID	LIB3165-059-P1-K1-D12
Method	BLASTX
NCBI GI	g2995384
BLAST score	262
E value	4.0e-23
Match length	86
% identity	63
NCBI Description	(AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No.	223930
Seq. ID	LIB3165-059-P1-K1-E5
Method	BLASTX
NCBI GI	g1352821
BLAST score	152
E value	2.0e-10
Match length	33
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223931
Seq. ID	LIB3165-059-P1-K1-F11
Method	BLASTX
NCBI GI	g1168411
BLAST score	162
E value	4.0e-15
Match length	83
% identity	67
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.	223932
Seq. ID	LIB3165-059-P1-K1-G11
Method	BLASTX
NCBI GI	g3702339
BLAST score	154
E value	2.0e-10
Match length	59
% identity	56
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	223933
Seq. ID	LIB3165-059-P1-K1-G12
Method	BLASTX
NCBI GI	g2119719
BLAST score	192
E value	6.0e-15
Match length	80
% identity	56
NCBI Description	heat-shock cognate protein 70-3 - tomato >gi_762844 (L41253) Hsc70 [Lycopersicon esculentum]

Seq. No.	223934
Seq. ID	LIB3165-059-P1-K1-H10
Method	BLASTX
NCBI GI	g1431629
BLAST score	165
E value	8.0e-12
Match length	57
% identity	61
NCBI Description	(X99348) pectinacetylesterase precursor [Vigna radiata]

Seq. No.	223935
Seq. ID	LIB3165-060-Q1-K1-A1
Method	BLASTX
NCBI GI	g2507153
BLAST score	189
E value	3.0e-14
Match length	134
% identity	35
NCBI Description	VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS16 >gi_2133204_pir__S62031 vacuolar protein sorting-associated protein VPS16 - yeast (Saccharomyces cerevisiae)

	>gi_1171414 (U44030) Vsp16p: Vacuolar sorting protein [Saccharomyces cerevisiae]
Seq. No.	223936
Seq. ID	LIB3165-060-Q1-K1-A3
Method	BLASTX
NCBI GI	g3914603
BLAST score	517
E value	3.0e-62
Match length	134
% identity	83
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]
Seq. No.	223937
Seq. ID	LIB3165-060-Q1-K1-A4
Method	BLASTX
NCBI GI	g2832783
BLAST score	488
E value	2.0e-49
Match length	98
% identity	91
NCBI Description	(AJ225806) potassium channel beta subunit [Egeria densa]
Seq. No.	223938
Seq. ID	LIB3165-060-Q1-K1-A5
Method	BLASTX
NCBI GI	g232029
BLAST score	377
E value	1.0e-36
Match length	74
% identity	99
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_100154_pir__S21989 translation elongation factor eEF-1 alpha chain - carrot >gi_18339_emb_CAA42843_ (X60302) elongation factor 1A [Daucus carota]
Seq. No.	223939
Seq. ID	LIB3165-060-Q1-K1-A6
Method	BLASTX
NCBI GI	g1928981
BLAST score	510
E value	5.0e-52
Match length	109
% identity	93
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]
Seq. No.	223940
Seq. ID	LIB3165-060-Q1-K1-A8
Method	BLASTX
NCBI GI	g3121825
BLAST score	322
E value	7.0e-30
Match length	123

% identity	65
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea]

Seq. No.	223941
Seq. ID	LIB3165-060-Q1-K1-B1
Method	BLASTX
NCBI GI	g1351408
BLAST score	437
E value	2.0e-43
Match length	104
% identity	78
NCBI Description	VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) >gi_1076563_pir__S51117 cystein proteinase - sweet orange >gi_633185_emb_CAA87720_ (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi_1588548_prf__2208463A vascular processing protease [Citrus sinensis]

Seq. No.	223942
Seq. ID	LIB3165-060-Q1-K1-B11
Method	BLASTX
NCBI GI	g2501353
BLAST score	438
E value	1.0e-43
Match length	89
% identity	93
NCBI Description	TRANSKETOLASE, CHLOROPLAST (TK) >gi_1084440_pir__S54300 transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) >gi_664901_emb_CAA86607_ (Z46646) transketolase [Craterostigma plantagineum]

Seq. No.	223943
Seq. ID	LIB3165-060-Q1-K1-B12
Method	BLASTX
NCBI GI	g3421102
BLAST score	332
E value	3.0e-31
Match length	77
% identity	81
NCBI Description	(AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis thaliana]

Seq. No.	223944
Seq. ID	LIB3165-060-Q1-K1-B2
Method	BLASTX
NCBI GI	g2832643
BLAST score	281
E value	3.0e-25
Match length	70
% identity	81
NCBI Description	(AL021710) hypothetical protein [Arabidopsis thaliana]

Seq. No.	223945
Seq. ID	LIB3165-060-Q1-K1-B3
Method	BLASTX
NCBI GI	g4325041

BLAST score 478
E value 2.0e-48
Match length 102
% identity 94
NCBI Description (AF117339) FtsH-like protein Pftf precursor [Nicotiana tabacum]

Seq. No. 223946
Seq. ID LIB3165-060-Q1-K1-B8
Method BLASTX
NCBI GI g1684851
BLAST score 318
E value 2.0e-29
Match length 114
% identity 60
NCBI Description (U77935) DnaJ-like protein [Phaseolus vulgaris]

Seq. No. 223947
Seq. ID LIB3165-060-Q1-K1-B9
Method BLASTX
NCBI GI g20729
BLAST score 392
E value 4.0e-38
Match length 108
% identity 74
NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No. 223948
Seq. ID LIB3165-060-Q1-K1-C1
Method BLASTX
NCBI GI g1352821
BLAST score 431
E value 9.0e-43
Match length 83
% identity 98
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223949
Seq. ID LIB3165-060-Q1-K1-C10
Method BLASTX
NCBI GI g267120
BLAST score 198
E value 2.0e-15
Match length 83
% identity 55
NCBI Description THIOREDOXIN F-TYPE PRECURSOR (TRX-F) >gi_100070_pir__S20929 thioredoxin f precursor - garden pea >gi_20907_emb_CAA45098_ (X63537) thioredoxin F [Pisum sativum] >gi_1388086 (U35830) thioredoxin f [Pisum sativum]

Seq. No. 223950
Seq. ID LIB3165-060-Q1-K1-C11
Method BLASTX

NCBI GI	g1351271
BLAST score	181
E value	9.0e-17
Match length	97
% identity	60
NCBI Description	TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) >gi_1084309_pir__S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi_806312 (L36387) triosephosphate isomerase, chloroplast isozyme [Spinacia oleracea]

Seq. No.	223951
Seq. ID	LIB3165-060-Q1-K1-C7
Method	BLASTX
NCBI GI	g1130682
BLAST score	642
E value	2.0e-67
Match length	127
% identity	100
NCBI Description	(Z46959) acetohydroxyacid synthase [Gossypium hirsutum]

Seq. No.	223952
Seq. ID	LIB3165-060-Q1-K1-C8
Method	BLASTX
NCBI GI	g4206194
BLAST score	462
E value	3.0e-46
Match length	131
% identity	66
NCBI Description	(AF071527) GH3-like protein [Arabidopsis thaliana] >gi_4262168_gb_AAD14468_ (AC005275) putative GH3-like protein [Arabidopsis thaliana]

Seq. No.	223953
Seq. ID	LIB3165-060-Q1-K1-D12
Method	BLASTX
NCBI GI	g2943789
BLAST score	269
E value	1.0e-23
Match length	90
% identity	62
NCBI Description	(AB000875) RD22BP1 [Arabidopsis thaliana]

Seq. No.	223954
Seq. ID	LIB3165-060-Q1-K1-D2
Method	BLASTX
NCBI GI	g68200
BLAST score	438
E value	1.0e-43
Match length	113
% identity	80
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	223955
Seq. ID	LIB3165-060-Q1-K1-D3

Method	BLASTX
NCBI GI	g1532135
BLAST score	495
E value	3.0e-50
Match length	106
% identity	86
NCBI Description	(U49442) chloroplast mRNA-binding protein CSP41 precursor [Spinacia oleracea]

Seq. No.	223956
Seq. ID	LIB3165-060-Q1-K1-D4
Method	BLASTX
NCBI GI	g4091806
BLAST score	377
E value	2.0e-36
Match length	96
% identity	72
NCBI Description	(AF052585) CONSTANS-like protein 2 [Malus domestica]

Seq. No.	223957
Seq. ID	LIB3165-060-Q1-K1-D5
Method	BLASTX
NCBI GI	g4406530
BLAST score	169
E value	4.0e-12
Match length	56
% identity	66
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223958
Seq. ID	LIB3165-060-Q1-K1-D6
Method	BLASTX
NCBI GI	g1946368
BLAST score	452
E value	3.0e-45
Match length	104
% identity	85
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	223959
Seq. ID	LIB3165-060-Q1-K1-D8
Method	BLASTX
NCBI GI	g3024126
BLAST score	444
E value	3.0e-44
Match length	87
% identity	97
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine synthetase 1 [Catharanthus roseus]

Seq. No.	223960
Seq. ID	LIB3165-060-Q1-K1-E11
Method	BLASTX
NCBI GI	g3822036
BLAST score	221

E value 4.0e-18
Match length 115
% identity 45
NCBI Description (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]

Seq. No. 223961
Seq. ID LIB3165-060-Q1-K1-E12
Method BLASTX
NCBI GI g4204849
BLAST score 515
E value 1.0e-52
Match length 120
% identity 81
NCBI Description (U55875) protein kinase [Arabidopsis thaliana]

Seq. No. 223962
Seq. ID LIB3165-060-Q1-K1-E2
Method BLASTX
NCBI GI g3127838
BLAST score 220
E value 3.0e-18
Match length 88
% identity 49
NCBI Description (AL023496) hypothetical protein [Streptomyces coelicolor]

Seq. No. 223963
Seq. ID LIB3165-060-Q1-K1-E4
Method BLASTX
NCBI GI g3023752
BLAST score 160
E value 3.0e-11
Match length 54
% identity 65
NCBI Description FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520) ferredoxin-I [Lycopersicon esculentum]

Seq. No. 223964
Seq. ID LIB3165-060-Q1-K1-E5
Method BLASTX
NCBI GI g1170897
BLAST score 288
E value 4.0e-26
Match length 67
% identity 87
NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi_1076276_pir__S52039 NAD-malate dehydrogenase - cucumber >gi_695311 (L31900) glyoxysomal malate dehydrogenase [Cucumis sativus]

Seq. No. 223965
Seq. ID LIB3165-060-Q1-K1-F10
Method BLASTX
NCBI GI g1352821
BLAST score 482
E value 1.0e-48
Match length 96
% identity 95

NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	223966
Seq. ID	LIB3165-060-Q1-K1-F11
Method	BLASTX
NCBI GI	g3763916
BLAST score	331
E value	6.0e-31
Match length	126
% identity	53
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana] >gi_4531439_gb_AAD22124.1_AC006224_6 (AC006224) unknown protein [Arabidopsis thaliana]
Seq. No.	223967
Seq. ID	LIB3165-060-Q1-K1-F12
Method	BLASTX
NCBI GI	g729668
BLAST score	242
E value	1.0e-20
Match length	55
% identity	84
NCBI Description	HISTONE H1 >gi_2147479_pir__S65059 histone H1, drought-inducible - Lycopersicon pennellii >gi_436823 (U01890) Solanum pennellii histone H1 [Solanum pennellii]
Seq. No.	223968
Seq. ID	LIB3165-060-Q1-K1-F3
Method	BLASTX
NCBI GI	g1352821
BLAST score	352
E value	1.0e-33
Match length	67
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	223969
Seq. ID	LIB3165-060-Q1-K1-F5
Method	BLASTX
NCBI GI	g4455223
BLAST score	403
E value	2.0e-39
Match length	126
% identity	32
NCBI Description	(AL035440) putative DNA binding protein [Arabidopsis thaliana]
Seq. No.	223970
Seq. ID	LIB3165-060-Q1-K1-F6

Method	BLASTX
NCBI GI	g464775
BLAST score	447
E value	1.0e-44
Match length	89
% identity	92
NCBI Description	SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi_542013_pir__S39492 superoxide dismutase - Para rubber tree >gi_348137 (L11707) superoxide dismutase (manganese) [Hevea brasiliensis]

Seq. No.	223971
Seq. ID	LIB3165-060-Q1-K1-F7
Method	BLASTX
NCBI GI	g3549626
BLAST score	294
E value	1.0e-26
Match length	99
% identity	55
NCBI Description	(AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]

Seq. No.	223972
Seq. ID	LIB3165-060-Q1-K1-G1
Method	BLASTX
NCBI GI	g289920
BLAST score	429
E value	1.0e-42
Match length	82
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	223973
Seq. ID	LIB3165-060-Q1-K1-G10
Method	BLASTX
NCBI GI	g1352821
BLAST score	495
E value	3.0e-50
Match length	95
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223974
Seq. ID	LIB3165-060-Q1-K1-G12
Method	BLASTX
NCBI GI	g1781348
BLAST score	572
E value	3.0e-59
Match length	119
% identity	92
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No.	223975

Seq. ID	LIB3165-060-Q1-K1-G2
Method	BLASTX
NCBI GI	g1170567
BLAST score	280
E value	3.0e-25
Match length	56
% identity	89
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1085960_pir__S52648 INO1 protein - Citrus paradisi >gi_602565_emb_CAA83565_ (Z32632) INO1 [Citrus x paradisi]

Seq. No.	223976
Seq. ID	LIB3165-060-Q1-K1-G4
Method	BLASTX
NCBI GI	g3687652
BLAST score	503
E value	3.0e-51
Match length	106
% identity	92
NCBI Description	(AF047352) rubisco activase precursor [Datisca glomerata]

Seq. No.	223977
Seq. ID	LIB3165-060-Q1-K1-G5
Method	BLASTX
NCBI GI	g1871192
BLAST score	140
E value	1.0e-08
Match length	64
% identity	44
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	223978
Seq. ID	LIB3165-060-Q1-K1-G7
Method	BLASTX
NCBI GI	g1352821
BLAST score	302
E value	8.0e-28
Match length	63
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223979
Seq. ID	LIB3165-060-Q1-K1-H1
Method	BLASTX
NCBI GI	g2980770
BLAST score	260
E value	5.0e-23
Match length	67
% identity	78
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	223980

Seq. ID	LIB3165-060-Q1-K1-H11
Method	BLASTX
NCBI GI	g131393
BLAST score	350
E value	3.0e-33
Match length	106
% identity	72
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_100360_pir__S15005 photosystem II oxygen-evolving complex protein 2 - common tobacco >gi_19911_emb_CAA39039.1_ (X55354) photosystem II 23kDa polypeptide [Nicotiana tabacum]

Seq. No.	223981
Seq. ID	LIB3165-060-Q1-K1-H12
Method	BLASTX
NCBI GI	g267122
BLAST score	422
E value	1.0e-41
Match length	100
% identity	77
NCBI Description	THIOREDOXIN H-TYPE (TRX-H) >gi_478400_pir__JQ2242 thioredoxin h - Arabidopsis thaliana >gi_16552_emb_CAA78462_ (Z14084) Thioredoxin H [Arabidopsis thaliana] >gi_1388080 (U35827) thioredoxin h [Arabidopsis thaliana]

Seq. No.	223982
Seq. ID	LIB3165-060-Q1-K1-H4
Method	BLASTX
NCBI GI	g120659
BLAST score	396
E value	1.0e-38
Match length	79
% identity	94
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST >gi_81721_pir__B24796 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13), chloroplast - white mustard (fragment) >gi_829288_emb_CAA27845_ (X04302) chloroplast GAPDH (233aa) [Sinapis alba]

Seq. No.	223983
Seq. ID	LIB3165-060-Q1-K1-H6
Method	BLASTX
NCBI GI	g1749546
BLAST score	222
E value	3.0e-18
Match length	77
% identity	60
NCBI Description	(D89169) similar to Saccharomyces cerevisiae SCD6 protein, SWISS-PROT Accession Number P45978 [Schizosaccharomyces pombe]

Seq. No.	223984
Seq. ID	LIB3165-060-Q1-K1-H7

Method	BLASTX
NCBI GI	g1352821
BLAST score	320
E value	8.0e-30
Match length	63
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	223985
Seq. ID	LIB3165-060-Q1-K1-H9
Method	BLASTX
NCBI GI	g4406530
BLAST score	259
E value	5.0e-26
Match length	92
% identity	74
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	223986
Seq. ID	LIB3166-001-Q1-K1-A1
Method	BLASTX
NCBI GI	g4102600
BLAST score	543
E value	9.0e-56
Match length	124
% identity	86
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]

Seq. No.	223987
Seq. ID	LIB3166-001-Q1-K1-A11
Method	BLASTX
NCBI GI	g2584721
BLAST score	631
E value	4.0e-66
Match length	139
% identity	83
NCBI Description	(Y10157) sulfite reductase [Arabidopsis thaliana]

Seq. No.	223988
Seq. ID	LIB3166-001-Q1-K1-A2
Method	BLASTX
NCBI GI	g967125
BLAST score	691
E value	4.0e-73
Match length	135
% identity	96
NCBI Description	(U08140) calcium dependent protein kinase [Vigna radiata]

Seq. No.	223989
Seq. ID	LIB3166-001-Q1-K1-A3
Method	BLASTX
NCBI GI	g1263291
BLAST score	556

E value	2.0e-57
Match length	120
% identity	87
NCBI Description	(U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No.	223990
Seq. ID	LIB3166-001-Q1-K1-A5
Method	BLASTX
NCBI GI	g3169182
BLAST score	360
E value	2.0e-34
Match length	78
% identity	85
NCBI Description	(AC004401) unknown protein [Arabidopsis thaliana]

Seq. No.	223991
Seq. ID	LIB3166-001-Q1-K1-A6
Method	BLASTX
NCBI GI	g4455202
BLAST score	392
E value	5.0e-38
Match length	106
% identity	73
NCBI Description	(AL035440) putative APG protein [Arabidopsis thaliana]

Seq. No.	223992
Seq. ID	LIB3166-001-Q1-K1-A8
Method	BLASTX
NCBI GI	g2191129
BLAST score	301
E value	2.0e-27
Match length	135
% identity	55
NCBI Description	(AF007269) similar to SPF1 DNA-binding protein [Arabidopsis thaliana]

Seq. No.	223993
Seq. ID	LIB3166-001-Q1-K1-A9
Method	BLASTX
NCBI GI	g3046815
BLAST score	544
E value	7.0e-56
Match length	130
% identity	82
NCBI Description	(AL021687) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	223994
Seq. ID	LIB3166-001-Q1-K1-B1
Method	BLASTX
NCBI GI	g3122116
BLAST score	296
E value	8.0e-27
Match length	132
% identity	48
NCBI Description	CELL DIVISION PROTEIN FTSH HOMOLOG >gi_2660540_emb_CAA05102_ (AJ001932) cell cycle protein [Helicobacter felis]

Seq. No.	223995
Seq. ID	LIB3166-001-Q1-K1-B10
Method	BLASTX
NCBI GI	g3023195
BLAST score	605
E value	5.0e-63
Match length	135
% identity	88
NCBI Description	14-3-3-LIKE PROTEIN B (SGF14B) >gi_1575727 (U70534) SGF14B [Glycine max]

Seq. No.	223996
Seq. ID	LIB3166-001-Q1-K1-B11
Method	BLASTX
NCBI GI	g2541876
BLAST score	221
E value	5.0e-18
Match length	76
% identity	51
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	223997
Seq. ID	LIB3166-001-Q1-K1-B3
Method	BLASTX
NCBI GI	g3608485
BLAST score	649
E value	3.0e-68
Match length	127
% identity	94
NCBI Description	(AF088915) proteasome beta subunit [Petunia x hybrida]

Seq. No.	223998
Seq. ID	LIB3166-001-Q1-K1-B7
Method	BLASTX
NCBI GI	g886116
BLAST score	516
E value	1.0e-52
Match length	131
% identity	70
NCBI Description	(U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473 (AF051338) xyloglucan endotransglycosylase related protein [Arabidopsis thaliana]

Seq. No.	223999
Seq. ID	LIB3166-001-Q1-K1-B9
Method	BLASTX
NCBI GI	g3955021
BLAST score	174
E value	2.0e-12
Match length	35
% identity	89
NCBI Description	(AJ010811) HB2 homeodomain protein [Populus tremula x Populus tremuloides]

Seq. No.	224000

Seq. ID	LIB3166-001-Q1-K1-C1
Method	BLASTX
NCBI GI	g3790567
BLAST score	196
E value	4.0e-15
Match length	116
% identity	36
NCBI Description	(AF078821) RING-H2 finger protein RHA1b [Arabidopsis thaliana]

Seq. No.	224001
Seq. ID	LIB3166-001-Q1-K1-C11
Method	BLASTX
NCBI GI	g1495804
BLAST score	631
E value	4.0e-66
Match length	137
% identity	86
NCBI Description	(X96406) 13-lipoxygenase [Solanum tuberosum]

Seq. No.	224002
Seq. ID	LIB3166-001-Q1-K1-C12
Method	BLASTX
NCBI GI	g1170504
BLAST score	175
E value	1.0e-12
Match length	68
% identity	49
NCBI Description	EUKARYOTIC INITIATION FACTOR (ISO)4F SUBUNIT P82 (IEIF-(ISO)4F P82) >gi_452440 (M95747) initiation factor (iso)4f p82 subunit [Triticum aestivum]

Seq. No.	224003
Seq. ID	LIB3166-001-Q1-K1-C2
Method	BLASTX
NCBI GI	g4455340
BLAST score	235
E value	1.0e-19
Match length	65
% identity	68
NCBI Description	(AL035522) putative protein [Arabidopsis thaliana]

Seq. No.	224004
Seq. ID	LIB3166-001-Q1-K1-C3
Method	BLASTX
NCBI GI	g1408471
BLAST score	511
E value	5.0e-52
Match length	113
% identity	81
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	224005
Seq. ID	LIB3166-001-Q1-K1-C6
Method	BLASTX

NCBI GI	g3021355
BLAST score	409
E value	5.0e-40
Match length	89
% identity	88
NCBI Description	(AJ005081) UDP-galactose 4-epimerase [Cyamopsis tetragonoloba]

Seq. No.	224006
Seq. ID	LIB3166-001-Q1-K1-C7
Method	BLASTX
NCBI GI	g2829918
BLAST score	548
E value	2.0e-56
Match length	129
% identity	81
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No.	224007
Seq. ID	LIB3166-001-Q1-K1-C8
Method	BLASTX
NCBI GI	g4314378
BLAST score	343
E value	3.0e-32
Match length	136
% identity	51
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	224008
Seq. ID	LIB3166-001-Q1-K1-D10
Method	BLASTX
NCBI GI	g4263712
BLAST score	408
E value	6.0e-40
Match length	98
% identity	77
NCBI Description	(AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]

Seq. No.	224009
Seq. ID	LIB3166-001-Q1-K1-D11
Method	BLASTX
NCBI GI	g1706482
BLAST score	169
E value	6.0e-12
Match length	107
% identity	40
NCBI Description	DNA LIGASE IV (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)) >gi_860937_emb_CAA58467_ (X83441) DNA ligase IV [Homo sapiens] >gi_4504997_ref_NP_002303.1_pLIG4_ ligase IV, DNA, ATP-dependent

Seq. No.	224010
Seq. ID	LIB3166-001-Q1-K1-D3
Method	BLASTX
NCBI GI	g2459429

BLAST score	502
E value	6.0e-51
Match length	126
% identity	71
NCBI Description	(AC002332) unknown protein [Arabidopsis thaliana]

Seq. No.	224011
Seq. ID	LIB3166-001-Q1-K1-D5
Method	BLASTX
NCBI GI	g2501572
BLAST score	387
E value	2.0e-37
Match length	107
% identity	63
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi_1350545 (L47118) EMB8 gene product [Picea glauca]

Seq. No.	224012
Seq. ID	LIB3166-001-Q1-K1-D6
Method	BLASTX
NCBI GI	g310587
BLAST score	160
E value	5.0e-11
Match length	51
% identity	65
NCBI Description	(L20864) ascorbate peroxidase [Spinacia oleracea] >gi_1384110_dbj_BAA12890_ (D85864) cytosolic ascorbate peroxidase [Spinacia oleracea]

Seq. No.	224013
Seq. ID	LIB3166-001-Q1-K1-D7
Method	BLASTX
NCBI GI	g4539348
BLAST score	142
E value	9.0e-09
Match length	50
% identity	80
NCBI Description	(AL035539) putative pollen allergen [Arabidopsis thaliana]

Seq. No.	224014
Seq. ID	LIB3166-001-Q1-K1-E1
Method	BLASTX
NCBI GI	g4249410
BLAST score	563
E value	4.0e-58
Match length	128
% identity	82
NCBI Description	(AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.	224015
Seq. ID	LIB3166-001-Q1-K1-E11
Method	BLASTX
NCBI GI	g2344901
BLAST score	252
E value	8.0e-22
Match length	84
% identity	64

NCBI Description	(AC002388) serine/threonine protein kinase isolog [Arabidopsis thaliana]
Seq. No.	224016
Seq. ID	LIB3166-001-Q1-K1-E12
Method	BLASTX
NCBI GI	g3775989
BLAST score	557
E value	2.0e-57
Match length	137
% identity	75
NCBI Description	(AJ010458) RNA helicase [Arabidopsis thaliana]
Seq. No.	224017
Seq. ID	LIB3166-001-Q1-K1-E3
Method	BLASTX
NCBI GI	g4206789
BLAST score	457
E value	9.0e-46
Match length	129
% identity	71
NCBI Description	(AF112864) syntaxin-related protein At-SYR1 [Arabidopsis thaliana]
Seq. No.	224018
Seq. ID	LIB3166-001-Q1-K1-E7
Method	BLASTX
NCBI GI	g4204313
BLAST score	481
E value	2.0e-48
Match length	107
% identity	83
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]
Seq. No.	224019
Seq. ID	LIB3166-001-Q1-K1-E9
Method	BLASTX
NCBI GI	g136636
BLAST score	469
E value	4.0e-47
Match length	87
% identity	98
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]
Seq. No.	224020
Seq. ID	LIB3166-001-Q1-K1-F10
Method	BLASTX
NCBI GI	g479406

BLAST score	404
E value	5.0e-50
Match length	119
% identity	62
NCBI Description	chlorophyll a/b-binding protein - garden pea >gi_20671_emb_CAA49149_ (X69215) chlorophyll a/b-binding protein [Pisum sativum]

Seq. No.	224021
Seq. ID	LIB3166-001-Q1-K1-F11
Method	BLASTX
NCBI GI	g3281846
BLAST score	176
E value	1.0e-12
Match length	132
% identity	33
NCBI Description	(AJ006404) late elongated hypocotyl [Arabidopsis thaliana]

Seq. No.	224022
Seq. ID	LIB3166-001-Q1-K1-F3
Method	BLASTX
NCBI GI	g3281848
BLAST score	188
E value	4.0e-14
Match length	132
% identity	46
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	224023
Seq. ID	LIB3166-001-Q1-K1-F5
Method	BLASTX
NCBI GI	g2218152
BLAST score	693
E value	2.0e-73
Match length	136
% identity	90
NCBI Description	(AF005279) type IIIa membrane protein cp-wap13 [Vigna unguiculata]

Seq. No.	224024
Seq. ID	LIB3166-001-Q1-K1-G12
Method	BLASTX
NCBI GI	g3218467
BLAST score	221
E value	5.0e-18
Match length	138
% identity	38
NCBI Description	(AJ006529) putative phosphatase [Gallus gallus]

Seq. No.	224025
Seq. ID	LIB3166-001-Q1-K1-G2
Method	BLASTX
NCBI GI	g1854386
BLAST score	487
E value	3.0e-49
Match length	137
% identity	68

NCBI Description	(AB001375) similar to soluble NSF attachment protein [Vitis vinifera]

Seq. No.	224026
Seq. ID	LIB3166-001-Q1-K1-G3
Method	BLASTX
NCBI GI	g2780194
BLAST score	546
E value	4.0e-56
Match length	123
% identity	58
NCBI Description	(AJ003197) adenine nucleotide translocator [Lupinus albus]

Seq. No.	224027
Seq. ID	LIB3166-001-Q1-K1-G5
Method	BLASTX
NCBI GI	g4262250
BLAST score	370
E value	2.0e-35
Match length	108
% identity	74
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	224028
Seq. ID	LIB3166-001-Q1-K1-G6
Method	BLASTX
NCBI GI	g3859116
BLAST score	360
E value	2.0e-34
Match length	120
% identity	59
NCBI Description	(AF031609) unknown [Oryza sativa]

Seq. No.	224029
Seq. ID	LIB3166-001-Q1-K1-G8
Method	BLASTX
NCBI GI	g1946369
BLAST score	142
E value	9.0e-09
Match length	84
% identity	44
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	224030
Seq. ID	LIB3166-001-Q1-K1-G9
Method	BLASTX
NCBI GI	g1346769
BLAST score	501
E value	8.0e-51
Match length	136
% identity	65
NCBI Description	PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING ENZYME) (PE) >gi_558596_emb_CAA52605_ (X74496) prolyl oligopeptidase [Homo sapiens] >gi_1585155_prf__2124300A Pro oligopeptidase [Homo sapiens] >gi_4506043_ref_NP_002717.1_pPREP_ prolyl endopeptidase

Seq. No.	224031
Seq. ID	LIB3166-001-Q1-K1-H2
Method	BLASTX
NCBI GI	g3402704
BLAST score	344
E value	2.0e-32
Match length	119
% identity	66
NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224032
Seq. ID	LIB3166-001-Q1-K1-H4
Method	BLASTX
NCBI GI	g421836
BLAST score	603
E value	8.0e-63
Match length	139
% identity	84
NCBI Description	G-box-binding factor GF14 - Arabidopsis thaliana >gi_553040 (M96855) GF14 [Arabidopsis thaliana]

Seq. No.	224033
Seq. ID	LIB3166-001-Q1-K1-H5
Method	BLASTX
NCBI GI	g2252631
BLAST score	158
E value	1.0e-10
Match length	63
% identity	49
NCBI Description	(U95973) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224034
Seq. ID	LIB3166-001-Q1-K1-H6
Method	BLASTX
NCBI GI	g3319342
BLAST score	164
E value	2.0e-11
Match length	45
% identity	64
NCBI Description	(AF077407) similar to mitochondrial carrier proteins (Pfam: mit_carr.hmm, score: 79.74 and 42.50) [Arabidopsis thaliana]

Seq. No.	224035
Seq. ID	LIB3166-001-Q1-K1-H7
Method	BLASTX
NCBI GI	g1352076
BLAST score	162
E value	4.0e-11
Match length	134
% identity	33
NCBI Description	BETA-GALACTOSIDASE (LACTASE) >gi_144746 (M35107) beta-D-galactosidase (cbgA) [Clostridium acetobutylicum]

Seq. No.	224036
Seq. ID	LIB3166-001-Q1-K1-H8
Method	BLASTX

NCBI GI	g4262225
BLAST score	464
E value	2.0e-46
Match length	139
% identity	58
NCBI Description	(AC006200) putative phosphatidic acid phosphatase [Arabidopsis thaliana]

Seq. No.	224037
Seq. ID	LIB3166-001-Q1-K2-A1
Method	BLASTX
NCBI GI	g4102600
BLAST score	543
E value	8.0e-56
Match length	124
% identity	86
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]

Seq. No.	224038
Seq. ID	LIB3166-001-Q1-K3-A1
Method	BLASTX
NCBI GI	g4102600
BLAST score	543
E value	8.0e-56
Match length	124
% identity	86
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]

Seq. No.	224039
Seq. ID	LIB3166-001-Q1-K3-A2
Method	BLASTX
NCBI GI	g1220196
BLAST score	535
E value	7.0e-55
Match length	115
% identity	88
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	224040
Seq. ID	LIB3166-001-Q1-K3-A3
Method	BLASTX
NCBI GI	g3122116
BLAST score	266
E value	2.0e-23
Match length	123
% identity	48
NCBI Description	CELL DIVISION PROTEIN FTSH HOMOLOG >gi_2660540_emb_CAA05102_ (AJ001932) cell cycle protein [Helicobacter felis]

Seq. No.	224041
Seq. ID	LIB3166-001-Q1-K3-A7
Method	BLASTX
NCBI GI	g3169182
BLAST score	360
E value	2.0e-34
Match length	78

% identity	85
NCBI Description	(AC004401) unknown protein [Arabidopsis thaliana]

Seq. No.	224042
Seq. ID	LIB3166-001-Q1-K3-B1
Method	BLASTX
NCBI GI	g3608485
BLAST score	597
E value	4.0e-62
Match length	117
% identity	95
NCBI Description	(AF088915) proteasome beta subunit [Petunia x hybrida]

Seq. No.	224043
Seq. ID	LIB3166-001-Q1-K3-B11
Method	BLASTX
NCBI GI	g3859116
BLAST score	223
E value	6.0e-29
Match length	121
% identity	64
NCBI Description	(AF031609) unknown [Oryza sativa]

Seq. No.	224044
Seq. ID	LIB3166-001-Q1-K3-B2
Method	BLASTX
NCBI GI	g3790567
BLAST score	161
E value	5.0e-11
Match length	108
% identity	33
NCBI Description	(AF078821) RING-H2 finger protein RHA1b [Arabidopsis thaliana]

Seq. No.	224045
Seq. ID	LIB3166-001-Q1-K3-B3
Method	BLASTX
NCBI GI	g1408471
BLAST score	455
E value	1.0e-45
Match length	102
% identity	79
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	224046
Seq. ID	LIB3166-001-Q1-K3-B5
Method	BLASTX
NCBI GI	g1854386
BLAST score	462
E value	2.0e-46
Match length	127
% identity	69
NCBI Description	(AB001375) similar to soluble NSF attachment protein [Vitis vinifera]

Seq. No.	224047
Seq. ID	LIB3166-001-Q1-K3-B7
Method	BLASTX
NCBI GI	g886116
BLAST score	481
E value	1.0e-48
Match length	124
% identity	69
NCBI Description	(U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473 (AF051338) xyloglucan endotransglycosylase related protein [Arabidopsis thaliana]

Seq. No.	224048
Seq. ID	LIB3166-001-Q1-K3-B9
Method	BLASTX
NCBI GI	g2829918
BLAST score	511
E value	4.0e-52
Match length	121
% identity	80
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No.	224049
Seq. ID	LIB3166-001-Q1-K3-C1
Method	BLASTX
NCBI GI	g1545805
BLAST score	159
E value	5.0e-11
Match length	89
% identity	48
NCBI Description	(D64052) cytochrome P450 like_TBP [Nicotiana tabacum]

Seq. No.	224050
Seq. ID	LIB3166-001-Q1-K3-C11
Method	BLASTX
NCBI GI	g4262225
BLAST score	304
E value	6.0e-28
Match length	108
% identity	51
NCBI Description	(AC006200) putative phosphatidic acid phosphatase [Arabidopsis thaliana]

Seq. No.	224051
Seq. ID	LIB3166-001-Q1-K3-C2
Method	BLASTX
NCBI GI	g2459429
BLAST score	461
E value	3.0e-46
Match length	116
% identity	73
NCBI Description	(AC002332) unknown protein [Arabidopsis thaliana]

Seq. No.	224052
Seq. ID	LIB3166-001-Q1-K3-C3
Method	BLASTX

NCBI GI	g4249410
BLAST score	519
E value	5.0e-53
Match length	119
% identity	81
NCBI Description	(AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.	224053
Seq. ID	LIB3166-001-Q1-K3-C4
Method	BLASTX
NCBI GI	g3402704
BLAST score	312
E value	1.0e-28
Match length	107
% identity	67
NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224054
Seq. ID	LIB3166-001-Q1-K3-C7
Method	BLASTX
NCBI GI	g2501572
BLAST score	387
E value	2.0e-37
Match length	107
% identity	63
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi_1350545 (L47118) EMB8 gene product [Picea glauca]

Seq. No.	224055
Seq. ID	LIB3166-001-Q1-K3-D1
Method	BLASTX
NCBI GI	g4206789
BLAST score	517
E value	7.0e-53
Match length	123
% identity	82
NCBI Description	(AF112864) syntaxin-related protein At-SYR1 [Arabidopsis thaliana]

Seq. No.	224056
Seq. ID	LIB3166-001-Q1-K3-D3
Method	BLASTX
NCBI GI	g3281848
BLAST score	164
E value	2.0e-11
Match length	113
% identity	46
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	224057
Seq. ID	LIB3166-001-Q1-K3-D7
Method	BLASTX
NCBI GI	g4204313
BLAST score	414
E value	9.0e-41
Match length	91
% identity	85

NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	224058
Seq. ID	LIB3166-001-Q1-K3-D8
Method	BLASTX
NCBI GI	g2218152
BLAST score	531
E value	2.0e-54
Match length	125
% identity	78
NCBI Description	(AF005279) type IIIa membrane protein cp-wap13 [Vigna unguiculata]

Seq. No.	224059
Seq. ID	LIB3166-001-Q1-K3-E2
Method	BLASTX
NCBI GI	g2780194
BLAST score	336
E value	1.0e-41
Match length	107
% identity	86
NCBI Description	(AJ003197) adenine nucleotide translocator [Lupinus albus]

Seq. No.	224060
Seq. ID	LIB3166-001-Q1-K3-E7
Method	BLASTX
NCBI GI	g4262250
BLAST score	312
E value	9.0e-29
Match length	96
% identity	72
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	224061
Seq. ID	LIB3166-001-Q1-K3-F2
Method	BLASTX
NCBI GI	g1399273
BLAST score	619
E value	9.0e-65
Match length	123
% identity	94
NCBI Description	(U31834) calmodulin-domain protein kinase CDPK isoform 5 [Arabidopsis thaliana] >gi_3080419_emb_CAA18738_ (AL022604) calmodulin-domain protein kinase CDPK isoform 5 (CPK5) [Arabidopsis thaliana]

Seq. No.	224062
Seq. ID	LIB3166-001-Q1-K3-F7
Method	BLASTX
NCBI GI	g98554
BLAST score	150
E value	9.0e-10
Match length	119
% identity	34
NCBI Description	beta-galactosidase (EC 3.2.1.23) - Clostridium acetobutylicum

Seq. No.	224063
Seq. ID	LIB3166-001-Q1-K3-F8
Method	BLASTX
NCBI GI	g4455202
BLAST score	327
E value	2.0e-30
Match length	109
% identity	60
NCBI Description	(AL035440) putative APG protein [Arabidopsis thaliana]

Seq. No.	224064
Seq. ID	LIB3166-001-Q1-K3-F9
Method	BLASTX
NCBI GI	g2191129
BLAST score	225
E value	1.0e-18
Match length	115
% identity	51
NCBI Description	(AF007269) similar to SPF1 DNA-binding protein [Arabidopsis thaliana]

Seq. No.	224065
Seq. ID	LIB3166-001-Q1-K3-G3
Method	BLASTX
NCBI GI	g4455340
BLAST score	172
E value	2.0e-12
Match length	64
% identity	58
NCBI Description	(AL035522) putative protein [Arabidopsis thaliana]

Seq. No.	224066
Seq. ID	LIB3166-001-Q1-K3-G9
Method	BLASTX
NCBI GI	g3021355
BLAST score	409
E value	4.0e-40
Match length	89
% identity	88
NCBI Description	(AJ005081) UDP-galactose 4-epimerase [Cyamopsis tetragonoloba]

Seq. No.	224067
Seq. ID	LIB3166-001-Q1-K3-H7
Method	BLASTX
NCBI GI	g4314378
BLAST score	293
E value	2.0e-26
Match length	124
% identity	48
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	224068
Seq. ID	LIB3166-001-Q1-K3-H8
Method	BLASTX
NCBI GI	g310587

BLAST score 143
E value 6.0e-09
Match length 51
% identity 59
NCBI Description (L20864) ascorbate peroxidase [Spinacia oleracea] >gi_1384110_dbj_BAA12890_ (D85864) cytosolic ascorbate peroxidase [Spinacia oleracea]

Seq. No. 224069
Seq. ID LIB3166-002-Q1-K1-A10
Method BLASTX
NCBI GI g4539301
BLAST score 247
E value 3.0e-21
Match length 68
% identity 74
NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No. 224070
Seq. ID LIB3166-002-Q1-K1-A2
Method BLASTX
NCBI GI g2827524
BLAST score 366
E value 3.0e-35
Match length 77
% identity 82
NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No. 224071
Seq. ID LIB3166-002-Q1-K1-A3
Method BLASTX
NCBI GI g3249081
BLAST score 347
E value 9.0e-33
Match length 136
% identity 11
NCBI Description (AC004473) Strong similarity to AROGP2 gene gb_1762634 from Lycopersicon esculentum. [Arabidopsis thaliana]

Seq. No. 224072
Seq. ID LIB3166-002-Q1-K1-A4
Method BLASTX
NCBI GI g4510430
BLAST score 498
E value 2.0e-50
Match length 107
% identity 85
NCBI Description (AC006929) unknown protein, 3' partial [Arabidopsis thaliana]

Seq. No. 224073
Seq. ID LIB3166-002-Q1-K1-A6
Method BLASTX
NCBI GI g2558938
BLAST score 234
E value 9.0e-20

Match length	93
% identity	55
NCBI Description	(AF024625) arm repeat containing protein [Brassica napus]

Seq. No.	224074
Seq. ID	LIB3166-002-Q1-K1-A7
Method	BLASTX
NCBI GI	g4105782
BLAST score	293
E value	2.0e-26
Match length	67
% identity	87
NCBI Description	(AF049922) PGP169-12 [Petunia x hybrida]

Seq. No.	224075
Seq. ID	LIB3166-002-Q1-K1-A8
Method	BLASTX
NCBI GI	g3461846
BLAST score	372
E value	1.0e-35
Match length	108
% identity	30
NCBI Description	(AC005315) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No.	224076
Seq. ID	LIB3166-002-Q1-K1-A9
Method	BLASTX
NCBI GI	g1762428
BLAST score	356
E value	8.0e-34
Match length	94
% identity	68
NCBI Description	(U59467) aromatic rich glycoprotein JP630 [Arabidopsis thaliana]

Seq. No.	224077
Seq. ID	LIB3166-002-Q1-K1-B1
Method	BLASTX
NCBI GI	g3688123
BLAST score	395
E value	2.0e-38
Match length	120
% identity	66
NCBI Description	(AJ006293) granule-bound starch synthase [Antirrhinum majus]

Seq. No.	224078
Seq. ID	LIB3166-002-Q1-K1-B10
Method	BLASTX
NCBI GI	g418507
BLAST score	167
E value	1.0e-11
Match length	71
% identity	48
NCBI Description	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE >gi_541097_pir__S40872 hypothetical

protein f161 - Escherichia coli >gi_305032 (L19201) ORF_f161 [Escherichia coli] >gi_1336002 (U56082) S-adenosylmethionine:2-demethylmenaquinone methyltransferase [Escherichia coli] >gi_1790364 (AE000467) menaquinone biosynthesis, unknown [Escherichia coli]

Seq. No.	224079
Seq. ID	LIB3166-002-Q1-K1-B2
Method	BLASTX
NCBI GI	g3688123
BLAST score	352
E value	2.0e-33
Match length	122
% identity	61
NCBI Description	(AJ006293) granule-bound starch synthase [Antirrhinum majus]

Seq. No.	224080
Seq. ID	LIB3166-002-Q1-K1-B3
Method	BLASTX
NCBI GI	g3559811
BLAST score	498
E value	2.0e-50
Match length	137
% identity	72
NCBI Description	(AJ010735) gr1-protein [Arabidopsis thaliana]

Seq. No.	224081
Seq. ID	LIB3166-002-Q1-K1-B4
Method	BLASTX
NCBI GI	g1483563
BLAST score	157
E value	1.0e-10
Match length	39
% identity	74
NCBI Description	(X99825) leucine aminopeptidase [Petroselinum crispum]

Seq. No.	224082
Seq. ID	LIB3166-002-Q1-K1-B5
Method	BLASTX
NCBI GI	g1666096
BLAST score	453
E value	3.0e-45
Match length	129
% identity	73
NCBI Description	(Y09113) dioxygenase [Marah macrocarpus]

Seq. No.	224083
Seq. ID	LIB3166-002-Q1-K1-B8
Method	BLASTX
NCBI GI	g2827528
BLAST score	460
E value	5.0e-46
Match length	117
% identity	74
NCBI Description	(AL021633) predicted protein [Arabidopsis thaliana]

Seq. No.	224084
Seq. ID	LIB3166-002-Q1-K1-B9
Method	BLASTX
NCBI GI	g1170031
BLAST score	634
E value	2.0e-66
Match length	135
% identity	89
NCBI Description	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT) >gi_541940_pir__JQ2263 glutamate 1-semialdehyde aminotransferase (EC 2.6.1.-) precursor - soybean >gi_310567 (L12453) glutamate 1-semialdehyde aminotransferase [Glycine max] >gi_747968 (U20260) glutamate 1-semialdehyde aminotransferase [Glycine max]

Seq. No.	224085
Seq. ID	LIB3166-002-Q1-K1-C1
Method	BLASTX
NCBI GI	g1707018
BLAST score	456
E value	1.0e-45
Match length	132
% identity	70
NCBI Description	(U78721) CutA isolog [Arabidopsis thaliana]

Seq. No.	224086
Seq. ID	LIB3166-002-Q1-K1-C10
Method	BLASTX
NCBI GI	g3859536
BLAST score	626
E value	2.0e-65
Match length	125
% identity	90
NCBI Description	(AF095453) asparagine synthetase [Arabidopsis thaliana]

Seq. No.	224087
Seq. ID	LIB3166-002-Q1-K1-C11
Method	BLASTX
NCBI GI	g4469020
BLAST score	469
E value	4.0e-47
Match length	123
% identity	76
NCBI Description	(AL035602) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	224088
Seq. ID	LIB3166-002-Q1-K1-C12
Method	BLASTX
NCBI GI	g1255954
BLAST score	534
E value	1.0e-54
Match length	118
% identity	83
NCBI Description	(Z70677) thioredoxin [Ricinus communis]

Seq. No.	224089
Seq. ID	LIB3166-002-Q1-K1-C2
Method	BLASTX
NCBI GI	g3603401
BLAST score	288
E value	7.0e-26
Match length	126
% identity	49
NCBI Description	(AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No.	224090
Seq. ID	LIB3166-002-Q1-K1-C3
Method	BLASTX
NCBI GI	g2829870
BLAST score	275
E value	2.0e-24
Match length	117
% identity	58
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	224091
Seq. ID	LIB3166-002-Q1-K1-C4
Method	BLASTX
NCBI GI	g1708934
BLAST score	176
E value	9.0e-13
Match length	60
% identity	50
NCBI Description	CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1 (RING FINGER PROTEIN MAT1) (MENAGE A TROIS) (CDK7/CYCLIN H ASSEMBLY FACTOR) (P36) (P35) >gi_2137198_pir__A57235 CDK-activating kinase p36 - mouse >gi_1015999 (U35249) CDK-activating kinase assembly factor p36/MAT1 [Mus musculus]

Seq. No.	224092
Seq. ID	LIB3166-002-Q1-K1-C7
Method	BLASTX
NCBI GI	g1709007
BLAST score	187
E value	5.0e-14
Match length	107
% identity	40
NCBI Description	O-SUCCINYLHOMOSERINE SULFHYDRYLASE (OSH SULFHYDRYLASE) >gi_607830 (U10904) O-succinylhomoserine sulfhydrylase [Pseudomonas aeruginosa]

Seq. No.	224093
Seq. ID	LIB3166-002-Q1-K1-D10
Method	BLASTX
NCBI GI	g3242789
BLAST score	549
E value	2.0e-56
Match length	114
% identity	87
NCBI Description	(AF055357) respiratory burst oxidase protein D [Arabidopsis thaliana]

Seq. No.	224094
Seq. ID	LIB3166-002-Q1-K1-D11
Method	BLASTX
NCBI GI	g1469930
BLAST score	294
E value	1.0e-26
Match length	92
% identity	70
NCBI Description	(U48777) fiber-specific acyl carrier protein [Gossypium hirsutum]

Seq. No.	224095
Seq. ID	LIB3166-002-Q1-K1-D2
Method	BLASTX
NCBI GI	g4432859
BLAST score	326
E value	2.0e-30
Match length	106
% identity	61
NCBI Description	(AC006300) unknown protein [Arabidopsis thaliana]

Seq. No.	224096
Seq. ID	LIB3166-002-Q1-K1-D4
Method	BLASTX
NCBI GI	g3024126
BLAST score	524
E value	1.0e-53
Match length	102
% identity	97
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine synthetase 1 [Catharanthus roseus]

Seq. No.	224097
Seq. ID	LIB3166-002-Q1-K1-D5
Method	BLASTX
NCBI GI	g3877579
BLAST score	216
E value	2.0e-17
Match length	108
% identity	49
NCBI Description	(Z82271) Similarity to Mouse kinensin-like protein KIF4 (SW:P33174); cDNA EST EMBL:D27320 comes from this gene; cDNA EST EMBL:D27322 comes from this gene; cDNA EST EMBL:D27321 comes from this gene; cDNA EST EMBL:D35764 comes fr... >gi_3879321_emb_CAB07273_ (Z92811) Similarity to Mouse kinensin-like protein KIF4 (SW:P33174); cDNA EST EMBL:D27320 comes from this gene; cDNA EST EMBL:D27322 comes from this gene; cDNA EST EMBL:D27321 comes from this gene; cDNA EST EMBL:D35764 comes fr

Seq. No.	224098
Seq. ID	LIB3166-002-Q1-K1-D6
Method	BLASTX
NCBI GI	g4455159
BLAST score	181

E value	1.0e-20
Match length	72
% identity	62
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]

Seq. No.	224099
Seq. ID	LIB3166-002-Q1-K1-D7
Method	BLASTX
NCBI GI	g4416347
BLAST score	416
E value	7.0e-41
Match length	87
% identity	92
NCBI Description	(AF109403) MADS C-2 protein; MADS-box protein [Sinapis alba]

Seq. No.	224100
Seq. ID	LIB3166-002-Q1-K1-D9
Method	BLASTX
NCBI GI	g4559358
BLAST score	208
E value	2.0e-16
Match length	65
% identity	57
NCBI Description	(AC006585) putative steroid binding protein [Arabidopsis thaliana]

Seq. No.	224101
Seq. ID	LIB3166-002-Q1-K1-E1
Method	BLASTX
NCBI GI	g516118
BLAST score	221
E value	5.0e-18
Match length	125
% identity	43
NCBI Description	(L08469) envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	224102
Seq. ID	LIB3166-002-Q1-K1-E10
Method	BLASTX
NCBI GI	g2827143
BLAST score	621
E value	6.0e-65
Match length	137
% identity	84
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	224103
Seq. ID	LIB3166-002-Q1-K1-E11
Method	BLASTX
NCBI GI	g3046815
BLAST score	468
E value	6.0e-47
Match length	93
% identity	90
NCBI Description	(AL021687) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	224104
Seq. ID	LIB3166-002-Q1-K1-E12
Method	BLASTX
NCBI GI	g3953465
BLAST score	116
E value	8.0e-12
Match length	91
% identity	51
NCBI Description	(AC002328) F20N2.10 [Arabidopsis thaliana]

Seq. No.	224105
Seq. ID	LIB3166-002-Q1-K1-E4
Method	BLASTX
NCBI GI	g3434971
BLAST score	240
E value	3.0e-20
Match length	62
% identity	71
NCBI Description	(AB008105) ethylene responsive element binding factor 3 [Arabidopsis thaliana]

Seq. No.	224106
Seq. ID	LIB3166-002-Q1-K1-E5
Method	BLASTX
NCBI GI	g2982303
BLAST score	205
E value	4.0e-16
Match length	46
% identity	87
NCBI Description	(AF051236) hypothetical protein [Picea mariana]

Seq. No.	224107
Seq. ID	LIB3166-002-Q1-K1-E6
Method	BLASTX
NCBI GI	g4432857
BLAST score	190
E value	2.0e-14
Match length	106
% identity	46
NCBI Description	(AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224108
Seq. ID	LIB3166-002-Q1-K1-E8
Method	BLASTX
NCBI GI	g4049348
BLAST score	271
E value	2.0e-26
Match length	136
% identity	46
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	224109
Seq. ID	LIB3166-002-Q1-K1-E9
Method	BLASTX
NCBI GI	g3983665
BLAST score	516

E value	1.0e-52
Match length	129
% identity	80
NCBI Description	(AB011271) importin-beta2 [Oryza sativa]

Seq. No.	224110
Seq. ID	LIB3166-002-Q1-K1-F10
Method	BLASTX
NCBI GI	g3834310
BLAST score	520
E value	1.0e-53
Match length	115
% identity	96
NCBI Description	(AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122 come from this gene. [Arabidopsis thaliana]

Seq. No.	224111
Seq. ID	LIB3166-002-Q1-K1-F12
Method	BLASTX
NCBI GI	g3928084
BLAST score	377
E value	3.0e-36
Match length	136
% identity	57
NCBI Description	(AC005770) retrotransposon-like protein [Arabidopsis thaliana]

Seq. No.	224112
Seq. ID	LIB3166-002-Q1-K1-F3
Method	BLASTX
NCBI GI	g2970641
BLAST score	664
E value	6.0e-70
Match length	129
% identity	94
NCBI Description	(AF052194) xyloglucan endotransglycosylase precursor [Actinidia deliciosa]

Seq. No.	224113
Seq. ID	LIB3166-002-Q1-K1-F4
Method	BLASTX
NCBI GI	g3434973
BLAST score	219
E value	8.0e-18
Match length	76
% identity	61
NCBI Description	(AB008106) ethylene responsive element binding factor 4 [Arabidopsis thaliana]

Seq. No.	224114
Seq. ID	LIB3166-002-Q1-K1-F5
Method	BLASTX
NCBI GI	g1076515
BLAST score	258
E value	2.0e-22

Match length	115
% identity	49
NCBI Description	pectinesterase precursor - kidney bean >gi_732913_emb_CAA59482_ (X85216) pectinesterase [Phaseolus vulgaris]

Seq. No.	224115
Seq. ID	LIB3166-002-Q1-K1-F8
Method	BLASTX
NCBI GI	g2642448
BLAST score	384
E value	3.0e-37
Match length	118
% identity	29
NCBI Description	(AC002391) hypothetical protein [Arabidopsis thaliana] >gi_3169187 (AC004401) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224116
Seq. ID	LIB3166-002-Q1-K1-G10
Method	BLASTX
NCBI GI	g710626
BLAST score	287
E value	9.0e-26
Match length	86
% identity	65
NCBI Description	(D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941 (AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis thaliana]

Seq. No.	224117
Seq. ID	LIB3166-002-Q1-K1-G11
Method	BLASTX
NCBI GI	g710626
BLAST score	187
E value	3.0e-14
Match length	79
% identity	53
NCBI Description	(D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941 (AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis thaliana]

Seq. No.	224118
Seq. ID	LIB3166-002-Q1-K1-G3
Method	BLASTX
NCBI GI	g4572679
BLAST score	388
E value	1.0e-37
Match length	106
% identity	69
NCBI Description	(AC006954) RSZp22 splicing factor; contains RNA recognition motif [Arabidopsis thaliana]

Seq. No.	224119
Seq. ID	LIB3166-002-Q1-K1-G4

Method	BLASTX
NCBI GI	g3962377
BLAST score	523
E value	2.0e-53
Match length	121
% identity	85
NCBI Description	(AJ002551) heat shock protein 70 [Arabidopsis thaliana]

Seq. No.	224120
Seq. ID	LIB3166-002-Q1-K1-G7
Method	BLASTX
NCBI GI	g4572679
BLAST score	234
E value	8.0e-20
Match length	67
% identity	66
NCBI Description	(AC006954) RSZp22 splicing factor; contains RNA recognition motif [Arabidopsis thaliana]

Seq. No.	224121
Seq. ID	LIB3166-002-Q1-K1-H12
Method	BLASTX
NCBI GI	g1332579
BLAST score	393
E value	2.0e-56
Match length	121
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	224122
Seq. ID	LIB3166-002-Q1-K1-H3
Method	BLASTX
NCBI GI	g266946
BLAST score	233
E value	9.0e-20
Match length	54
% identity	85
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN) >gi_71143_pir__R5UBP0 acidic ribosomal protein P0 - red goosefoot >gi_18141_emb_CAA33276_ (X15206) 34kD light-induced protein [Chenopodium rubrum]

Seq. No.	224123
Seq. ID	LIB3166-002-Q1-K1-H4
Method	BLASTX
NCBI GI	g100351
BLAST score	437
E value	2.0e-43
Match length	130
% identity	65
NCBI Description	pathogenesis-related protein 4A - common tobacco >gi_19962_emb_CAA41437_ (X58546) pathogenesis-related protein 4A [Nicotiana tabacum]

Seq. No.	224124
Seq. ID	LIB3166-002-Q1-K1-H6
Method	BLASTX

NCBI GI	g3955021
BLAST score	423
E value	1.0e-41
Match length	96
% identity	85
NCBI Description	(AJ010811) HB2 homeodomain protein [Populus tremula x Populus tremuloides]

Seq. No.	224125
Seq. ID	LIB3166-002-Q1-K1-H7
Method	BLASTX
NCBI GI	g2738949
BLAST score	335
E value	1.0e-31
Match length	68
% identity	90
NCBI Description	(AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa]

Seq. No.	224126
Seq. ID	LIB3166-002-Q1-K1-H8
Method	BLASTX
NCBI GI	g70644
BLAST score	562
E value	5.0e-58
Match length	124
% identity	18
NCBI Description	ubiquitin precursor - common sunflower (fragment)

Seq. No.	224127
Seq. ID	LIB3166-003-P1-K1-A10
Method	BLASTX
NCBI GI	g3757521
BLAST score	492
E value	9.0e-50
Match length	143
% identity	64
NCBI Description	(AC005167) unknown protein [Arabidopsis thaliana]

Seq. No.	224128
Seq. ID	LIB3166-003-P1-K1-A2
Method	BLASTX
NCBI GI	g4539370
BLAST score	221
E value	3.0e-18
Match length	59
% identity	71
NCBI Description	(AL049525) UDP-galactose 4-epimerase-like protein [Arabidopsis thaliana]

Seq. No.	224129
Seq. ID	LIB3166-003-P1-K1-A3
Method	BLASTX
NCBI GI	g224293
BLAST score	386
E value	2.0e-37
Match length	78

% identity	100
NCBI Description	histone H4 [Triticum aestivum]

Seq. No.	224130
Seq. ID	LIB3166-003-P1-K1-B1
Method	BLASTX
NCBI GI	g3335060
BLAST score	150
E value	1.0e-09
Match length	110
% identity	36
NCBI Description	(AF025842) plasma membrane-type calcium ATPase [Arabidopsis thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]

Seq. No.	224131
Seq. ID	LIB3166-003-P1-K1-B12
Method	BLASTX
NCBI GI	g2146797
BLAST score	429
E value	2.0e-42
Match length	138
% identity	40
NCBI Description	protein disulfide-isomerase (EC 5.3.4.1) - Castor bean >gi_1134968 (U41385) protein disulphide isomerase PDI [Ricinus communis] >gi_1587210_prf__2206331A protein disulfide isomerase [Ricinus communis]

Seq. No.	224132
Seq. ID	LIB3166-003-P1-K1-B2
Method	BLASTX
NCBI GI	g2244999
BLAST score	220
E value	7.0e-18
Match length	96
% identity	47
NCBI Description	(Z97341) similarity to phaseolin G-box binding protein PG2 [Arabidopsis thaliana]

Seq. No.	224133
Seq. ID	LIB3166-003-P1-K1-B8
Method	BLASTX
NCBI GI	g131399
BLAST score	442
E value	5.0e-44
Match length	105
% identity	79
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi_82277_pir__S00411 photosystem II 10K protein precursor - potato >gi_21489_emb_CAA28450_ (X04753) ST-LS1 protein [Solanum tuberosum]

Seq. No.	224134
Seq. ID	LIB3166-003-P1-K1-C1
Method	BLASTX
NCBI GI	g3176726

BLAST score	299
E value	4.0e-27
Match length	82
% identity	76
NCBI Description	(AC002392) putative serine proteinase [Arabidopsis thaliana]

Seq. No.	224135
Seq. ID	LIB3166-003-P1-K1-C12
Method	BLASTX
NCBI GI	g1174162
BLAST score	638
E value	7.0e-67
Match length	121
% identity	93
NCBI Description	(U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi_3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No.	224136
Seq. ID	LIB3166-003-P1-K1-C2
Method	BLASTX
NCBI GI	g4218011
BLAST score	518
E value	8.0e-53
Match length	130
% identity	75
NCBI Description	(AC006135) putative protein kinase [Arabidopsis thaliana] >gi_4309721_gb_AAD15491_ (AC006439) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	224137
Seq. ID	LIB3166-003-P1-K1-C4
Method	BLASTX
NCBI GI	g3600031
BLAST score	226
E value	1.0e-18
Match length	111
% identity	51
NCBI Description	(AF080119) similar to 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolases [Arabidopsis thaliana]

Seq. No.	224138
Seq. ID	LIB3166-003-P1-K1-C9
Method	BLASTX
NCBI GI	g2244734
BLAST score	710
E value	2.0e-75
Match length	142
% identity	99
NCBI Description	(D88414) actin [Gossypium hirsutum]

Seq. No.	224139
Seq. ID	LIB3166-003-P1-K1-D10
Method	BLASTX
NCBI GI	g3122049
BLAST score	206

E value	1.0e-17
Match length	123
% identity	46
NCBI Description	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP) >gi_1330236_dbj_BAA11189_ (D78011) dihydropyrimidinase [Homo sapiens] >gi_3608122_dbj_BAA33067_ (AB004678) dihydropyrimidinase [Homo sapiens] >gi_4503375_ref_NP_001376.1_pDPYS_ dihydropyrimidinase

Seq. No.	224140
Seq. ID	LIB3166-003-P1-K1-D11
Method	BLASTX
NCBI GI	g4455208
BLAST score	554
E value	5.0e-57
Match length	138
% identity	78
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	224141
Seq. ID	LIB3166-003-P1-K1-D4
Method	BLASTX
NCBI GI	g466172
BLAST score	146
E value	3.0e-09
Match length	61
% identity	52
NCBI Description	GTP-BINDING PROTEIN YPTM2 >gi_283056_pir__B38202 ypt family - maize >gi_287835_emb_CAA44919_ (X63278) yptm2 [Zea mays]

Seq. No.	224142
Seq. ID	LIB3166-003-P1-K1-D8
Method	BLASTX
NCBI GI	g3935168
BLAST score	223
E value	2.0e-25
Match length	122
% identity	54
NCBI Description	(AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No.	224143
Seq. ID	LIB3166-003-P1-K1-E6
Method	BLASTX
NCBI GI	g3688191
BLAST score	201
E value	1.0e-15
Match length	84
% identity	52
NCBI Description	(AJ010090) MAP3K alpha protein kinase [Arabidopsis thaliana]

Seq. No.	224144
Seq. ID	LIB3166-003-P1-K1-E7
Method	BLASTX
NCBI GI	g4115377
BLAST score	428
E value	2.0e-42

Match length	100
% identity	79
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	224145
Seq. ID	LIB3166-003-P1-K1-F2
Method	BLASTX
NCBI GI	g115833
BLAST score	308
E value	6.0e-44
Match length	130
% identity	66
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi_170394 (M32605) a-binding protein [Lycopersicon esculentum]

Seq. No.	224146
Seq. ID	LIB3166-003-P1-K1-F5
Method	BLASTX
NCBI GI	g3142290
BLAST score	487
E value	3.0e-49
Match length	126
% identity	80
NCBI Description	(AC002411) Contains similarity to gb_Z69902 from C. elegans. [Arabidopsis thaliana]

Seq. No.	224147
Seq. ID	LIB3166-003-P1-K1-F6
Method	BLASTX
NCBI GI	g2244865
BLAST score	158
E value	1.0e-10
Match length	127
% identity	33
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224148
Seq. ID	LIB3166-003-P1-K1-G10
Method	BLASTX
NCBI GI	g3860263
BLAST score	330
E value	9.0e-31
Match length	126
% identity	56
NCBI Description	(AC005824) putative cytochrome p450 protein [Arabidopsis thaliana]

Seq. No.	224149
Seq. ID	LIB3166-003-P1-K1-G2
Method	BLASTX
NCBI GI	g3201541
BLAST score	245
E value	2.0e-21
Match length	50
% identity	90

NCBI Description	(AJ005077) TCTR2 protein [Lycopersicon esculentum]
Seq. No.	224150
Seq. ID	LIB3166-003-P1-K1-G5
Method	BLASTX
NCBI GI	g2894534
BLAST score	243
E value	2.0e-34
Match length	100
% identity	79
NCBI Description	(AJ224327) aquaporin [Oryza sativa]
Seq. No.	224151
Seq. ID	LIB3166-003-P1-K1-G6
Method	BLASTX
NCBI GI	g2245066
BLAST score	180
E value	9.0e-14
Match length	55
% identity	60
NCBI Description	(Z97342) Beta-Amylase [Arabidopsis thaliana]
Seq. No.	224152
Seq. ID	LIB3166-003-P1-K1-G7
Method	BLASTX
NCBI GI	g1730630
BLAST score	207
E value	2.0e-16
Match length	134
% identity	37
NCBI Description	HYPOTHETICAL 82.6 KD PROTEIN B0361.8 IN CHROMOSOME III >gi_458956 (U00031) similar to cytoplasmic domain of synaptobrevin [Caenorhabditis elegans]
Seq. No.	224153
Seq. ID	LIB3166-003-P1-K1-H10
Method	BLASTX
NCBI GI	g1142621
BLAST score	219
E value	9.0e-18
Match length	139
% identity	44
NCBI Description	(U18349) phaseolin G-box binding protein PG2 [Phaseolus vulgaris]
Seq. No.	224154
Seq. ID	LIB3166-003-P1-K1-H12
Method	BLASTX
NCBI GI	g1657948
BLAST score	180
E value	1.0e-13
Match length	37
% identity	86
NCBI Description	(U73466) MipC [Mesembryanthemum crystallinum]
Seq. No.	224155
Seq. ID	LIB3166-003-P1-K1-H2

Method	BLASTX
NCBI GI	g1351135
BLAST score	280
E value	2.0e-29
Match length	90
% identity	75
NCBI Description	SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE) >gi_436792_emb_CAA50317_ (X70990) sucrose synthase [Arabidopsis thaliana]

Seq. No.	224156
Seq. ID	LIB3166-003-P1-K1-H6
Method	BLASTX
NCBI GI	g1657948
BLAST score	137
E value	9.0e-09
Match length	41
% identity	66
NCBI Description	(U73466) MipC [Mesembryanthemum crystallinum]

Seq. No.	224157
Seq. ID	LIB3166-003-P1-K1-H9
Method	BLASTX
NCBI GI	g1174592
BLAST score	734
E value	4.0e-78
Match length	142
% identity	99
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	224158
Seq. ID	LIB3166-004-P1-K1-A12
Method	BLASTX
NCBI GI	g586339
BLAST score	158
E value	1.0e-10
Match length	58
% identity	47
NCBI Description	PEROXISOMAL-COENZYME A SYNTHETASE >gi_626794_pir__S46098 probable AMP-binding protein - yeast (Saccharomyces cerevisiae) >gi_536615_emb_CAA85185_ (Z36091) ORF YBR222c [Saccharomyces cerevisiae]

Seq. No.	224159
Seq. ID	LIB3166-004-P1-K1-A4
Method	BLASTX
NCBI GI	g2244916
BLAST score	160
E value	7.0e-11
Match length	131
% identity	31
NCBI Description	(Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224160
Seq. ID	LIB3166-004-P1-K1-A6

Method	BLASTX
NCBI GI	g2190548
BLAST score	229
E value	3.0e-21
Match length	81
% identity	65
NCBI Description	(AC001229) EST gb_ATTS1121 comes from this gene. [Arabidopsis thaliana]

Seq. No.	224161
Seq. ID	LIB3166-004-P1-K1-A7
Method	BLASTX
NCBI GI	g3551999
BLAST score	364
E value	7.0e-35
Match length	102
% identity	58
NCBI Description	(AF085081) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3552001 (AF085082) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140628 (AF090163) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140630 (AF090164) alcohol dehydrogenase A [Gossypium hirsutum]

Seq. No.	224162
Seq. ID	LIB3166-004-P1-K1-A9
Method	BLASTX
NCBI GI	g3914442
BLAST score	359
E value	3.0e-34
Match length	99
% identity	73
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No.	224163
Seq. ID	LIB3166-004-P1-K1-B1
Method	BLASTX
NCBI GI	g1351014
BLAST score	339
E value	8.0e-32
Match length	72
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010) ribosomal protein S8 [Oryza sativa]

Seq. No.	224164
Seq. ID	LIB3166-004-P1-K1-B11
Method	BLASTX
NCBI GI	g3759184
BLAST score	272
E value	5.0e-24
Match length	121
% identity	50
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	224165

Seq. ID	LIB3166-004-P1-K1-B12
Method	BLASTX
NCBI GI	g1279542
BLAST score	505
E value	2.0e-51
Match length	118
% identity	89
NCBI Description	(Z71276) small GTPase [Mangifera indica]

Seq. No.	224166
Seq. ID	LIB3166-004-P1-K1-B3
Method	BLASTX
NCBI GI	g4538939
BLAST score	300
E value	4.0e-52
Match length	125
% identity	89
NCBI Description	(AL049483) Col-0 casein kinase I-like protein [Arabidopsis thaliana]

Seq. No.	224167
Seq. ID	LIB3166-004-P1-K1-B8
Method	BLASTX
NCBI GI	g3402683
BLAST score	146
E value	3.0e-09
Match length	39
% identity	74
NCBI Description	(AC004697) patatin-like protein [Arabidopsis thaliana]

Seq. No.	224168
Seq. ID	LIB3166-004-P1-K1-C1
Method	BLASTX
NCBI GI	g2130024
BLAST score	350
E value	4.0e-33
Match length	103
% identity	62
NCBI Description	DNA-binding protein ABF2 - wild oat >gi_1159879_emb_CAA88331_ (Z48431) DNA-binding protein [Avena fatua]

Seq. No.	224169
Seq. ID	LIB3166-004-P1-K1-C10
Method	BLASTX
NCBI GI	g2129604
BLAST score	210
E value	1.0e-16
Match length	58
% identity	74
NCBI Description	GTP-binding protein 1 - Arabidopsis thaliana >gi_2129607_pir__S71584 GTP-binding protein ATBG1 - Arabidopsis thaliana >gi_1184981 (U46924) ATGB1 [Arabidopsis thaliana]

Seq. No.	224170
Seq. ID	LIB3166-004-P1-K1-C11

Method	BLASTX
NCBI GI	g3850583
BLAST score	330
E value	8.0e-31
Match length	125
% identity	56
NCBI Description	(AC005278) Contains similarity to transcription initiation factor IIE, alpha subunit gb_X63468 from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	224171
Seq. ID	LIB3166-004-P1-K1-C12
Method	BLASTX
NCBI GI	g1931640
BLAST score	454
E value	3.0e-45
Match length	124
% identity	66
NCBI Description	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]

Seq. No.	224172
Seq. ID	LIB3166-004-P1-K1-C5
Method	BLASTX
NCBI GI	g2102696
BLAST score	228
E value	8.0e-19
Match length	110
% identity	40
NCBI Description	(U72761) karyopherin beta 3 [Homo sapiens] >gi_4504909_ref_NP_002262.1_pKPNB3_ karyopherin (importin) beta

Seq. No.	224173
Seq. ID	LIB3166-004-P1-K1-C6
Method	BLASTX
NCBI GI	g3687243
BLAST score	249
E value	3.0e-21
Match length	68
% identity	72
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	224174
Seq. ID	LIB3166-004-P1-K1-D5
Method	BLASTX
NCBI GI	g1173218
BLAST score	575
E value	2.0e-59
Match length	113
% identity	98
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	224175

Seq. ID	LIB3166-004-P1-K1-D6
Method	BLASTX
NCBI GI	g232024
BLAST score	301
E value	2.0e-27
Match length	85
% identity	69
NCBI Description	PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland cotton >gi_2129498_pir__S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	224176
Seq. ID	LIB3166-004-P1-K1-D7
Method	BLASTX
NCBI GI	g3068705
BLAST score	201
E value	7.0e-16
Match length	64
% identity	69
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	224177
Seq. ID	LIB3166-004-P1-K1-E1
Method	BLASTX
NCBI GI	g1171579
BLAST score	273
E value	1.0e-24
Match length	66
% identity	80
NCBI Description	(X95342) cytochrome P450 [Nicotiana tabacum]

Seq. No.	224178
Seq. ID	LIB3166-004-P1-K1-E10
Method	BLASTX
NCBI GI	g4185740
BLAST score	354
E value	1.0e-33
Match length	139
% identity	56
NCBI Description	(AF079999) putative glutamate receptor [Arabidopsis thaliana]

Seq. No.	224179
Seq. ID	LIB3166-004-P1-K1-F12
Method	BLASTX
NCBI GI	g541881
BLAST score	306
E value	4.0e-28
Match length	75
% identity	73
NCBI Description	MYB homolog transcription ATMYB2 - Arabidopsis thaliana >gi_506189_dbj_BAA03534_ (D14712) ATMYB2 [Arabidopsis thaliana] >gi_2275197 (AC002337) Atmyb2 [Arabidopsis thaliana]

Seq. No.	224180
Seq. ID	LIB3166-004-P1-K1-F5
Method	BLASTX
NCBI GI	g4510375
BLAST score	460
E value	5.0e-46
Match length	116
% identity	77
NCBI Description	(AC007017) putative homeotic protein BEL1 [Arabidopsis thaliana]

Seq. No.	224181
Seq. ID	LIB3166-004-P1-K1-F8
Method	BLASTX
NCBI GI	g2443891
BLAST score	163
E value	3.0e-11
Match length	116
% identity	49
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No.	224182
Seq. ID	LIB3166-004-P1-K1-G10
Method	BLASTX
NCBI GI	g2347199
BLAST score	176
E value	9.0e-13
Match length	72
% identity	64
NCBI Description	(AC002338) protein kinase isolog [Arabidopsis thaliana]

Seq. No.	224183
Seq. ID	LIB3166-004-P1-K1-G11
Method	BLASTX
NCBI GI	g4538911
BLAST score	379
E value	1.0e-36
Match length	120
% identity	63
NCBI Description	(AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224184
Seq. ID	LIB3166-004-P1-K1-G3
Method	BLASTX
NCBI GI	g2970051
BLAST score	225
E value	1.0e-18
Match length	63
% identity	63
NCBI Description	(AB012110) ARG10 [Vigna radiata]

Seq. No.	224185
Seq. ID	LIB3166-004-P1-K1-G4
Method	BLASTX
NCBI GI	g1531758
BLAST score	174
E value	2.0e-12

Match length	36
% identity	78
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	224186
Seq. ID	LIB3166-004-P1-K1-G6
Method	BLASTX
NCBI GI	g1174592
BLAST score	629
E value	7.0e-66
Match length	118
% identity	97
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	224187
Seq. ID	LIB3166-004-P1-K1-G7
Method	BLASTX
NCBI GI	g3004555
BLAST score	316
E value	4.0e-29
Match length	136
% identity	5
NCBI Description	(AC003673) similar to salt inducible protein [Arabidopsis thaliana]

Seq. No.	224188
Seq. ID	LIB3166-004-P1-K1-H2
Method	BLASTX
NCBI GI	g1653702
BLAST score	254
E value	5.0e-22
Match length	80
% identity	65
NCBI Description	(D90915) dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex [Synechocystis sp.]

Seq. No.	224189
Seq. ID	LIB3166-004-P1-K1-H5
Method	BLASTX
NCBI GI	g3582342
BLAST score	278
E value	1.0e-24
Match length	139
% identity	44
NCBI Description	(AC005496) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	224190
Seq. ID	LIB3166-005-P1-K1-A1
Method	BLASTX
NCBI GI	g3046696
BLAST score	289
E value	2.0e-37
Match length	113

% identity	73
NCBI Description	(AL022224) CTP synthase like protein [Arabidopsis thaliana]

Seq. No.	224191
Seq. ID	LIB3166-005-P1-K1-A11
Method	BLASTX
NCBI GI	g4056494
BLAST score	438
E value	2.0e-43
Match length	108
% identity	76
NCBI Description	(AC005896) putative protein translocase [Arabidopsis thaliana]

Seq. No.	224192
Seq. ID	LIB3166-005-P1-K1-A12
Method	BLASTX
NCBI GI	g2262178
BLAST score	277
E value	1.0e-24
Match length	129
% identity	50
NCBI Description	(AC002329) putative Mlo-like protein [Arabidopsis thaliana]

Seq. No.	224193
Seq. ID	LIB3166-005-P1-K1-A2
Method	BLASTX
NCBI GI	g2642648
BLAST score	715
E value	6.0e-76
Match length	143
% identity	98
NCBI Description	(AF033852) cytosolic heat shock 70 protein; HSC70-3 [Spinacia oleracea] >gi_2660768 (AF034616) cytosolic heat shock 70 protein [Spinacia oleracea] >gi_2660770 (AF034617) cytosolic heat shock 70 protein [Spinacia oleracea]

Seq. No.	224194
Seq. ID	LIB3166-005-P1-K1-A3
Method	BLASTX
NCBI GI	g2661021
BLAST score	594
E value	9.0e-62
Match length	117
% identity	95
NCBI Description	(AF035255) catalase [Glycine max]

Seq. No.	224195
Seq. ID	LIB3166-005-P1-K1-A4
Method	BLASTX
NCBI GI	g1297190
BLAST score	413
E value	2.0e-40
Match length	103
% identity	77
NCBI Description	(U53501) Theoretical protein with similarity to GenBank Accession Number L22302 serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No.	224196
Seq. ID	LIB3166-005-P1-K1-A8
Method	BLASTX
NCBI GI	g1345684
BLAST score	455
E value	2.0e-45
Match length	105
% identity	85
NCBI Description	CATALASE ISOZYME 3 >gi_536787_emb_CAA85426_ (Z36977) catalase [Nicotiana plumbaginifolia]

Seq. No.	224197
Seq. ID	LIB3166-005-P1-K1-A9
Method	BLASTX
NCBI GI	g2078350
BLAST score	255
E value	6.0e-22
Match length	119
% identity	51
NCBI Description	(U95923) transaldolase [Solanum tuberosum]

Seq. No.	224198
Seq. ID	LIB3166-005-P1-K1-B1
Method	BLASTX
NCBI GI	g3776559
BLAST score	323
E value	6.0e-30
Match length	109
% identity	54
NCBI Description	(AC005388) Strong similarity to gene F14J9.26 gi_3482933 cdc2 protein kinase homolog from A. thaliana BAC gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this gene. [Arabidopsis thaliana]

Seq. No.	224199
Seq. ID	LIB3166-005-P1-K1-B11
Method	BLASTX
NCBI GI	g729092
BLAST score	662
E value	1.0e-69
Match length	134
% identity	92
NCBI Description	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM AK1 (CDPK) >gi_477484_pir__A49082 calcium-dependent protein kinase isoform AK1 - Arabidopsis thaliana >gi_304105 (L14771) calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	224200
Seq. ID	LIB3166-005-P1-K1-B12
Method	BLASTX
NCBI GI	g1168446
BLAST score	495
E value	4.0e-50
Match length	123
% identity	76

NCBI Description	AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE) >gi_1073840_pir__F64132 aminopeptidase N (pepN) homolog - Haemophilus influenzae (strain Rd KW20) >gi_1574460 (U32835) aminopeptidase N (pepN) [Haemophilus influenzae Rd]
Seq. No.	224201
Seq. ID	LIB3166-005-P1-K1-B3
Method	BLASTX
NCBI GI	g1326161
BLAST score	142
E value	1.0e-08
Match length	55
% identity	60
NCBI Description	(U54703) dehydrin [Phaseolus vulgaris]
Seq. No.	224202
Seq. ID	LIB3166-005-P1-K1-B7
Method	BLASTX
NCBI GI	g548770
BLAST score	165
E value	1.0e-11
Match length	63
% identity	60
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630) ribosomal protein L3 [Oryza sativa]
Seq. No.	224203
Seq. ID	LIB3166-005-P1-K1-C11
Method	BLASTX
NCBI GI	g100200
BLAST score	160
E value	4.0e-11
Match length	72
% identity	51
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato
Seq. No.	224204
Seq. ID	LIB3166-005-P1-K1-C2
Method	BLASTX
NCBI GI	g4539348
BLAST score	359
E value	4.0e-34
Match length	123
% identity	54
NCBI Description	(AL035539) putative pollen allergen [Arabidopsis thaliana]
Seq. No.	224205
Seq. ID	LIB3166-005-P1-K1-C3
Method	BLASTX
NCBI GI	g418854
BLAST score	622
E value	5.0e-65
Match length	131
% identity	17
NCBI Description	ubiquitin precursor - parsley >gi_288112_emb_CAA45621_

	(X64344) polyubiquitin [Petroselinum crispum] >gi_288114_emb_CAA45622_ (X64345) polyubiquitin [Petroselinum crispum]
Seq. No.	224206
Seq. ID	LIB3166-005-P1-K1-D1
Method	BLASTX
NCBI GI	g225242
BLAST score	154
E value	2.0e-10
Match length	36
% identity	86
NCBI Description	ORF 1708 [Nicotiana tabacum]
Seq. No.	224207
Seq. ID	LIB3166-005-P1-K1-D11
Method	BLASTX
NCBI GI	g1946220
BLAST score	180
E value	3.0e-13
Match length	34
% identity	94
NCBI Description	(Z71979) kn1-like protein [Malus domestica]
Seq. No.	224208
Seq. ID	LIB3166-005-P1-K1-D12
Method	BLASTX
NCBI GI	g3901012
BLAST score	199
E value	1.0e-15
Match length	44
% identity	75
NCBI Description	(AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]
Seq. No.	224209
Seq. ID	LIB3166-005-P1-K1-D5
Method	BLASTX
NCBI GI	g3249084
BLAST score	236
E value	2.0e-34
Match length	155
% identity	29
NCBI Description	(AC004473) Similar to red-1 (related to thioredoxin) gene gb_X92750 from Mus musculus. ESTs gb_AA712687 and gb_Z37223 come from this gene [Arabidopsis thaliana]
Seq. No.	224210
Seq. ID	LIB3166-005-P1-K1-D6
Method	BLASTX
NCBI GI	g4559372
BLAST score	357
E value	6.0e-34
Match length	87
% identity	76
NCBI Description	(AC006585) putative CONSTANS protein [Arabidopsis thaliana]

Seq. No.	224211
Seq. ID	LIB3166-005-P1-K1-E1
Method	BLASTX
NCBI GI	g1076708
BLAST score	619
E value	1.0e-64
Match length	126
% identity	28
NCBI Description	seed tetraubiquitin - common sunflower >gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max] >gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max] >gi_556688_emb_CAA84440_ (Z34988) seed tetraubiquitin [Helianthus annuus] >gi_994785_dbj_BAA05085_ (D26092) Ubiquitin [Glycine max] >gi_4263514_gb_AAD15340_ (AC004044) putative polyubiquitin [Arabidopsis thaliana] >gi_1096513_prf__2111434A tetraubiquitin [Helianthus annuus]

Seq. No.	224212
Seq. ID	LIB3166-005-P1-K1-E12
Method	BLASTX
NCBI GI	g3928095
BLAST score	399
E value	8.0e-54
Match length	138
% identity	76
NCBI Description	(AC005770) putative protein kinase [Arabidopsis thaliana]

Seq. No.	224213
Seq. ID	LIB3166-005-P1-K1-E3
Method	BLASTX
NCBI GI	g951427
BLAST score	453
E value	3.0e-45
Match length	134
% identity	61
NCBI Description	(M59857) stearoyl-acyl-carrier protein desaturase [Ricinus communis]

Seq. No.	224214
Seq. ID	LIB3166-005-P1-K1-E4
Method	BLASTX
NCBI GI	g951427
BLAST score	539
E value	3.0e-55
Match length	135
% identity	75
NCBI Description	(M59857) stearoyl-acyl-carrier protein desaturase [Ricinus communis]

Seq. No.	224215
Seq. ID	LIB3166-005-P1-K1-E5
Method	BLASTX
NCBI GI	g134945
BLAST score	444
E value	4.0e-44
Match length	134

% identity	64
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) (DELTA(9) STEAROYL-ACYL CARRIER PROTEIN DESATURASE) >gi_66360_pir__OHCSAD acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) precursor - castor bean >gi_21093_emb_CAA39859_ (X56508) acyl-[acyl-carrier protein] desatu [Ricinus communis] >gi_228313_prf__1802405A stearoyl acyl carrier desaturase [Ricinus communis]
Seq. No.	224216
Seq. ID	LIB3166-005-P1-K1-E6
Method	BLASTX
NCBI GI	g1703129
BLAST score	578
E value	7.0e-60
Match length	114
% identity	95
NCBI Description	ACTIN 11 >gi_2129522_pir__S68109 actin 11 - Arabidopsis thaliana >gi_1002533 (U27981) actin-11 [Arabidopsis thaliana]
Seq. No.	224217
Seq. ID	LIB3166-005-P1-K1-E9
Method	BLASTX
NCBI GI	g4455318
BLAST score	327
E value	9.0e-31
Match length	88
% identity	72
NCBI Description	(AL035528) glycine hydroxymethyltransferase-like protein [Arabidopsis thaliana]
Seq. No.	224218
Seq. ID	LIB3166-005-P1-K1-F1
Method	BLASTX
NCBI GI	g3559816
BLAST score	699
E value	5.0e-74
Match length	142
% identity	93
NCBI Description	(Y15782) transketolase 2 [Capsicum annuum]
Seq. No.	224219
Seq. ID	LIB3166-005-P1-K1-F10
Method	BLASTX
NCBI GI	g4105794
BLAST score	298
E value	5.0e-27
Match length	79
% identity	62
NCBI Description	(AF049928) PGP224 [Petunia x hybrida]
Seq. No.	224220
Seq. ID	LIB3166-005-P1-K1-F11
Method	BLASTX
NCBI GI	g4468978

BLAST score	356
E value	8.0e-34
Match length	139
% identity	55
NCBI Description	(AL035605) peroxidase-like protein [Arabidopsis thaliana]

Seq. No.	224221
Seq. ID	LIB3166-005-P1-K1-F3
Method	BLASTX
NCBI GI	g4063749
BLAST score	116
E value	4.0e-11
Match length	91
% identity	46
NCBI Description	(AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224222
Seq. ID	LIB3166-005-P1-K1-F5
Method	BLASTX
NCBI GI	g4455276
BLAST score	502
E value	6.0e-51
Match length	143
% identity	72
NCBI Description	(AL035527) peptide transporter-like protein [Arabidopsis thaliana]

Seq. No.	224223
Seq. ID	LIB3166-005-P1-K1-F6
Method	BLASTX
NCBI GI	g1076715
BLAST score	196
E value	4.0e-15
Match length	86
% identity	41
NCBI Description	abscisic acid-induced protein HVA22 - barley >gi_404589 (L19119) A22 [Hordeum vulgare]

Seq. No.	224224
Seq. ID	LIB3166-005-P1-K1-G7
Method	BLASTX
NCBI GI	g1769903
BLAST score	347
E value	9.0e-33
Match length	140
% identity	54
NCBI Description	(X95738) proline transporter 2 [Arabidopsis thaliana]

Seq. No.	224225
Seq. ID	LIB3166-005-P1-K1-G8
Method	BLASTX
NCBI GI	g1220196
BLAST score	311
E value	6.0e-56
Match length	129
% identity	85
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	224226
Seq. ID	LIB3166-005-P1-K1-H10
Method	BLASTX
NCBI GI	g1694976
BLAST score	337
E value	1.0e-31
Match length	74
% identity	84
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis thaliana]

Seq. No.	224227
Seq. ID	LIB3166-005-P1-K1-H12
Method	BLASTX
NCBI GI	g3688123
BLAST score	436
E value	3.0e-43
Match length	119
% identity	71
NCBI Description	(AJ006293) granule-bound starch synthase [Antirrhinum majus]

Seq. No.	224228
Seq. ID	LIB3166-005-P1-K1-H3
Method	BLASTX
NCBI GI	g3036951
BLAST score	390
E value	5.0e-38
Match length	74
% identity	100
NCBI Description	(AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	224229
Seq. ID	LIB3166-005-P1-K1-H4
Method	BLASTX
NCBI GI	g3193327
BLAST score	223
E value	3.0e-18
Match length	84
% identity	56
NCBI Description	(AF069299) No definition line found [Arabidopsis thaliana]

Seq. No.	224230
Seq. ID	LIB3166-005-P1-K1-H5
Method	BLASTX
NCBI GI	g2494842
BLAST score	148
E value	3.0e-10
Match length	79
% identity	48
NCBI Description	GLUCOSYLTRANSFERASE ALG6 >gi_2131171_pir__S61985 ALG6 protein - yeast (Saccharomyces cerevisiae) >gi_1150997 (U43491) hypothetical protein UNA544 [Saccharomyces cerevisiae] >gi_1420090_emb_CAA99190_ (Z74910) ORF YOR002w

[Saccharomyces cerevisiae]

Seq. No.	224231
Seq. ID	LIB3166-005-P1-K1-H6
Method	BLASTX
NCBI GI	g170354
BLAST score	538
E value	3.0e-55
Match length	109
% identity	21
NCBI Description	(M74156) pentameric polyubiquitin [Nicotiana sylvestris]

Seq. No.	224232
Seq. ID	LIB3166-005-P1-K1-H7
Method	BLASTX
NCBI GI	g3928529
BLAST score	152
E value	9.0e-16
Match length	88
% identity	53
NCBI Description	(AB015502) alcohol dehydrogenase [Arabis hirsuta]

Seq. No.	224233
Seq. ID	LIB3166-005-P1-K1-H8
Method	BLASTX
NCBI GI	g2493146
BLAST score	223
E value	3.0e-18
Match length	61
% identity	75
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_755148 (U13669) vacuolar H+-ATPase proteolipid (16 kDa) subunit [Gossypium hirsutum] >gi_4519415_dbj_BAA75542.1_ (AB024275) vacuolar H+-ATPase c subunit [Citrus unshiu]

Seq. No.	224234
Seq. ID	LIB3166-005-P1-K1-H9
Method	BLASTX
NCBI GI	g2244732
BLAST score	751
E value	4.0e-80
Match length	141
% identity	99
NCBI Description	(D88413) endo-xyloglucan transferase [Gossypium hirsutum]

Seq. No.	224235
Seq. ID	LIB3166-006-P1-K1-A10
Method	BLASTX
NCBI GI	g2827709
BLAST score	280
E value	6.0e-25
Match length	133
% identity	47
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	224236
Seq. ID	LIB3166-006-P1-K1-A11

Method	BLASTX
NCBI GI	g3319921
BLAST score	190
E value	1.0e-14
Match length	60
% identity	63
NCBI Description	(AJ223388) Hev b 3 [Hevea brasiliensis] >gi_3319923_emb_CAA11304_ (AJ223389) Hev b 3 [Hevea brasiliensis] >gi_3319925_emb_CAA11305_ (AJ223390) Hev b 3 [Hevea brasiliensis] >gi_3818475 (AF051317) small rubber particle protein [Hevea brasiliensis]

Seq. No.	224237
Seq. ID	LIB3166-006-P1-K1-A12
Method	BLASTX
NCBI GI	g3335366
BLAST score	190
E value	1.0e-14
Match length	80
% identity	46
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	224238
Seq. ID	LIB3166-006-P1-K1-A2
Method	BLASTX
NCBI GI	g3122785
BLAST score	410
E value	2.0e-40
Match length	88
% identity	92
NCBI Description	40S RIBOSOMAL PROTEIN S14 >gi_2565340 (AF026079) ribosomal protein S14 [Lupinus luteus]

Seq. No.	224239
Seq. ID	LIB3166-006-P1-K1-A3
Method	BLASTX
NCBI GI	g4249385
BLAST score	263
E value	1.0e-44
Match length	99
% identity	90
NCBI Description	(AC005966) T2K10.11 [Arabidopsis thaliana]

Seq. No.	224240
Seq. ID	LIB3166-006-P1-K1-A4
Method	BLASTX
NCBI GI	g117988
BLAST score	521
E value	3.0e-53
Match length	99
% identity	95
NCBI Description	CYTOCHROME C >gi_65503_pir__CCCN cytochrome c - sea-island cotton

Seq. No.	224241
Seq. ID	LIB3166-006-P1-K1-A7
Method	BLASTX

NCBI GI	g4490321
BLAST score	169
E value	4.0e-12
Match length	70
% identity	51
NCBI Description	(AJ011604) nitrate transporter [Arabidopsis thaliana]

Seq. No.	224242
Seq. ID	LIB3166-006-P1-K1-A9
Method	BLASTX
NCBI GI	g2392769
BLAST score	145
E value	3.0e-12
Match length	87
% identity	52
NCBI Description	(AC002534) putative histone deacetylase [Arabidopsis thaliana]

Seq. No.	224243
Seq. ID	LIB3166-006-P1-K1-B1
Method	BLASTX
NCBI GI	g4512698
BLAST score	548
E value	2.0e-56
Match length	112
% identity	91
NCBI Description	(AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224244
Seq. ID	LIB3166-006-P1-K1-B10
Method	BLASTX
NCBI GI	g1076365
BLAST score	218
E value	4.0e-18
Match length	76
% identity	57
NCBI Description	pectinesterase (EC 3.1.1.11) PME1 precursor - Arabidopsis thaliana >gi_2129666_pir__JC4778 pectinesterase (EC 3.1.1.11) 1 - Arabidopsis thaliana >gi_550306_emb_CAA57275_ (X81585) ATPME1 [Arabidopsis thaliana] >gi_903895 (U25649) ATPME1 precursor [Arabidopsis thaliana]

Seq. No.	224245
Seq. ID	LIB3166-006-P1-K1-B11
Method	BLASTX
NCBI GI	g3790100
BLAST score	422
E value	8.0e-42
Match length	94
% identity	90
NCBI Description	(AF095520) pyrophosphate-dependent phosphofructokinase beta subunit [Citrus X paradisi]

Seq. No.	224246
Seq. ID	LIB3166-006-P1-K1-B12
Method	BLASTX
NCBI GI	g2244900

BLAST score	366
E value	2.0e-41
Match length	132
% identity	61
NCBI Description	(Z97338) similarity to hypothetical protein HYP1 - Arabidopsis [Arabidopsis thaliana]

Seq. No.	224247
Seq. ID	LIB3166-006-P1-K1-B2
Method	BLASTX
NCBI GI	g125887
BLAST score	157
E value	1.0e-10
Match length	89
% identity	37
NCBI Description	ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR >gi_82092_pir__S04765 LAT52 protein precursor - tomato >gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon esculentum]

Seq. No.	224248
Seq. ID	LIB3166-006-P1-K1-B4
Method	BLASTX
NCBI GI	g1332579
BLAST score	486
E value	2.0e-52
Match length	115
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	224249
Seq. ID	LIB3166-006-P1-K1-B5
Method	BLASTX
NCBI GI	g4218122
BLAST score	276
E value	1.0e-24
Match length	95
% identity	61
NCBI Description	(AL035353) putative protein [Arabidopsis thaliana]

Seq. No.	224250
Seq. ID	LIB3166-006-P1-K1-C1
Method	BLASTX
NCBI GI	g2213643
BLAST score	250
E value	1.0e-28
Match length	91
% identity	71
NCBI Description	(U57338) glossy1 homolog [Oryza sativa]

Seq. No.	224251
Seq. ID	LIB3166-006-P1-K1-C11
Method	BLASTX
NCBI GI	g2065531
BLAST score	254
E value	5.0e-22
Match length	81

% identity	64
NCBI Description	(U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No.	224252
Seq. ID	LIB3166-006-P1-K1-C12
Method	BLASTX
NCBI GI	g1345787
BLAST score	678
E value	1.0e-71
Match length	134
% identity	94
NCBI Description	CHALCONE SYNTHASE 2 (NARINGENIN-CHALCONE SYNTHASE 2) >gi_567937_dbj_BAA05641_ (D26594) chalcone synthase [Camellia sinensis]

Seq. No.	224253
Seq. ID	LIB3166-006-P1-K1-C4
Method	BLASTX
NCBI GI	g2244732
BLAST score	446
E value	2.0e-44
Match length	90
% identity	94
NCBI Description	(D88413) endo-xyloglucan transferase [Gossypium hirsutum]

Seq. No.	224254
Seq. ID	LIB3166-006-P1-K1-C5
Method	BLASTX
NCBI GI	g2979551
BLAST score	174
E value	9.0e-13
Match length	57
% identity	65
NCBI Description	(AC003680) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	224255
Seq. ID	LIB3166-006-P1-K1-C7
Method	BLASTX
NCBI GI	g128190
BLAST score	530
E value	2.0e-54
Match length	122
% identity	80
NCBI Description	NITRATE REDUCTASE 2 (NR2) >gi_66205_pir__RDNTNS nitrate reductase (NADH) (EC 1.6.6.1) nia-2 - common tobacco >gi_19891_emb_CAA32217_ (X14059) nitrate reductase [Nicotiana tabacum]

Seq. No.	224256
Seq. ID	LIB3166-006-P1-K1-D1
Method	BLASTX
NCBI GI	g4490341
BLAST score	172
E value	3.0e-12
Match length	124
% identity	39

NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]
Seq. No.	224257
Seq. ID	LIB3166-006-P1-K1-D10
Method	BLASTX
NCBI GI	g3249084
BLAST score	185
E value	3.0e-14
Match length	58
% identity	29
NCBI Description	(AC004473) Similar to red-1 (related to thioredoxin) gene gb_X92750 from Mus musculus. ESTs gb_AA712687 and gb_Z37223 come from this gene [Arabidopsis thaliana]
Seq. No.	224258
Seq. ID	LIB3166-006-P1-K1-D11
Method	BLASTX
NCBI GI	g3738285
BLAST score	278
E value	9.0e-25
Match length	69
% identity	75
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.	224259
Seq. ID	LIB3166-006-P1-K1-D12
Method	BLASTX
NCBI GI	g1173256
BLAST score	629
E value	7.0e-66
Match length	123
% identity	98
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal protein S4 - upland cotton >gi_488739_emb_CAA55882_ (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]
Seq. No.	224260
Seq. ID	LIB3166-006-P1-K1-D6
Method	BLASTX
NCBI GI	g2078350
BLAST score	173
E value	7.0e-15
Match length	54
% identity	81
NCBI Description	(U95923) transaldolase [Solanum tuberosum]
Seq. No.	224261
Seq. ID	LIB3166-006-P1-K1-D7
Method	BLASTX
NCBI GI	g1749596
BLAST score	252
E value	2.0e-27
Match length	101
% identity	61
NCBI Description	(D89194) similar to Rat ATP citrate-lyase, SWISS-PROT Accession Number P16638 [Schizosaccharomyces pombe]

Seq. No.	224262
Seq. ID	LIB3166-006-P1-K1-D9
Method	BLASTX
NCBI GI	g2505870
BLAST score	575
E value	1.0e-59
Match length	128
% identity	89
NCBI Description	(Y12227) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224263
Seq. ID	LIB3166-006-P1-K1-E10
Method	BLASTX
NCBI GI	g4468993
BLAST score	302
E value	2.0e-27
Match length	134
% identity	51
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	224264
Seq. ID	LIB3166-006-P1-K1-E11
Method	BLASTX
NCBI GI	g4510363
BLAST score	125
E value	6.0e-12
Match length	59
% identity	67
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	224265
Seq. ID	LIB3166-006-P1-K1-E2
Method	BLASTX
NCBI GI	g1351974
BLAST score	568
E value	1.0e-58
Match length	110
% identity	100
NCBI Description	ADP-RIBOSYLATION FACTOR >gi_1076788_pir__S49325 ADP-ribosylation factor - maize >gi_1076789_pir__S53486 ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_ (X80042) ADP-ribosylation factor [Zea mays]

Seq. No.	224266
Seq. ID	LIB3166-006-P1-K1-E3
Method	BLASTX
NCBI GI	g125606
BLAST score	463
E value	2.0e-46
Match length	99
% identity	88
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir__S12248 pyruvate kinase (EC 2.7.1.40) - potato >gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum tuberosum]

Seq. No.	224267
Seq. ID	LIB3166-006-P1-K1-E4
Method	BLASTX
NCBI GI	g4102861
BLAST score	540
E value	2.0e-55
Match length	111
% identity	86
NCBI Description	(AF016893) copper/zinc-superoxide dismutase [Populus tremuloides]

Seq. No.	224268
Seq. ID	LIB3166-006-P1-K1-E6
Method	BLASTX
NCBI GI	g1895084
BLAST score	172
E value	3.0e-12
Match length	101
% identity	47
NCBI Description	(U89897) golgi associated protein se-wap41 [Zea mays]

Seq. No.	224269
Seq. ID	LIB3166-006-P1-K1-E7
Method	BLASTX
NCBI GI	g4263507
BLAST score	444
E value	3.0e-44
Match length	133
% identity	61
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224270
Seq. ID	LIB3166-006-P1-K1-E8
Method	BLASTX
NCBI GI	g4220534
BLAST score	242
E value	2.0e-20
Match length	66
% identity	77
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	224271
Seq. ID	LIB3166-006-P1-K1-E9
Method	BLASTX
NCBI GI	g4093157
BLAST score	204
E value	5.0e-16
Match length	93
% identity	56
NCBI Description	(AF087936) phytochrome-associated protein 2 [Arabidopsis thaliana]

Seq. No.	224272
Seq. ID	LIB3166-006-P1-K1-F1
Method	BLASTX
NCBI GI	g1769903

BLAST score	482
E value	1.0e-48
Match length	124
% identity	73
NCBI Description	(X95738) proline transporter 2 [Arabidopsis thaliana]

Seq. No.	224273
Seq. ID	LIB3166-006-P1-K1-F2
Method	BLASTX
NCBI GI	g1742961
BLAST score	169
E value	5.0e-12
Match length	99
% identity	48
NCBI Description	(X94756) cystathionine gamma-synthase [Arabidopsis thaliana]

Seq. No.	224274
Seq. ID	LIB3166-006-P1-K1-F5
Method	BLASTX
NCBI GI	g1263291
BLAST score	511
E value	5.0e-52
Match length	115
% identity	80
NCBI Description	(U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No.	224275
Seq. ID	LIB3166-006-P1-K1-F6
Method	BLASTX
NCBI GI	g1531758
BLAST score	552
E value	4.0e-63
Match length	133
% identity	92
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	224276
Seq. ID	LIB3166-006-P1-K1-G1
Method	BLASTX
NCBI GI	g3901012
BLAST score	501
E value	6.0e-51
Match length	125
% identity	73
NCBI Description	(AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]

Seq. No.	224277
Seq. ID	LIB3166-006-P1-K1-G2
Method	BLASTX
NCBI GI	g2462762
BLAST score	169
E value	2.0e-12
Match length	70
% identity	59

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NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.	224278
Seq. ID	LIB3166-006-P1-K1-G3
Method	BLASTX
NCBI GI	g1518540
BLAST score	428
E value	2.0e-42
Match length	95
% identity	84
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]
Seq. No.	224279
Seq. ID	LIB3166-006-P1-K1-G4
Method	BLASTX
NCBI GI	g3668086
BLAST score	223
E value	3.0e-18
Match length	72
% identity	74
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.	224280
Seq. ID	LIB3166-006-P1-K1-G5
Method	BLASTX
NCBI GI	g2245131
BLAST score	304
E value	7.0e-28
Match length	125
% identity	50
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]
Seq. No.	224281
Seq. ID	LIB3166-006-P1-K1-G6
Method	BLASTX
NCBI GI	g4539348
BLAST score	167
E value	5.0e-12
Match length	56
% identity	55
NCBI Description	(AL035539) putative pollen allergen [Arabidopsis thaliana]
Seq. No.	224282
Seq. ID	LIB3166-006-P1-K1-G7
Method	BLASTX
NCBI GI	g3915023
BLAST score	318
E value	9.0e-30
Match length	86
% identity	70
NCBI Description	SUCROSE-PHOSPHATE SYNTHASE 1 (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1) >gi_2588888_dbj_BAA23213_ (AB005023) sucrose-phosphate synthase [Citrus unshiu]
Seq. No.	224283

Seq. ID	LIB3166-006-P1-K1-H10
Method	BLASTX
NCBI GI	g2498731
BLAST score	318
E value	2.0e-29
Match length	84
% identity	68
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi_1362013_pir__S57611 zeta-crystallin homolog - Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	224284
Seq. ID	LIB3166-006-P1-K1-H3
Method	BLASTX
NCBI GI	g2443329
BLAST score	373
E value	6.0e-36
Match length	113
% identity	66
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.	224285
Seq. ID	LIB3166-006-P1-K1-H4
Method	BLASTX
NCBI GI	g3668089
BLAST score	302
E value	2.0e-27
Match length	104
% identity	51
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	224286
Seq. ID	LIB3166-006-P1-K1-H7
Method	BLASTX
NCBI GI	g4263777
BLAST score	176
E value	8.0e-13
Match length	85
% identity	47
NCBI Description	(AC006068) putative serine carboxypeptidase II [Arabidopsis thaliana] >gi_4510391_gb_AAD21479.1_ (AC007017) putative serine carboxypeptidase II [Arabidopsis thaliana]

Seq. No.	224287
Seq. ID	LIB3166-007-P1-K1-A12
Method	BLASTX
NCBI GI	g2497742
BLAST score	186
E value	6.0e-14
Match length	37
% identity	95
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) >gi_995907 (U15153) nonspecific lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	224288

Seq. ID	LIB3166-007-P1-K1-A2
Method	BLASTX
NCBI GI	g116923
BLAST score	172
E value	2.0e-12
Match length	102
% identity	44
NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi_111414_pir__S13520 beta-COP protein - rat >gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus norvegicus]

Seq. No.	224289
Seq. ID	LIB3166-007-P1-K1-A3
Method	BLASTX
NCBI GI	g4158232
BLAST score	511
E value	4.0e-52
Match length	107
% identity	90
NCBI Description	(Y18626) reversibly glycosylated polypeptide [Triticum aestivum]

Seq. No.	224290
Seq. ID	LIB3166-007-P1-K1-A4
Method	BLASTX
NCBI GI	g4455364
BLAST score	304
E value	9.0e-28
Match length	107
% identity	54
NCBI Description	(AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No.	224291
Seq. ID	LIB3166-007-P1-K1-A9
Method	BLASTX
NCBI GI	g3193287
BLAST score	275
E value	2.0e-24
Match length	104
% identity	54
NCBI Description	(AF069298) Arabidopsis predicted protein of unknown function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]

Seq. No.	224292
Seq. ID	LIB3166-007-P1-K1-B1
Method	BLASTX
NCBI GI	g3128216
BLAST score	282
E value	3.0e-25
Match length	85
% identity	61
NCBI Description	(AC004077) putative GA4 protein [Arabidopsis thaliana]

Seq. No.	224293
Seq. ID	LIB3166-007-P1-K1-B11

Method	BLASTX
NCBI GI	g3046703
BLAST score	421
E value	4.0e-65
Match length	136
% identity	91
NCBI Description	(AL021749) protein kinase ADK1-like protein [Arabidopsis thaliana]

Seq. No.	224294
Seq. ID	LIB3166-007-P1-K1-B12
Method	BLASTX
NCBI GI	g3219353
BLAST score	453
E value	2.0e-47
Match length	135
% identity	73
NCBI Description	(AF061514) manganese superoxide dismutase [Gossypium hirsutum]

Seq. No.	224295
Seq. ID	LIB3166-007-P1-K1-B9
Method	BLASTX
NCBI GI	g4105696
BLAST score	275
E value	7.0e-25
Match length	57
% identity	93
NCBI Description	(AF049870) beta tubulin 1 [Arabidopsis thaliana]

Seq. No.	224296
Seq. ID	LIB3166-007-P1-K1-C1
Method	BLASTX
NCBI GI	g4049399
BLAST score	158
E value	1.0e-10
Match length	101
% identity	37
NCBI Description	(Y09581) FRO2 [Arabidopsis thaliana]

Seq. No.	224297
Seq. ID	LIB3166-007-P1-K1-C11
Method	BLASTX
NCBI GI	g3738291
BLAST score	241
E value	2.0e-20
Match length	95
% identity	46
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	224298
Seq. ID	LIB3166-007-P1-K1-C6
Method	BLASTX
NCBI GI	g2827634
BLAST score	163
E value	3.0e-11
Match length	91

% identity	43
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	224299
Seq. ID	LIB3166-007-P1-K1-C7
Method	BLASTX
NCBI GI	g1418331
BLAST score	195
E value	6.0e-15
Match length	102
% identity	39
NCBI Description	(X95909) receptor like protein kinase [Arabidopsis thaliana]

Seq. No.	224300
Seq. ID	LIB3166-007-P1-K1-C8
Method	BLASTX
NCBI GI	g115833
BLAST score	163
E value	2.0e-16
Match length	94
% identity	57
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi_170394 (M32605) a-binding protein [Lycopersicon esculentum]

Seq. No.	224301
Seq. ID	LIB3166-007-P1-K1-C9
Method	BLASTX
NCBI GI	g4210451
BLAST score	163
E value	5.0e-19
Match length	71
% identity	76
NCBI Description	(AB016472) ARR2 protein [Arabidopsis thaliana]

Seq. No.	224302
Seq. ID	LIB3166-007-P1-K1-D1
Method	BLASTX
NCBI GI	g120669
BLAST score	564
E value	3.0e-58
Match length	113
% identity	94
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	224303
Seq. ID	LIB3166-007-P1-K1-D10
Method	BLASTX
NCBI GI	g541818
BLAST score	490
E value	1.0e-49

Match length	135
% identity	71
NCBI Description	protein kinase - common ice plant (fragment) >gi_457693_emb_CAA82994_ (Z30333) protein kinase [Mesembryanthemum crystallinum]

Seq. No.	224304
Seq. ID	LIB3166-007-P1-K1-D12
Method	BLASTX
NCBI GI	g3522945
BLAST score	183
E value	1.0e-13
Match length	95
% identity	35
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	224305
Seq. ID	LIB3166-007-P1-K1-D3
Method	BLASTX
NCBI GI	g2407790
BLAST score	414
E value	1.0e-40
Match length	115
% identity	18
NCBI Description	(AF019910) grr1 [Glycine max]

Seq. No.	224306
Seq. ID	LIB3166-007-P1-K1-D4
Method	BLASTX
NCBI GI	g3688123
BLAST score	434
E value	5.0e-43
Match length	134
% identity	66
NCBI Description	(AJ006293) granule-bound starch synthase [Antirrhinum majus]

Seq. No.	224307
Seq. ID	LIB3166-007-P1-K1-D6
Method	BLASTX
NCBI GI	g4107323
BLAST score	592
E value	2.0e-61
Match length	131
% identity	86
NCBI Description	(AL035077) 60s ribosomal protein l10 [Schizosaccharomyces pombe]

Seq. No.	224308
Seq. ID	LIB3166-007-P1-K1-D7
Method	BLASTX
NCBI GI	g464707
BLAST score	560
E value	9.0e-58
Match length	114
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal

	protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]
Seq. No.	224309
Seq. ID	LIB3166-007-P1-K1-E1
Method	BLASTX
NCBI GI	g3128215
BLAST score	215
E value	3.0e-17
Match length	113
% identity	49
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana]
Seq. No.	224310
Seq. ID	LIB3166-007-P1-K1-E10
Method	BLASTX
NCBI GI	g3901014
BLAST score	235
E value	1.0e-19
Match length	55
% identity	76
NCBI Description	(AJ130886) metallothionein-like protein class II [Fagus sylvatica]
Seq. No.	224311
Seq. ID	LIB3166-007-P1-K1-E3
Method	BLASTX
NCBI GI	g2738949
BLAST score	488
E value	2.0e-49
Match length	99
% identity	93
NCBI Description	(AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa]
Seq. No.	224312
Seq. ID	LIB3166-007-P1-K1-E6
Method	BLASTX
NCBI GI	g3894183
BLAST score	264
E value	5.0e-23
Match length	109
% identity	31
NCBI Description	(AC005662) calmodulin-like protein [Arabidopsis thaliana]

Seq. No.	224313
Seq. ID	LIB3166-007-P1-K1-E7
Method	BLASTX
NCBI GI	g2558660
BLAST score	194
E value	8.0e-15
Match length	73
% identity	52
NCBI Description	(AC002354) No definition line found [Arabidopsis thaliana]

Seq. No.	224314
Seq. ID	LIB3166-007-P1-K1-E9
Method	BLASTX
NCBI GI	g462195
BLAST score	462
E value	3.0e-46
Match length	96
% identity	93
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir__S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No.	224315
Seq. ID	LIB3166-007-P1-K1-F12
Method	BLASTX
NCBI GI	g4098246
BLAST score	653
E value	1.0e-68
Match length	138
% identity	91
NCBI Description	(U76410) homeobox 2 protein [Lycopersicon esculentum]

Seq. No.	224316
Seq. ID	LIB3166-007-P1-K1-F2
Method	BLASTX
NCBI GI	g4163997
BLAST score	385
E value	3.0e-47
Match length	140
% identity	72
NCBI Description	(AF087483) alpha-xylosidase precursor [Arabidopsis thaliana]

Seq. No.	224317
Seq. ID	LIB3166-007-P1-K1-F5
Method	BLASTX
NCBI GI	g3250676
BLAST score	325
E value	1.0e-35
Match length	109
% identity	76
NCBI Description	(AL024486) putative protein [Arabidopsis thaliana]

Seq. No.	224318
Seq. ID	LIB3166-007-P1-K1-F6

Method	BLASTX
NCBI GI	g2760349
BLAST score	375
E value	4.0e-36
Match length	122
% identity	13
NCBI Description	(U84969) ubiquitin [Arabidopsis thaliana]

Seq. No.	224319
Seq. ID	LIB3166-007-P1-K1-F7
Method	BLASTX
NCBI GI	g3426038
BLAST score	478
E value	2.0e-49
Match length	135
% identity	29
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	224320
Seq. ID	LIB3166-007-P1-K1-F9
Method	BLASTX
NCBI GI	g2443878
BLAST score	310
E value	2.0e-28
Match length	119
% identity	57
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No.	224321
Seq. ID	LIB3166-007-P1-K1-G1
Method	BLASTX
NCBI GI	g2160156
BLAST score	477
E value	6.0e-52
Match length	138
% identity	75
NCBI Description	(AC000132) Strong similarity to S. pombe leucyl-tRNA synthetase (gb_Z73100). [Arabidopsis thaliana]

Seq. No.	224322
Seq. ID	LIB3166-007-P1-K1-G10
Method	BLASTX
NCBI GI	g3582342
BLAST score	226
E value	1.0e-18
Match length	126
% identity	41
NCBI Description	(AC005496) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	224323
Seq. ID	LIB3166-007-P1-K1-G12
Method	BLASTX
NCBI GI	g2058313
BLAST score	271
E value	7.0e-24
Match length	65

% identity	77
NCBI Description	(X97433) cinnamoyl-CoA reductase [Eucalyptus gunnii]

Seq. No.	224324
Seq. ID	LIB3166-007-P1-K1-G4
Method	BLASTX
NCBI GI	g2464855
BLAST score	382
E value	2.0e-38
Match length	92
% identity	87
NCBI Description	(Z99707) myb-related protein [Arabidopsis thaliana]

Seq. No.	224325
Seq. ID	LIB3166-007-P1-K1-G5
Method	BLASTX
NCBI GI	g3915037
BLAST score	621
E value	6.0e-65
Match length	132
% identity	91
NCBI Description	SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi_2570067_emb_CAA04512_ (AJ001071) second sucrose synthase [Pisum sativum]

Seq. No.	224326
Seq. ID	LIB3166-007-P1-K1-G6
Method	BLASTX
NCBI GI	g1703446
BLAST score	379
E value	1.0e-36
Match length	116
% identity	68
NCBI Description	L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE) >gi_1076292_pir__S53127 asparaginase - Arabidopsis thaliana >gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis thaliana]

Seq. No.	224327
Seq. ID	LIB3166-007-P1-K1-G7
Method	BLASTX
NCBI GI	g3264767
BLAST score	415
E value	9.0e-41
Match length	125
% identity	61
NCBI Description	(AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No.	224328
Seq. ID	LIB3166-007-P1-K1-H10
Method	BLASTX
NCBI GI	g3341685
BLAST score	205
E value	4.0e-16
Match length	102
% identity	49
NCBI Description	(AC003672) unknown protein [Arabidopsis thaliana]

Seq. No.	224329
Seq. ID	LIB3166-007-P1-K1-H11
Method	BLASTX
NCBI GI	g2224927
BLAST score	320
E value	4.0e-49
Match length	122
% identity	80
NCBI Description	(AF004213) ethylene-insensitive3-like1 [Arabidopsis thaliana]

Seq. No.	224330
Seq. ID	LIB3166-007-P1-K1-H12
Method	BLASTX
NCBI GI	g2495365
BLAST score	399
E value	5.0e-39
Match length	112
% identity	73
NCBI Description	HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B heat shock protein HSP81-2 [Arabidopsis thaliana]

Seq. No.	224331
Seq. ID	LIB3166-007-P1-K1-H2
Method	BLASTX
NCBI GI	g4539292
BLAST score	475
E value	7.0e-48
Match length	103
% identity	84
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	224332
Seq. ID	LIB3166-007-P1-K1-H3
Method	BLASTX
NCBI GI	g2618721
BLAST score	150
E value	3.0e-10
Match length	41
% identity	76
NCBI Description	(U49072) IAA16 [Arabidopsis thaliana]

Seq. No.	224333
Seq. ID	LIB3166-008-P1-K1-A11
Method	BLASTX
NCBI GI	g1621268
BLAST score	268
E value	9.0e-24
Match length	93
% identity	63
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	224334
Seq. ID	LIB3166-008-P1-K1-A12
Method	BLASTX

NCBI GI	g3281861
BLAST score	375
E value	4.0e-36
Match length	127
% identity	56
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	224335
Seq. ID	LIB3166-008-P1-K1-A3
Method	BLASTX
NCBI GI	g3236253
BLAST score	569
E value	7.0e-59
Match length	129
% identity	81
NCBI Description	(AC004684) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	224336
Seq. ID	LIB3166-008-P1-K1-A7
Method	BLASTX
NCBI GI	g4234941
BLAST score	227
E value	3.0e-19
Match length	52
% identity	87
NCBI Description	(AF097938) cytosolic phosphoglucomutase [Populus tremula x Populus tremuloides]

Seq. No.	224337
Seq. ID	LIB3166-008-P1-K1-B1
Method	BLASTX
NCBI GI	g1750376
BLAST score	531
E value	2.0e-54
Match length	119
% identity	83
NCBI Description	(U80808) ubiquitin activating enzyme [Arabidopsis thaliana] >gi_3150409 (AC004165) ubiquitin activating enzyme (UBA1) [Arabidopsis thaliana]

Seq. No.	224338
Seq. ID	LIB3166-008-P1-K1-B12
Method	BLASTX
NCBI GI	g2979548
BLAST score	202
E value	5.0e-16
Match length	97
% identity	39
NCBI Description	(AC003680) putative 7-ethoxycoumarin O-deethylase [Arabidopsis thaliana]

Seq. No.	224339
Seq. ID	LIB3166-008-P1-K1-B3
Method	BLASTX
NCBI GI	g478713
BLAST score	414

E value	1.0e-40
Match length	84
% identity	96
NCBI Description	AP1 protein - Arabidopsis thaliana >gi_383297_prf__1902329A APETALA1 gene [Arabidopsis thaliana]

Seq. No.	224340
Seq. ID	LIB3166-008-P1-K1-B4
Method	BLASTX
NCBI GI	g2618691
BLAST score	179
E value	4.0e-13
Match length	75
% identity	55
NCBI Description	(AC002510) putative chloroplast envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	224341
Seq. ID	LIB3166-008-P1-K1-B7
Method	BLASTX
NCBI GI	g4510375
BLAST score	182
E value	8.0e-14
Match length	72
% identity	58
NCBI Description	(AC007017) putative homeotic protein BEL1 [Arabidopsis thaliana]

Seq. No.	224342
Seq. ID	LIB3166-008-P1-K1-C10
Method	BLASTX
NCBI GI	g2959781
BLAST score	480
E value	2.0e-48
Match length	106
% identity	86
NCBI Description	(AJ223508) Zwille protein [Arabidopsis thaliana]

Seq. No.	224343
Seq. ID	LIB3166-008-P1-K1-C3
Method	BLASTX
NCBI GI	g3927836
BLAST score	341
E value	4.0e-32
Match length	114
% identity	62
NCBI Description	(AC005727) unknown protein [Arabidopsis thaliana]

Seq. No.	224344
Seq. ID	LIB3166-008-P1-K1-C4
Method	BLASTX
NCBI GI	g4220480
BLAST score	279
E value	8.0e-25
Match length	119
% identity	50
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	224345
Seq. ID	LIB3166-008-P1-K1-C5
Method	BLASTX
NCBI GI	g2833386
BLAST score	275
E value	2.0e-24
Match length	81
% identity	74
NCBI Description	RIBULOSE-PHOSPHATE 3-EPIMERASE PRECURSOR (PENTOSE-5-PHOSPHATE 3-EPIMERASE) (PPE) (RPE) (R5P3E) >gi_2129493_pir__S62724 ribulose-phosphate 3-epimerase (EC 5.1.3.1) precursor - spinach >gi_1162980 (L42328) ribulose-5-phosphate 3-epimerase [Spinacia oleracea] >gi_3264788 (AF070941) ribulose-phosphate 3-epimerase [Spinacia oleracea] >gi_1587969_prf__2207382A D-ribulose-5-phosphate 3-epimerase [Sorghum bicolor]

Seq. No.	224346
Seq. ID	LIB3166-008-P1-K1-C9
Method	BLASTX
NCBI GI	g3367568
BLAST score	429
E value	2.0e-42
Match length	117
% identity	70
NCBI Description	(AL031135) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	224347
Seq. ID	LIB3166-008-P1-K1-D10
Method	BLASTX
NCBI GI	g3378430
BLAST score	188
E value	1.0e-14
Match length	61
% identity	66
NCBI Description	(AF079317) semialdehyde dehydrogenase [Sphingomonas aromaticivorans]

Seq. No.	224348
Seq. ID	LIB3166-008-P1-K1-D11
Method	BLASTX
NCBI GI	g2463569
BLAST score	343
E value	2.0e-32
Match length	73
% identity	86
NCBI Description	(AB007503) squalene synthase [Glycine max]

Seq. No.	224349
Seq. ID	LIB3166-008-P1-K1-D12
Method	BLASTX
NCBI GI	g2443881
BLAST score	163
E value	3.0e-11
Match length	77

% identity	28
NCBI Description	(AC002294) contains beta-transducin motif [Arabidopsis thaliana]
Seq. No.	224350
Seq. ID	LIB3166-008-P1-K1-D4
Method	BLASTX
NCBI GI	g2911043
BLAST score	234
E value	1.0e-19
Match length	106
% identity	53
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]
Seq. No.	224351
Seq. ID	LIB3166-008-P1-K1-D5
Method	BLASTX
NCBI GI	g3582333
BLAST score	587
E value	6.0e-61
Match length	131
% identity	79
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]
Seq. No.	224352
Seq. ID	LIB3166-008-P1-K1-D6
Method	BLASTX
NCBI GI	g3986750
BLAST score	226
E value	8.0e-19
Match length	50
% identity	86
NCBI Description	(AF107464) serine/threonine protein phosphatase type 2A [Hevea brasiliensis]
Seq. No.	224353
Seq. ID	LIB3166-008-P1-K1-E6
Method	BLASTX
NCBI GI	g4574320
BLAST score	106
E value	1.0e-08
Match length	59
% identity	63
NCBI Description	(AF117224) wound-induced protein WI12 [Mesembryanthemum crystallinum]
Seq. No.	224354
Seq. ID	LIB3166-008-P1-K1-E9
Method	BLASTX
NCBI GI	g4510376
BLAST score	331
E value	6.0e-31
Match length	122
% identity	54
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.	224355

Seq. ID	LIB3166-008-P1-K1-F1
Method	BLASTX
NCBI GI	g2129915
BLAST score	330
E value	8.0e-31
Match length	115
% identity	57
NCBI Description	ferredoxin precursor - sweet orange >gi_1360725_emb_CAA87068_ (Z46944) non-photosynthetic ferredoxin [Citrus sinensis]

Seq. No.	224356
Seq. ID	LIB3166-008-P1-K1-F11
Method	BLASTX
NCBI GI	g2501850
BLAST score	507
E value	1.0e-51
Match length	102
% identity	92
NCBI Description	(AF012823) GDP dissociation inhibitor [Nicotiana tabacum]

Seq. No.	224357
Seq. ID	LIB3166-008-P1-K1-F3
Method	BLASTX
NCBI GI	g3033400
BLAST score	284
E value	7.0e-26
Match length	91
% identity	69
NCBI Description	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	224358
Seq. ID	LIB3166-008-P1-K1-F4
Method	BLASTX
NCBI GI	g2809246
BLAST score	203
E value	6.0e-16
Match length	64
% identity	55
NCBI Description	(AC002560) F24O1.15 [Arabidopsis thaliana]

Seq. No.	224359
Seq. ID	LIB3166-008-P1-K1-F6
Method	BLASTX
NCBI GI	g4432842
BLAST score	204
E value	5.0e-16
Match length	135
% identity	39
NCBI Description	(AC006283) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224360
Seq. ID	LIB3166-008-P1-K1-F7
Method	BLASTX
NCBI GI	g417073
BLAST score	472

E value	2.0e-47
Match length	118
% identity	75
NCBI Description	GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT) >gi_484529_pir__JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate synthase [Medicago sativa]

Seq. No.	224361
Seq. ID	LIB3166-008-P1-K1-F8
Method	BLASTX
NCBI GI	g417073
BLAST score	140
E value	4.0e-09
Match length	39
% identity	64
NCBI Description	GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT) >gi_484529_pir__JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate synthase [Medicago sativa]

Seq. No.	224362
Seq. ID	LIB3166-008-P1-K1-G12
Method	BLASTX
NCBI GI	g1168734
BLAST score	258
E value	7.0e-31
Match length	106
% identity	71
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi_288753_emb_CAA79622_ (Z19568) cinnamyl alcohol dehydrogenase [Populus deltoides]

Seq. No.	224363
Seq. ID	LIB3166-008-P1-K1-G2
Method	BLASTX
NCBI GI	g3142300
BLAST score	508
E value	1.0e-51
Match length	121
% identity	81
NCBI Description	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this gene. [Arabidopsis thaliana]

Seq. No.	224364
Seq. ID	LIB3166-008-P1-K1-G3
Method	BLASTX
NCBI GI	g4376592
BLAST score	163
E value	3.0e-11
Match length	121
% identity	11
NCBI Description	(AE001616) S1 Ribosomal Protein [Chlamydia pneumoniae]

Seq. No.	224365

Seq. ID	LIB3166-008-P1-K1-G4
Method	BLASTX
NCBI GI	g2224733
BLAST score	171
E value	4.0e-12
Match length	91
% identity	51
NCBI Description	(AB004933) Aux22e [Vigna radiata]

Seq. No.	224366
Seq. ID	LIB3166-008-P1-K1-G7
Method	BLASTX
NCBI GI	g1220196
BLAST score	279
E value	8.0e-31
Match length	104
% identity	70
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	224367
Seq. ID	LIB3166-008-P1-K1-G9
Method	BLASTX
NCBI GI	g4220538
BLAST score	416
E value	5.0e-41
Match length	101
% identity	80
NCBI Description	(AL035356) NADPH-ferrihemoprotein reductase ATR1 [Arabidopsis thaliana]

Seq. No.	224368
Seq. ID	LIB3166-008-P1-K1-H1
Method	BLASTX
NCBI GI	g4580460
BLAST score	431
E value	1.0e-42
Match length	114
% identity	79
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No.	224369
Seq. ID	LIB3166-008-P1-K1-H2
Method	BLASTX
NCBI GI	g3549667
BLAST score	554
E value	4.0e-57
Match length	121
% identity	87
NCBI Description	(AL031394) Arabidopsis dynamin-like protein ADL2 [Arabidopsis thaliana]

Seq. No.	224370
Seq. ID	LIB3166-008-P1-K1-H9
Method	BLASTX
NCBI GI	g1657382
BLAST score	497

E value	4.0e-52
Match length	117
% identity	86
NCBI Description	(Y09101) cholinephosphate cytidylyltransferase [Pisum sativum]

Seq. No.	224371
Seq. ID	LIB3166-009-P1-K1-A7
Method	BLASTX
NCBI GI	g2119278
BLAST score	622
E value	5.0e-65
Match length	141
% identity	87
NCBI Description	tubulin beta-1 chain - rice

Seq. No.	224372
Seq. ID	LIB3166-009-P1-K1-B10
Method	BLASTX
NCBI GI	g462147
BLAST score	258
E value	2.0e-22
Match length	71
% identity	69
NCBI Description	GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI) (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) >gi_541866_pir__S41808 glucose-6-phosphate isomerase (EC 5.3.1.9) - Arabidopsis thaliana >gi_415923_emb_CAA48940_ (X69195) glucose-6-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	224373
Seq. ID	LIB3166-009-P1-K1-B3
Method	BLASTX
NCBI GI	g2252839
BLAST score	447
E value	2.0e-44
Match length	142
% identity	59
NCBI Description	(AF013293) Similar to receptor-like protein kinase precusor [Arabidopsis thaliana]

Seq. No.	224374
Seq. ID	LIB3166-009-P1-K1-B4
Method	BLASTX
NCBI GI	g421941
BLAST score	326
E value	3.0e-30
Match length	70
% identity	90
NCBI Description	GTP-binding protein, ras-related - common tobacco >gi_296878_emb_CAA50609_ (X71609) ras-related GTP-binding protein [Nicotiana tabacum]

Seq. No.	224375
Seq. ID	LIB3166-009-P1-K1-B6
Method	BLASTX

NCBI GI	g115833
BLAST score	529
E value	4.0e-54
Match length	129
% identity	78
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi_170394 (M32605) a-binding protein [Lycopersicon esculentum]

Seq. No.	224376
Seq. ID	LIB3166-009-P1-K1-C1
Method	BLASTX
NCBI GI	g1702983
BLAST score	325
E value	3.0e-30
Match length	110
% identity	56
NCBI Description	AUXIN-REPRESSED 12.5 KD PROTEIN >gi_99855_pir__S11850 hypothetical protein - garden strawberry >gi_22573_emb_CAA36676_ (X52429) 12.5 kDa protein [Fragaria x ananassa] >gi_927034 (L44142) auxin-repressed protein [Fragaria ananassa]

Seq. No.	224377
Seq. ID	LIB3166-009-P1-K1-C11
Method	BLASTX
NCBI GI	g3395427
BLAST score	169
E value	6.0e-12
Match length	103
% identity	36
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	224378
Seq. ID	LIB3166-009-P1-K1-C3
Method	BLASTX
NCBI GI	g1943751
BLAST score	624
E value	3.0e-65
Match length	141
% identity	89
NCBI Description	(U93845) Arabidopsis thaliana ER-type calcium pump protein, complete sequence >gi_2078292 (U96455) ER-type Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]

Seq. No.	224379
Seq. ID	LIB3166-009-P1-K1-C6
Method	BLASTX
NCBI GI	g2245066
BLAST score	402
E value	3.0e-39
Match length	134
% identity	62
NCBI Description	(Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No. 224380

Seq. ID	LIB3166-009-P1-K1-C7
Method	BLASTX
NCBI GI	g3608137
BLAST score	182
E value	2.0e-13
Match length	79
% identity	49
NCBI Description	(AC005314) unknown protein [Arabidopsis thaliana]

Seq. No.	224381
Seq. ID	LIB3166-009-P1-K1-D2
Method	BLASTX
NCBI GI	g2632254
BLAST score	371
E value	1.0e-35
Match length	102
% identity	70
NCBI Description	(Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No.	224382
Seq. ID	LIB3166-009-P1-K1-D6
Method	BLASTX
NCBI GI	g1944216
BLAST score	275
E value	7.0e-25
Match length	97
% identity	67
NCBI Description	(D84246) alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	224383
Seq. ID	LIB3166-009-P1-K1-D8
Method	BLASTX
NCBI GI	g541847
BLAST score	542
E value	1.0e-55
Match length	120
% identity	84
NCBI Description	alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana

Seq. No.	224384
Seq. ID	LIB3166-009-P1-K1-E12
Method	BLASTX
NCBI GI	g1403522
BLAST score	336
E value	2.0e-31
Match length	107
% identity	62
NCBI Description	(X57187) chitinase [Phaseolus vulgaris]

Seq. No.	224385
Seq. ID	LIB3166-009-P1-K1-E2
Method	BLASTX
NCBI GI	g4490297
BLAST score	279
E value	8.0e-25
Match length	120
% identity	55

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 224386
Seq. ID LIB3166-009-P1-K1-E3
Method BLASTX
NCBI GI g3287691
BLAST score 318
E value 2.0e-29
Match length 126
% identity 54
NCBI Description (AC003979) Contains similarity to RING zinc finger protein gb_X95455 from Gallus gallus. [Arabidopsis thaliana]

Seq. No. 224387
Seq. ID LIB3166-009-P1-K1-E4
Method BLASTX
NCBI GI g1871192
BLAST score 344
E value 2.0e-32
Match length 137
% identity 57
NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No. 224388
Seq. ID LIB3166-009-P1-K1-E6
Method BLASTX
NCBI GI g2708750
BLAST score 382
E value 7.0e-37
Match length 134
% identity 56
NCBI Description (AC003952) putative physical impedence protein [Arabidopsis thaliana]

Seq. No. 224389
Seq. ID LIB3166-009-P1-K1-E7
Method BLASTX
NCBI GI g115833
BLAST score 412
E value 2.0e-40
Match length 108
% identity 75
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi_170394 (M32605) a-binding protein [Lycopersicon esculentum]

Seq. No. 224390
Seq. ID LIB3166-009-P1-K1-F11
Method BLASTX
NCBI GI g4545262
BLAST score 215
E value 3.0e-17
Match length 48
% identity 85
NCBI Description (AF118230) metallothionein-like protein [Gossypium

hirsutum]

Seq. No.	224391
Seq. ID	LIB3166-009-P1-K1-F12
Method	BLASTX
NCBI GI	g4099482
BLAST score	266
E value	3.0e-23
Match length	127
% identity	46
NCBI Description	(U87791) eRFS [Homo sapiens]

Seq. No.	224392
Seq. ID	LIB3166-009-P1-K1-F2
Method	BLASTX
NCBI GI	g541847
BLAST score	268
E value	7.0e-24
Match length	63
% identity	76
NCBI Description	alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana

Seq. No.	224393
Seq. ID	LIB3166-009-P1-K1-F3
Method	BLASTX
NCBI GI	g1707944
BLAST score	635
E value	1.0e-66
Match length	137
% identity	93
NCBI Description	GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT PRECURSOR 2 (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) >gi_541976_pir__S41292 glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) - fava bean >gi_440595_emb_CAA54260_ (X76941) ADP-glucose pyrophosphorylase [Vicia faba]

Seq. No.	224394
Seq. ID	LIB3166-009-P1-K1-F4
Method	BLASTX
NCBI GI	g4335750
BLAST score	164
E value	7.0e-12
Match length	57
% identity	58
NCBI Description	(AC006284) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	224395
Seq. ID	LIB3166-009-P1-K1-F7
Method	BLASTX
NCBI GI	g3023536
BLAST score	388
E value	1.0e-37
Match length	127
% identity	58

NCBI Description	MADS BOX PROTEIN CMB1 >gi_695317 (L40404) MADS box protein [Dianthus caryophyllus]

Seq. No.	224396
Seq. ID	LIB3166-009-P1-K1-F9
Method	BLASTX
NCBI GI	g1345698
BLAST score	715
E value	6.0e-76
Match length	135
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR (CAB-151) (LHCP) >gi_99601_pir__S20917 chlorophyll a/b-binding protein - upland cotton >gi_452314_emb_CAA38025_ (X54090) chlorophyll ab binding protein [Gossypium hirsutum]

Seq. No.	224397
Seq. ID	LIB3166-009-P1-K1-G10
Method	BLASTX
NCBI GI	g464707
BLAST score	535
E value	6.0e-55
Match length	114
% identity	90
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	224398
Seq. ID	LIB3166-009-P1-K1-G11
Method	BLASTX
NCBI GI	g3176726
BLAST score	409
E value	4.0e-44
Match length	124
% identity	75
NCBI Description	(AC002392) putative serine proteinase [Arabidopsis thaliana]

Seq. No.	224399
Seq. ID	LIB3166-009-P1-K1-G2
Method	BLASTX
NCBI GI	g2244749
BLAST score	616

E value	3.0e-64
Match length	128
% identity	91
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	224400
Seq. ID	LIB3166-009-P1-K1-G3
Method	BLASTX
NCBI GI	g2109293
BLAST score	509
E value	9.0e-52
Match length	121
% identity	85
NCBI Description	(U97568) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	224401
Seq. ID	LIB3166-009-P1-K1-G4
Method	BLASTX
NCBI GI	g1708236
BLAST score	476
E value	5.0e-48
Match length	118
% identity	78
NCBI Description	HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana >gi_1143390_emb_CAA58763_ (X83882) hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi_1586548_prf__2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana]

Seq. No.	224402
Seq. ID	LIB3166-009-P1-K1-G5
Method	BLASTX
NCBI GI	g3334659
BLAST score	309
E value	2.0e-28
Match length	134
% identity	52
NCBI Description	(Y10489) putative cytochrome P450 [Glycine max]

Seq. No.	224403
Seq. ID	LIB3166-009-P1-K1-H2
Method	BLASTX
NCBI GI	g3763933
BLAST score	277
E value	1.0e-24
Match length	127
% identity	44
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana]

Seq. No.	224404
Seq. ID	LIB3166-009-P1-K1-H6
Method	BLASTX
NCBI GI	g441457

BLAST score	462
E value	3.0e-46
Match length	92
% identity	93
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]

Seq. No.	224405
Seq. ID	LIB3166-009-P1-K1-H8
Method	BLASTX
NCBI GI	g1946267
BLAST score	211
E value	8.0e-17
Match length	60
% identity	65
NCBI Description	(Y11415) myb [Oryza sativa]

Seq. No.	224406
Seq. ID	LIB3166-010-P1-K1-A1
Method	BLASTX
NCBI GI	g2827002
BLAST score	220
E value	2.0e-18
Match length	42
% identity	100
NCBI Description	(AF005993) HSP70 [Triticum aestivum]

Seq. No.	224407
Seq. ID	LIB3166-010-P1-K1-A10
Method	BLASTX
NCBI GI	g4580392
BLAST score	283
E value	3.0e-25
Match length	123
% identity	46
NCBI Description	(AC007171) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224408
Seq. ID	LIB3166-010-P1-K1-A11
Method	BLASTX
NCBI GI	g1399917
BLAST score	156
E value	2.0e-10
Match length	79
% identity	41
NCBI Description	(U60144) replication factor C large subunit [Anas platyrhynchos]

Seq. No.	224409
Seq. ID	LIB3166-010-P1-K1-A3
Method	BLASTX
NCBI GI	g1944216
BLAST score	329
E value	3.0e-31
Match length	72
% identity	85
NCBI Description	(D84246) alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	224410
Seq. ID	LIB3166-010-P1-K1-A8
Method	BLASTX
NCBI GI	g1169586
BLAST score	213
E value	1.0e-17
Match length	61
% identity	70
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) (CY-F1) >gi_542079_pir__S41287 fructose-bisphosphatase (EC 3.1.3.11) - potato >gi_440591_emb_CAA54265_ (X76946) fructose-1,6-bisphosphatase [Solanum tuberosum]

Seq. No.	224411
Seq. ID	LIB3166-010-P1-K1-A9
Method	BLASTX
NCBI GI	g289920
BLAST score	373
E value	4.0e-36
Match length	89
% identity	82
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	224412
Seq. ID	LIB3166-010-P1-K1-B10
Method	BLASTX
NCBI GI	g19464
BLAST score	329
E value	1.0e-30
Match length	85
% identity	62
NCBI Description	(X54464) ribulose bisphosphate carboxylase [Larix laricina]

Seq. No.	224413
Seq. ID	LIB3166-010-P1-K1-B11
Method	BLASTX
NCBI GI	g231806
BLAST score	267
E value	2.0e-36
Match length	102
% identity	83
NCBI Description	CHALCONE SYNTHASE (NAREGENIN-CHALCONE SYNTHASE) >gi_322681_pir__S29556 naringenin-chalcone synthase (EC 2.3.1.74) - apple tree (fragment) >gi_19589_emb_CAA48773_ (X68977) naregenin-chalcone synthase [Malus sp.]

Seq. No.	224414
Seq. ID	LIB3166-010-P1-K1-B2
Method	BLASTX
NCBI GI	g1173256
BLAST score	298
E value	2.0e-27
Match length	68

% identity	84
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal protein S4 - upland cotton >gi_488739_emb_CAA55882_ (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]

Seq. No.	224415
Seq. ID	LIB3166-010-P1-K1-B3
Method	BLASTX
NCBI GI	g218179
BLAST score	183
E value	7.0e-21
Match length	92
% identity	59
NCBI Description	(D10207) H-ATPase [Oryza sativa] >gi_444339_prf__1906387A H ATPase [Oryza sativa]

Seq. No.	224416
Seq. ID	LIB3166-010-P1-K1-B7
Method	BLASTX
NCBI GI	g2129655
BLAST score	192
E value	1.0e-14
Match length	71
% identity	58
NCBI Description	OBP32pep protein - Arabidopsis thaliana (fragment) >gi_1022799 (U37698) OBP32pep [Arabidopsis thaliana]

Seq. No.	224417
Seq. ID	LIB3166-010-P1-K1-B8
Method	BLASTX
NCBI GI	g3955021
BLAST score	381
E value	1.0e-36
Match length	103
% identity	73
NCBI Description	(AJ010811) HB2 homeodomain protein [Populus tremula x Populus tremuloides]

Seq. No.	224418
Seq. ID	LIB3166-010-P1-K1-C10
Method	BLASTX
NCBI GI	g125578
BLAST score	562
E value	5.0e-58
Match length	116
% identity	93
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_167266 (M73707) phosphoribulokinase [Mesembryanthemum crystallinum]

Seq. No.	224419
Seq. ID	LIB3166-010-P1-K1-C11
Method	BLASTX
NCBI GI	g4558547
BLAST score	277
E value	1.0e-24

Match length 141
% identity 45
NCBI Description (AC007138) hypothetical protein [Arabidopsis thaliana]

Seq. No. 224420
Seq. ID LIB3166-010-P1-K1-C12
Method BLASTX
NCBI GI g3834303
BLAST score 428
E value 3.0e-42
Match length 138
% identity 63
NCBI Description (AC005679) F9K20.3 [Arabidopsis thaliana]

Seq. No. 224421
Seq. ID LIB3166-010-P1-K1-C4
Method BLASTX
NCBI GI g543905
BLAST score 500
E value 1.0e-50
Match length 107
% identity 86
NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162) brassinosteroid-regulated protein [Glycine max]

Seq. No. 224422
Seq. ID LIB3166-010-P1-K1-C8
Method BLASTX
NCBI GI g3482973
BLAST score 429
E value 2.0e-42
Match length 127
% identity 71
NCBI Description (AL031369) putative protein [Arabidopsis thaliana]

Seq. No. 224423
Seq. ID LIB3166-010-P1-K1-D1
Method BLASTX
NCBI GI g2980773
BLAST score 234
E value 1.0e-19
Match length 79
% identity 45
NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 224424
Seq. ID LIB3166-010-P1-K1-D11
Method BLASTX
NCBI GI g4220533
BLAST score 378
E value 2.0e-36
Match length 127
% identity 34
NCBI Description (AL035356) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No. 224425

Seq. ID LIB3166-010-P1-K1-D4
Method BLASTX
NCBI GI g4454009
BLAST score 154
E value 4.0e-10
Match length 95
% identity 40
NCBI Description (AL035396) putative protein [Arabidopsis thaliana]

Seq. No. 224426
Seq. ID LIB3166-010-P1-K1-D7
Method BLASTX
NCBI GI g1621268
BLAST score 250
E value 1.0e-21
Match length 85
% identity 64
NCBI Description (Z81012) unknown [Ricinus communis]

Seq. No. 224427
Seq. ID LIB3166-010-P1-K1-D9
Method BLASTX
NCBI GI g2982251
BLAST score 290
E value 4.0e-26
Match length 76
% identity 71
NCBI Description (AF051208) putative RNA-binding protein [Picea mariana]

Seq. No. 224428
Seq. ID LIB3166-010-P1-K1-E12
Method BLASTX
NCBI GI g2129825
BLAST score 540
E value 2.0e-57
Match length 139
% identity 83
NCBI Description dynamin-like protein phragmoplastin 12 - soybean
>gi_1217994 (U25547) SDL [Glycine max]

Seq. No. 224429
Seq. ID LIB3166-010-P1-K1-E2
Method BLASTX
NCBI GI g4580389
BLAST score 272
E value 5.0e-24
Match length 109
% identity 56
NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]

Seq. No. 224430
Seq. ID LIB3166-010-P1-K1-E3
Method BLASTX
NCBI GI g1944216
BLAST score 358
E value 2.0e-34
Match length 80

% identity	85
NCBI Description	(D84246) alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	224431
Seq. ID	LIB3166-010-P1-K1-E4
Method	BLASTX
NCBI GI	g1871192
BLAST score	148
E value	1.0e-09
Match length	64
% identity	47
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	224432
Seq. ID	LIB3166-010-P1-K1-E6
Method	BLASTX
NCBI GI	g4545262
BLAST score	232
E value	3.0e-19
Match length	44
% identity	98
NCBI Description	(AF118230) metallothionein-like protein [Gossypium hirsutum]

Seq. No.	224433
Seq. ID	LIB3166-010-P1-K1-E7
Method	BLASTX
NCBI GI	g4415913
BLAST score	302
E value	2.0e-27
Match length	122
% identity	61
NCBI Description	(AC006282) unknown protein [Arabidopsis thaliana]

Seq. No.	224434
Seq. ID	LIB3166-010-P1-K1-F10
Method	BLASTX
NCBI GI	g3250675
BLAST score	253
E value	3.0e-22
Match length	75
% identity	67
NCBI Description	(AL024486) putative protein [Arabidopsis thaliana]

Seq. No.	224435
Seq. ID	LIB3166-010-P1-K1-F12
Method	BLASTX
NCBI GI	g3297818
BLAST score	373
E value	8.0e-36
Match length	104
% identity	63
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	224436
Seq. ID	LIB3166-010-P1-K1-F3

Method	BLASTX
NCBI GI	g4049410
BLAST score	419
E value	3.0e-41
Match length	118
% identity	66
NCBI Description	(Y10225) L-ascorbate oxidase [Cucumis melo]

Seq. No.	224437
Seq. ID	LIB3166-010-P1-K1-F6
Method	BLASTX
NCBI GI	g3885338
BLAST score	324
E value	3.0e-30
Match length	102
% identity	61
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	224438
Seq. ID	LIB3166-010-P1-K1-F7
Method	BLASTX
NCBI GI	g116923
BLAST score	251
E value	1.0e-21
Match length	82
% identity	61
NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi_111414_pir__S13520 beta-COP protein - rat >gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus norvegicus]

Seq. No.	224439
Seq. ID	LIB3166-010-P1-K1-F8
Method	BLASTX
NCBI GI	g1495804
BLAST score	657
E value	4.0e-69
Match length	142
% identity	85
NCBI Description	(X96406) 13-lipoxygenase [Solanum tuberosum]

Seq. No.	224440
Seq. ID	LIB3166-010-P1-K1-G1
Method	BLASTX
NCBI GI	g1707955
BLAST score	628
E value	9.0e-66
Match length	125
% identity	92
NCBI Description	GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME 1 (GLUTAMATE--AMMONIA LIGASE) >gi_1134896_emb_CAA63981_ (X94320) glutamine synthetase [Vitis vinifera]

Seq. No.	224441
Seq. ID	LIB3166-010-P1-K1-G10
Method	BLASTX
NCBI GI	g2935416

BLAST score 554
E value 5.0e-57
Match length 139
% identity 78
NCBI Description (AF047896) isoflavone reductase homolog [Betula pendula]

Seq. No. 224442
Seq. ID LIB3166-010-P1-K1-G12
Method BLASTX
NCBI GI g2408068
BLAST score 241
E value 2.0e-20
Match length 107
% identity 42
NCBI Description (Z99165) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 224443
Seq. ID LIB3166-010-P1-K1-G2
Method BLASTX
NCBI GI g2370312
BLAST score 399
E value 7.0e-39
Match length 139
% identity 58
NCBI Description (AJ000995) DnaJ-like protein [Medicago sativa] >gi_3202020 (AF069507) DnaJ-like protein MsJ1 [Medicago sativa]

Seq. No. 224444
Seq. ID LIB3166-010-P1-K1-G7
Method BLASTX
NCBI GI g2352492
BLAST score 190
E value 1.0e-14
Match length 68
% identity 59
NCBI Description (AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No. 224445
Seq. ID LIB3166-010-P1-K1-H4
Method BLASTX
NCBI GI g4417267
BLAST score 261
E value 1.0e-22
Match length 132
% identity 39
NCBI Description (AC007019) hypothetical protein [Arabidopsis thaliana]

Seq. No. 224446
Seq. ID LIB3166-010-P1-K1-H7
Method BLASTX
NCBI GI g116923
BLAST score 273
E value 4.0e-24
Match length 110
% identity 43

NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi_111414_pir__S13520 beta-COP protein - rat >gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus norvegicus]

Seq. No.	224447
Seq. ID	LIB3166-010-P1-K1-H9
Method	BLASTX
NCBI GI	g3935176
BLAST score	173
E value	2.0e-12
Match length	71
% identity	54
NCBI Description	(AC004557) F17L21.19 [Arabidopsis thaliana]

Seq. No.	224448
Seq. ID	LIB3166-011-P1-K1-A1
Method	BLASTX
NCBI GI	g4469023
BLAST score	323
E value	6.0e-30
Match length	98
% identity	68
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	224449
Seq. ID	LIB3166-011-P1-K1-A12
Method	BLASTX
NCBI GI	g3212869
BLAST score	495
E value	3.0e-50
Match length	120
% identity	74
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	224450
Seq. ID	LIB3166-011-P1-K1-A4
Method	BLASTX
NCBI GI	g2632252
BLAST score	271
E value	7.0e-24
Match length	134
% identity	46
NCBI Description	(Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No.	224451
Seq. ID	LIB3166-011-P1-K1-A5
Method	BLASTX
NCBI GI	g4544443
BLAST score	169
E value	5.0e-12
Match length	36
% identity	92
NCBI Description	(AC006592) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	224452

Seq. ID	LIB3166-011-P1-K1-A8
Method	BLASTX
NCBI GI	g3702332
BLAST score	176
E value	9.0e-13
Match length	124
% identity	27
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	224453
Seq. ID	LIB3166-011-P1-K1-B1
Method	BLASTX
NCBI GI	g2129769
BLAST score	497
E value	2.0e-50
Match length	112
% identity	81
NCBI Description	xyloglucan endo-transglycosylase precursor - Arabidopsis thaliana >gi_944810_dbj_BAA09783_ (D63508) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	224454
Seq. ID	LIB3166-011-P1-K1-B10
Method	BLASTX
NCBI GI	g4455214
BLAST score	577
E value	8.0e-60
Match length	126
% identity	89
NCBI Description	(AL035440) putative dihydrolipoamide succinyltransferase [Arabidopsis thaliana]

Seq. No.	224455
Seq. ID	LIB3166-011-P1-K1-B4
Method	BLASTX
NCBI GI	g2894612
BLAST score	485
E value	6.0e-49
Match length	112
% identity	79
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	224456
Seq. ID	LIB3166-011-P1-K1-B6
Method	BLASTX
NCBI GI	g485742
BLAST score	569
E value	7.0e-59
Match length	125
% identity	86
NCBI Description	(L32791) pyrophosphatase [Beta vulgaris]

Seq. No.	224457
Seq. ID	LIB3166-011-P1-K1-B8
Method	BLASTX
NCBI GI	g2129759
BLAST score	209

E value	1.0e-16
Match length	79
% identity	54
NCBI Description	UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana >gi_1143392_emb_CAA90941_ (Z54214) uridine diphosphate glucose epimerase [Arabidopsis thaliana]

Seq. No.	224458
Seq. ID	LIB3166-011-P1-K1-C1
Method	BLASTX
NCBI GI	g4539405
BLAST score	546
E value	4.0e-56
Match length	127
% identity	82
NCBI Description	(AL049524) putative ribosomal protein L9, cytosolic [Arabidopsis thaliana]

Seq. No.	224459
Seq. ID	LIB3166-011-P1-K1-C10
Method	BLASTX
NCBI GI	g1871577
BLAST score	383
E value	5.0e-37
Match length	106
% identity	67
NCBI Description	(Y11553) putative 21kD protein precursor [Medicago sativa]

Seq. No.	224460
Seq. ID	LIB3166-011-P1-K1-C11
Method	BLASTX
NCBI GI	g322750
BLAST score	546
E value	4.0e-56
Match length	109
% identity	99
NCBI Description	ubiquitin / ribosomal protein CEP52 - wood tobacco >gi_170217 (M74100) ubiquitin fusion protein [Nicotiana sylvestris]

Seq. No.	224461
Seq. ID	LIB3166-011-P1-K1-C12
Method	BLASTX
NCBI GI	g461942
BLAST score	525
E value	1.0e-53
Match length	135
% identity	74
NCBI Description	DNAJ PROTEIN HOMOLOG 1 (DNAJ-1) >gi_479277_pir__S33312 dnaJ protein - leek (fragment) >gi_16087_emb_CAA49211_ (X69436) DNA J protein [Allium porrum] >gi_447267_prf__1914140A DnaJ protein [Allium porrum]

Seq. No.	224462
Seq. ID	LIB3166-011-P1-K1-C2
Method	BLASTX
NCBI GI	g409756

BLAST score	146
E value	2.0e-09
Match length	88
% identity	30
NCBI Description	(L25643) ATP/GTP nucleotide-binding protein [Leishmania infantum]

Seq. No.	224463
Seq. ID	LIB3166-011-P1-K1-C3
Method	BLASTX
NCBI GI	g1142621
BLAST score	165
E value	3.0e-16
Match length	73
% identity	67
NCBI Description	(U18349) phaseolin G-box binding protein PG2 [Phaseolus vulgaris]

Seq. No.	224464
Seq. ID	LIB3166-011-P1-K1-C4
Method	BLASTX
NCBI GI	g4262239
BLAST score	273
E value	4.0e-24
Match length	133
% identity	43
NCBI Description	(AC006200) putative membrane transporter [Arabidopsis thaliana]

Seq. No.	224465
Seq. ID	LIB3166-011-P1-K1-C8
Method	BLASTX
NCBI GI	g3335060
BLAST score	418
E value	4.0e-41
Match length	95
% identity	88
NCBI Description	(AF025842) plasma membrane-type calcium ATPase [Arabidopsis thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]

Seq. No.	224466
Seq. ID	LIB3166-011-P1-K1-C9
Method	BLASTX
NCBI GI	g464707
BLAST score	538
E value	3.0e-55
Match length	110
% identity	95
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana]

	>gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]
Seq. No.	224467
Seq. ID	LIB3166-011-P1-K1-D12
Method	BLASTX
NCBI GI	g1071913
BLAST score	421
E value	2.0e-41
Match length	109
% identity	78
NCBI Description	cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial - spinach >gi_1066153_dbj_BAA07177_ (D37963) cysteine synthase [Spinacia oleracea]
Seq. No.	224468
Seq. ID	LIB3166-011-P1-K1-D4
Method	BLASTX
NCBI GI	g2262170
BLAST score	211
E value	7.0e-17
Match length	114
% identity	47
NCBI Description	(AC002329) predicted glycosyl hydrolase [Arabidopsis thaliana]
Seq. No.	224469
Seq. ID	LIB3166-011-P1-K1-D5
Method	BLASTX
NCBI GI	g4455364
BLAST score	428
E value	3.0e-42
Match length	121
% identity	65
NCBI Description	(AL035524) senescence-associated protein-like [Arabidopsis thaliana]
Seq. No.	224470
Seq. ID	LIB3166-011-P1-K1-D6
Method	BLASTX
NCBI GI	g2500378
BLAST score	416
E value	7.0e-41
Match length	83
% identity	90
NCBI Description	60S RIBOSOMAL PROTEIN L37
Seq. No.	224471
Seq. ID	LIB3166-011-P1-K1-E10
Method	BLASTX
NCBI GI	g1174592
BLAST score	608

E value	2.0e-63
Match length	113
% identity	99
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	224472
Seq. ID	LIB3166-011-P1-K1-E11
Method	BLASTX
NCBI GI	g2052379
BLAST score	169
E value	3.0e-12
Match length	35
% identity	86
NCBI Description	(U66343) calreticulin [Arabidopsis thaliana]

Seq. No.	224473
Seq. ID	LIB3166-011-P1-K1-E2
Method	BLASTX
NCBI GI	g3080400
BLAST score	302
E value	2.0e-35
Match length	119
% identity	65
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana] >gi_4455264_emb_CAB36800.1_ (AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	224474
Seq. ID	LIB3166-011-P1-K1-E3
Method	BLASTX
NCBI GI	g2292917
BLAST score	258
E value	2.0e-22
Match length	84
% identity	64
NCBI Description	(X99851) galactokinase [Arabidopsis thaliana]

Seq. No.	224475
Seq. ID	LIB3166-011-P1-K1-E5
Method	BLASTX
NCBI GI	g128194
BLAST score	462
E value	2.0e-46
Match length	113
% identity	80
NCBI Description	NITRATE REDUCTASE (NR) >gi_81572_pir__A41667 nitrate reductase (NADH) (EC 1.6.6.1) - winter squash >gi_167499 (M33154) nitrate reductase [Cucurbita maxima]

Seq. No.	224476
Seq. ID	LIB3166-011-P1-K1-E7
Method	BLASTX
NCBI GI	g3036807
BLAST score	324
E value	4.0e-30

Match length 88
% identity 74
NCBI Description (AL022373) putative protein [Arabidopsis thaliana]

Seq. No. 224477
Seq. ID LIB3166-011-P1-K1-F1
Method BLASTX
NCBI GI g498038
BLAST score 282
E value 2.0e-29
Match length 106
% identity 60
NCBI Description (L33792) lipid transfer protein [Senecio odorus]

Seq. No. 224478
Seq. ID LIB3166-011-P1-K1-F10
Method BLASTX
NCBI GI g3298441
BLAST score 270
E value 9.0e-24
Match length 103
% identity 58
NCBI Description (AB010879) chloroplast ribosomal protein L10 [Nicotiana tabacum]

Seq. No. 224479
Seq. ID LIB3166-011-P1-K1-F12
Method BLASTX
NCBI GI g2982303
BLAST score 551
E value 9.0e-57
Match length 127
% identity 81
NCBI Description (AF051236) hypothetical protein [Picea mariana]

Seq. No. 224480
Seq. ID LIB3166-011-P1-K1-F3
Method BLASTX
NCBI GI g4490736
BLAST score 331
E value 6.0e-31
Match length 132
% identity 66
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 224481
Seq. ID LIB3166-011-P1-K1-F7
Method BLASTX
NCBI GI g629541
BLAST score 484
E value 8.0e-49
Match length 115
% identity 81
NCBI Description plasma membrane intrinsic protein 1c - Arabidopsis thaliana >gi_472875_emb_CAA53476_ (X75882) plasma membrane intrinsic protein 1c [Arabidopsis thaliana]

Seq. No.	224482
Seq. ID	LIB3166-011-P1-K1-F8
Method	BLASTX
NCBI GI	g3341679
BLAST score	274
E value	3.0e-24
Match length	82
% identity	70
NCBI Description	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]

Seq. No.	224483
Seq. ID	LIB3166-011-P1-K1-F9
Method	BLASTX
NCBI GI	g3775997
BLAST score	391
E value	6.0e-38
Match length	90
% identity	84
NCBI Description	(AJ010462) RNA helicase [Arabidopsis thaliana]

Seq. No.	224484
Seq. ID	LIB3166-011-P1-K1-G1
Method	BLASTX
NCBI GI	g2511541
BLAST score	402
E value	1.0e-39
Match length	90
% identity	88
NCBI Description	(AF020787) DNA-binding protein GBP16 [Oryza sativa]

Seq. No.	224485
Seq. ID	LIB3166-011-P1-K1-G12
Method	BLASTX
NCBI GI	g3901012
BLAST score	602
E value	1.0e-62
Match length	135
% identity	76
NCBI Description	(AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]

Seq. No.	224486
Seq. ID	LIB3166-011-P1-K1-G2
Method	BLASTX
NCBI GI	g2961372
BLAST score	432
E value	8.0e-43
Match length	85
% identity	93
NCBI Description	(AL022141) putative ribosomal protein L8 [Arabidopsis thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	224487
Seq. ID	LIB3166-011-P1-K1-G3
Method	BLASTX

NCBI GI	g4544403
BLAST score	624
E value	3.0e-65
Match length	139
% identity	81
NCBI Description	(AC007047) putative glucan endo-1,3-beta-D-glucosidase precursor [Arabidopsis thaliana]

Seq. No.	224488
Seq. ID	LIB3166-011-P1-K1-G4
Method	BLASTX
NCBI GI	g1220196
BLAST score	508
E value	1.0e-51
Match length	112
% identity	85
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	224489
Seq. ID	LIB3166-011-P1-K1-G9
Method	BLASTX
NCBI GI	g3941543
BLAST score	241
E value	2.0e-20
Match length	72
% identity	68
NCBI Description	(AF069497) pelota [Arabidopsis thaliana] >gi_4469016_emb_CAB38277_ (AL035602) pelota (PEL1) [Arabidopsis thaliana]

Seq. No.	224490
Seq. ID	LIB3166-011-P1-K1-H1
Method	BLASTX
NCBI GI	g3434967
BLAST score	204
E value	4.0e-16
Match length	85
% identity	53
NCBI Description	(AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]

Seq. No.	224491
Seq. ID	LIB3166-011-P1-K1-H4
Method	BLASTX
NCBI GI	g2982453
BLAST score	291
E value	3.0e-26
Match length	99
% identity	62
NCBI Description	(AL022223) fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]

Seq. No.	224492
Seq. ID	LIB3166-011-P1-K1-H9
Method	BLASTX
NCBI GI	g3885328
BLAST score	157

E value	9.0e-11
Match length	83
% identity	40
NCBI Description	(AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	224493
Seq. ID	LIB3166-012-P1-K1-A4
Method	BLASTX
NCBI GI	g91035
BLAST score	608
E value	2.0e-63
Match length	127
% identity	93
NCBI Description	laminin receptor homolog - mouse >gi_52853_emb_CAA29696_ (X06406) protein p40 (AA 1 - 295) [Mus musculus] >gi_228997_prf__1815216A laminin receptor [Cricetinae gen. sp.]

Seq. No.	224494
Seq. ID	LIB3166-012-P1-K1-A5
Method	BLASTX
NCBI GI	g2894106
BLAST score	654
E value	8.0e-69
Match length	127
% identity	94
NCBI Description	(Z78279) Collagen alpha1 [Rattus norvegicus]

Seq. No.	224495
Seq. ID	LIB3166-012-P1-K1-A6
Method	BLASTX
NCBI GI	g3164123
BLAST score	643
E value	2.0e-67
Match length	126
% identity	94
NCBI Description	(AJ224880) collagen alpha 2 type V [Rattus norvegicus]

Seq. No.	224496
Seq. ID	LIB3166-012-P1-K1-A8
Method	BLASTX
NCBI GI	g127177
BLAST score	223
E value	2.0e-18
Match length	87
% identity	54
NCBI Description	MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM (G2) (DTNB) (MLC-2) >gi_71706_pir__MORTL2 myosin L2 (DTNB) regulatory light chain precursor, skeletal muscle - rat >gi_825539_emb_CAA25480_ (X00975) MLC2 [Rattus norvegicus]

Seq. No.	224497
Seq. ID	LIB3166-012-P1-K1-B10
Method	BLASTX
NCBI GI	g309233
BLAST score	413

E value	1.0e-40
Match length	79
% identity	100
NCBI Description	(M24509) ferritin heavy chain [Mus musculus] >gi_1435203 (U58829) ferritin-H subunit [Rattus norvegicus]

Seq. No.	224498
Seq. ID	LIB3166-012-P1-K1-B2
Method	BLASTX
NCBI GI	g1588365
BLAST score	382
E value	8.0e-37
Match length	104
% identity	74
NCBI Description	signal peptidase:SUBUNIT=12kD [Homo sapiens]

Seq. No.	224499
Seq. ID	LIB3166-012-P1-K1-B7
Method	BLASTX
NCBI GI	g2894106
BLAST score	337
E value	4.0e-32
Match length	66
% identity	98
NCBI Description	(Z78279) Collagen alpha1 [Rattus norvegicus]

Seq. No.	224500
Seq. ID	LIB3166-012-P1-K1-C1
Method	BLASTX
NCBI GI	g111946
BLAST score	407
E value	8.0e-40
Match length	84
% identity	88
NCBI Description	matrix Gla protein precursor - rat

Seq. No.	224501
Seq. ID	LIB3166-012-P1-K1-C10
Method	BLASTX
NCBI GI	g2135915
BLAST score	670
E value	1.0e-70
Match length	127
% identity	95
NCBI Description	phosphoenolpyruvate carboxykinase (GTP) (EC 4.1.1.32) precursor, mitochondrial - human >gi_1403050_emb_CAA63380_ (X92720) phosphoenolpyruvate carboxykinase (GTP) [Homo sapiens]

Seq. No.	224502
Seq. ID	LIB3166-012-P1-K1-C6
Method	BLASTX
NCBI GI	g4098993
BLAST score	474
E value	1.0e-47
Match length	121
% identity	79

NCBI Description	(U81491) polyhomeotic 2 [Mus musculus]

Seq. No.	224503
Seq. ID	LIB3166-012-P1-K1-C7
Method	BLASTX
NCBI GI	g417192
BLAST score	414
E value	1.0e-40
Match length	97
% identity	78
NCBI Description	MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (MCP-3) (MONOCYTE CHEMOATTRACTANT PROTEIN 3) (INTERCRINE/CHEMOKINE MARC) (FIC PROTEIN) >gi_57938_emb_CAA78169_ (Z12297) intercrine [Mus musculus] >gi_547089_bbs_149941 (S71251) monocyte chemotactic protein-3, MCP-3, Marc/Fic protein [mice, macrophage cell line WEHI-3, Peptide, 97 aa] [Mus sp.]

Seq. No.	224504
Seq. ID	LIB3166-012-P1-K1-E11
Method	BLASTX
NCBI GI	g123651
BLAST score	506
E value	5.0e-62
Match length	134
% identity	96
NCBI Description	HEAT SHOCK COGNATE 71 KD PROTEIN >gi_111759_pir__S07197 heat shock cognate protein hsc73 - rat >gi_2119718_pir__JC4853 heat-shock protein 73 - mouse >gi_56379_emb_CAA68265_ (Y00054) hsc73 [Rattus norvegicus] >gi_204667 (M11942) 70 kDa heat-shock-like protein [Rattus norvegicus] >gi_861213 (U27129) heat shock 73 protein [Mus musculus]

Seq. No.	224505
Seq. ID	LIB3166-012-P1-K1-E12
Method	BLASTX
NCBI GI	g3043917
BLAST score	345
E value	1.0e-32
Match length	113
% identity	63
NCBI Description	(AF029844) elongation factor 1-beta homolog [Mus musculus]

Seq. No.	224506
Seq. ID	LIB3166-012-P1-K1-E6
Method	BLASTX
NCBI GI	g114291
BLAST score	272
E value	1.0e-24
Match length	53
% identity	98
NCBI Description	ARGININOSUCCINATE SYNTHASE (CITRULLINE--ASPARTATE LIGASE) >gi_68637_pir__AJRTRS argininosuccinate synthase (EC 6.3.4.5) - rat >gi_55767_emb_CAA30999_ (X12459) argininosuccinate synthetase (AA 1-412) [Rattus norvegicus] >gi_203016 (M36708) argininosuccinate synthetase [Rattus norvegicus]

Seq. No.	224507
Seq. ID	LIB3166-012-P1-K1-F10
Method	BLASTX
NCBI GI	g137475
BLAST score	729
E value	1.0e-77
Match length	139
% identity	99
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (32 KD ACCESSORY PROTEIN) (P39) >gi_89602_pir__A32123 H+-transporting ATPase (EC 3.6.1.35) polypeptide IV, vacuolar - bovine

Seq. No.	224508
Seq. ID	LIB3166-012-P1-K1-F11
Method	BLASTX
NCBI GI	g2833633
BLAST score	611
E value	1.0e-63
Match length	136
% identity	81
NCBI Description	(AC003108) Unknown gene product [Homo sapiens]

Seq. No.	224509
Seq. ID	LIB3166-012-P1-K1-F12
Method	BLASTX
NCBI GI	g543201
BLAST score	611
E value	1.0e-63
Match length	132
% identity	84
NCBI Description	collagen alpha 1(I) chain precursor - mouse (fragments)

Seq. No.	224510
Seq. ID	LIB3166-012-P1-K1-F3
Method	BLASTX
NCBI GI	g117505
BLAST score	193
E value	6.0e-15
Match length	71
% identity	56
NCBI Description	CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (CALBP) (CALCIUM-BINDING PROTEIN 3) (CABP3) >gi_627974_pir__JH0819 calreticulin precursor - rat >gi_55855_emb_CAA37446_ (X53363) precursor (AA -17 to 399) [Rattus norvegicus] >gi_488841_emb_CAA55890_ (X79327) calreticulin [Rattus norvegicus] >gi_1845572_dbj_BAA11345_ (D78308) calreticulin [Rattus norvegicus]

Seq. No.	224511
Seq. ID	LIB3166-012-P1-K1-F4
Method	BLASTX
NCBI GI	g478811
BLAST score	232
E value	1.0e-19
Match length	74

% identity	17
NCBI Description	polyubiquitin - bovine >gi_645_emb_CAA79146_ (Z18245) polyubiquitin [Bos taurus]

Seq. No.	224512
Seq. ID	LIB3166-012-P1-K1-F9
Method	BLASTX
NCBI GI	g2961553
BLAST score	559
E value	9.0e-58
Match length	113
% identity	100
NCBI Description	(AF049878) amyloid beta-peptide binding protein; ERAB [Rattus norvegicus]

Seq. No.	224513
Seq. ID	LIB3166-012-P1-K1-G10
Method	BLASTX
NCBI GI	g231671
BLAST score	156
E value	2.0e-10
Match length	31
% identity	94
NCBI Description	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR >gi_284994_pir__A43291 collagen alpha 2(I) chain precursor - mouse >gi_50489_emb_CAA41205_ (X58251) pro-alpha-2(I) collagen [Mus musculus]

Seq. No.	224514
Seq. ID	LIB3166-012-P1-K1-G8
Method	BLASTX
NCBI GI	g119146
BLAST score	628
E value	6.0e-68
Match length	135
% identity	96
NCBI Description	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION FACTOR TU) (EF-TU) >gi_90198_pir__JU0133 translation elongation factor eEF-1 alpha chain - Chinese hamster >gi_111601_pir__S21055 translation elongation factor eEF-1 alpha chain - rat >gi_56080_emb_CAA43378_ (X61043) elongation factor 1 alpha [Rattus norvegicus] >gi_56093_emb_CAA45122_ (X63561) elongation factor 1-alpha [Rattus norvegicus] >gi_220279_dbj_BAA00409_ (D00522) EF-1 alpha [Cricetulus longicaudatus]

Seq. No.	224515
Seq. ID	LIB3166-012-P1-K1-H12
Method	BLASTX
NCBI GI	g3123887
BLAST score	267
E value	1.0e-23
Match length	63
% identity	81
NCBI Description	(AF027706) serine/threonine kinase RICK [Homo sapiens] >gi_3264574 (AC004003) serine/threonine kinase RICK; match to protein AF027706 (PID:g3123887) and mRNA AF027706

(NID:g3123886) [Homo sapiens] >gi_3290172 (AF064824) CARD-containing ICE associated kinase [Homo sapiens] >gi_3342910 (AF078530) receptor interacting protein 2 [Homo sapiens] >gi_4151948 (AF117829) serine/threonine kinase RICK [Homo sapiens] >gi_4506537_ref_NP_003812.1_pRIP2_ UNKNOWN

Seq. No.	224516
Seq. ID	LIB3166-012-P1-K1-H3
Method	BLASTX
NCBI GI	g809561
BLAST score	427
E value	3.0e-42
Match length	87
% identity	95
NCBI Description	(X13055) gamma-actin [Mus musculus]

Seq. No.	224517
Seq. ID	LIB3166-012-P1-K1-H6
Method	BLASTX
NCBI GI	g548747
BLAST score	312
E value	2.0e-32
Match length	71
% identity	92
NCBI Description	60S RIBOSOMAL PROTEIN L13A >gi_1363320_pir__A53204 ribosomal protein L13a - rat >gi_460776_emb_CAA48343_ (X68282) rat ribosomal protein L13a [Rattus norvegicus]

Seq. No.	224518
Seq. ID	LIB3166-012-P1-K1-H7
Method	BLASTX
NCBI GI	g1213490
BLAST score	200
E value	3.0e-20
Match length	56
% identity	95
NCBI Description	(U42719) C4 complement protein [Rattus norvegicus]

Seq. No.	224519
Seq. ID	LIB3166-012-P1-K1-H8
Method	BLASTX
NCBI GI	g1173177
BLAST score	471
E value	1.0e-47
Match length	93
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN S10 >gi_1362933_pir__S55918 ribosomal protein S10 - human >gi_550025 (U14972) ribosomal protein S10 [Homo sapiens] >gi_1096944_prf__2113200G ribosomal protein S10 [Homo sapiens] >gi_4506679_ref_NP_001005.1_pRPS10_ ribosomal protein S10

Seq. No.	224520
Seq. ID	LIB3166-013-P1-K1-A12
Method	BLASTX
NCBI GI	g2443757

BLAST score	306
E value	3.0e-28
Match length	90
% identity	67
NCBI Description	(AF020434) cyclophilin [Arabidopsis thaliana]

Seq. No.	224521
Seq. ID	LIB3166-013-P1-K1-A4
Method	BLASTX
NCBI GI	g4510376
BLAST score	362
E value	2.0e-34
Match length	144
% identity	54
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	224522
Seq. ID	LIB3166-013-P1-K1-B12
Method	BLASTX
NCBI GI	g4107276
BLAST score	261
E value	1.0e-22
Match length	59
% identity	90
NCBI Description	(X98506) acetyl-CoA synthetase [Solanum tuberosum]

Seq. No.	224523
Seq. ID	LIB3166-013-P1-K1-B2
Method	BLASTX
NCBI GI	g3451072
BLAST score	240
E value	2.0e-20
Match length	72
% identity	58
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	224524
Seq. ID	LIB3166-013-P1-K1-B6
Method	BLASTX
NCBI GI	g113363
BLAST score	511
E value	2.0e-54
Match length	129
% identity	77
NCBI Description	ALCOHOL DEHYDROGENASE 1 >gi_279445_pir__DEPJA1 alcohol dehydrogenase (EC 1.1.1.1) 1 - garden petunia >gi_20506_emb_CAA38039_ (X54106) alcohol dehydrogenase [Petunia x hybrida]

Seq. No.	224525
Seq. ID	LIB3166-013-P1-K1-B7
Method	BLASTX
NCBI GI	g4314355
BLAST score	305
E value	8.0e-28
Match length	88
% identity	60

NCBI Description (AC006340) unknown protein [Arabidopsis thaliana]

Seq. No. 224526
Seq. ID LIB3166-013-P1-K1-B9
Method BLASTX
NCBI GI g2522534
BLAST score 185
E value 2.0e-14
Match length 86
% identity 48
NCBI Description (AF027302) TNF-alpha stimulated ABC protein [Homo sapiens]

Seq. No. 224527
Seq. ID LIB3166-013-P1-K1-C1
Method BLASTX
NCBI GI g3269293
BLAST score 276
E value 1.0e-24
Match length 103
% identity 57
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 224528
Seq. ID LIB3166-013-P1-K1-C11
Method BLASTX
NCBI GI g2961378
BLAST score 574
E value 2.0e-59
Match length 143
% identity 39
NCBI Description (AL022141) putative protein [Arabidopsis thaliana]

Seq. No. 224529
Seq. ID LIB3166-013-P1-K1-C5
Method BLASTX
NCBI GI g3021489
BLAST score 164
E value 2.0e-15
Match length 88
% identity 62
NCBI Description (AJ224934) histone H2B [Lycopersicon esculentum]

Seq. No. 224530
Seq. ID LIB3166-013-P1-K1-C6
Method BLASTX
NCBI GI g3122388
BLAST score 610
E value 1.0e-63
Match length 131
% identity 31
NCBI Description WD-40 REPEAT PROTEIN MSI2 >gi_2394231 (AF016847) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No. 224531
Seq. ID LIB3166-013-P1-K1-C7
Method BLASTX
NCBI GI g4510345

BLAST score	275
E value	2.0e-24
Match length	63
% identity	75
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	224532
Seq. ID	LIB3166-013-P1-K1-C9
Method	BLASTX
NCBI GI	g3660552
BLAST score	221
E value	5.0e-18
Match length	51
% identity	76
NCBI Description	(AB013817) DREB1C [Arabidopsis thaliana] >gi_3738228_dbj_BAA33793_ (AB007789) DREB1C [Arabidopsis thaliana] >gi_3907541 (AF062925) transcriptional activator CBF1 homolog [Arabidopsis thaliana] >gi_4322228_gb_AAD15976_ (AF074601) CRT/DRE binding factor 2 [Arabidopsis thaliana]

Seq. No.	224533
Seq. ID	LIB3166-013-P1-K1-D2
Method	BLASTX
NCBI GI	g3367593
BLAST score	251
E value	2.0e-21
Match length	120
% identity	58
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana] >gi_3805841_emb_CAA21461_ (AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	224534
Seq. ID	LIB3166-013-P1-K1-D3
Method	BLASTX
NCBI GI	g1168734
BLAST score	503
E value	4.0e-51
Match length	133
% identity	77
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi_288753_emb_CAA79622_ (Z19568) cinnamyl alcohol dehydrogenase [Populus deltoides]

Seq. No.	224535
Seq. ID	LIB3166-013-P1-K1-E10
Method	BLASTX
NCBI GI	g3894173
BLAST score	146
E value	3.0e-09
Match length	32
% identity	75
NCBI Description	(AC005312) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224536
Seq. ID	LIB3166-013-P1-K1-E11

Method	BLASTX
NCBI GI	g3123271
BLAST score	262
E value	3.0e-23
Match length	59
% identity	86
NCBI Description	40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No.	224537
Seq. ID	LIB3166-013-P1-K1-E5
Method	BLASTX
NCBI GI	g3193292
BLAST score	517
E value	9.0e-53
Match length	122
% identity	85
NCBI Description	(AF069298) similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) [Arabidopsis thaliana]

Seq. No.	224538
Seq. ID	LIB3166-013-P1-K1-E9
Method	BLASTX
NCBI GI	g2754746
BLAST score	309
E value	2.0e-28
Match length	143
% identity	50
NCBI Description	(U85448) sucrose-phosphate synthase [Actinidia deliciosa]

Seq. No.	224539
Seq. ID	LIB3166-013-P1-K1-F1
Method	BLASTX
NCBI GI	g2736288
BLAST score	146
E value	3.0e-09
Match length	33
% identity	79
NCBI Description	(AF031080) isopentenyl diphosphate isomerase II [Camptotheca acuminata]

Seq. No.	224540
Seq. ID	LIB3166-013-P1-K1-F10
Method	BLASTX
NCBI GI	g1332579
BLAST score	267
E value	5.0e-24
Match length	72
% identity	7
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	224541
Seq. ID	LIB3166-013-P1-K1-F12
Method	BLASTX
NCBI GI	g1350777
BLAST score	324

E value	4.0e-30
Match length	75
% identity	87
NCBI Description	60S RIBOSOMAL PROTEIN L9 >gi_971282_dbj_BAA07209_ (D38012) ribosomal protein L9 [Oryza sativa]

Seq. No.	224542
Seq. ID	LIB3166-013-P1-K1-F2
Method	BLASTX
NCBI GI	g4090533
BLAST score	460
E value	3.0e-46
Match length	101
% identity	82
NCBI Description	(U68215) ACC oxidase [Carica papaya]

Seq. No.	224543
Seq. ID	LIB3166-013-P1-K1-F6
Method	BLASTX
NCBI GI	g2146739
BLAST score	262
E value	8.0e-23
Match length	118
% identity	51
NCBI Description	hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521 (U28214) hexokinase 1 [Arabidopsis thaliana]

Seq. No.	224544
Seq. ID	LIB3166-013-P1-K1-F7
Method	BLASTX
NCBI GI	g400976
BLAST score	426
E value	1.0e-48
Match length	108
% identity	96
NCBI Description	RAS-RELATED PROTEIN RHA1 >gi_478671_pir__S23727 GTP-binding protein RHA1 - Arabidopsis thaliana >gi_16484_emb_CAA41863_ (X59152) RHA1 [Arabidopsis thaliana] >gi_397594_emb_CAA80534_ (Z22958) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	224545
Seq. ID	LIB3166-013-P1-K1-F9
Method	BLASTX
NCBI GI	g1888357
BLAST score	499
E value	1.0e-50
Match length	123
% identity	76
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No.	224546
Seq. ID	LIB3166-013-P1-K1-G10
Method	BLASTX
NCBI GI	g2673910

BLAST score 148
E value 2.0e-09
Match length 67
% identity 54
NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No. 224547
Seq. ID LIB3166-013-P1-K1-G12
Method BLASTX
NCBI GI g1061420
BLAST score 512
E value 4.0e-52
Match length 127
% identity 82
NCBI Description (U38965) p-type H+-ATPase [Vicia faba]

Seq. No. 224548
Seq. ID LIB3166-013-P1-K1-G2
Method BLASTX
NCBI GI g3341468
BLAST score 170
E value 5.0e-12
Match length 85
% identity 45
NCBI Description (AJ009594) Dof zinc finger protein [Nicotiana tabacum]

Seq. No. 224549
Seq. ID LIB3166-013-P1-K1-G3
Method BLASTX
NCBI GI g1655653
BLAST score 113
E value 6.0e-09
Match length 100
% identity 38
NCBI Description (Z81368) hypothetical protein Rv2406c [Mycobacterium tuberculosis]

Seq. No. 224550
Seq. ID LIB3166-013-P1-K1-G5
Method BLASTX
NCBI GI g3136336
BLAST score 415
E value 6.0e-41
Match length 81
% identity 52
NCBI Description (AF064552) calmodulin; Cam [Apium graveolens]

Seq. No. 224551
Seq. ID LIB3166-013-P1-K1-G6
Method BLASTX
NCBI GI g2281090
BLAST score 394
E value 3.0e-38
Match length 115
% identity 65
NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224552
Seq. ID	LIB3166-013-P1-K1-G7
Method	BLASTX
NCBI GI	g629722
BLAST score	175
E value	1.0e-12
Match length	122
% identity	35
NCBI Description	finger protein pcp1 - potato >gi_563623_emb_CAA57772_ (X82328) putative DNA/RNA binding protein [Solanum tuberosum]

Seq. No.	224553
Seq. ID	LIB3166-013-P1-K1-G8
Method	BLASTX
NCBI GI	g4406787
BLAST score	388
E value	1.0e-37
Match length	102
% identity	77
NCBI Description	(AC006532) NADH dehydrogenase [Arabidopsis thaliana]

Seq. No.	224554
Seq. ID	LIB3166-013-P1-K1-G9
Method	BLASTX
NCBI GI	g3892059
BLAST score	270
E value	1.0e-23
Match length	143
% identity	48
NCBI Description	(AC002330) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	224555
Seq. ID	LIB3166-013-P1-K1-H10
Method	BLASTX
NCBI GI	g2983778
BLAST score	164
E value	2.0e-11
Match length	116
% identity	36
NCBI Description	(AE000736) hypothetical protein [Aquifex aeolicus]

Seq. No.	224556
Seq. ID	LIB3166-013-P1-K1-H5
Method	BLASTX
NCBI GI	g4512694
BLAST score	238
E value	6.0e-20
Match length	133
% identity	41
NCBI Description	(AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224557
Seq. ID	LIB3166-013-P1-K1-H7
Method	BLASTX
NCBI GI	g464621

BLAST score	278
E value	9.0e-25
Match length	104
% identity	54
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	224558
Seq. ID	LIB3166-013-P1-K1-H9
Method	BLASTX
NCBI GI	g3334320
BLAST score	482
E value	1.0e-48
Match length	108
% identity	92
NCBI Description	40S RIBOSOMAL PROTEIN SA (P40) >gi_2444420 (AF020553) ribosome-associated protein p40 [Glycine max]

Seq. No.	224559
Seq. ID	LIB3166-014-P1-K1-A1
Method	BLASTX
NCBI GI	g3540195
BLAST score	441
E value	8.0e-44
Match length	135
% identity	31
NCBI Description	(AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No.	224560
Seq. ID	LIB3166-014-P1-K1-A10
Method	BLASTX
NCBI GI	g4467147
BLAST score	194
E value	5.0e-22
Match length	110
% identity	56
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	224561
Seq. ID	LIB3166-014-P1-K1-A12
Method	BLASTX
NCBI GI	g541546
BLAST score	306
E value	6.0e-38
Match length	110
% identity	16
NCBI Description	ubiquitin precursor - Volvox carteri >gi_395295_emb_CAA52290_ (X74214) polyubiquitin [Volvox carteri]

Seq. No.	224562
Seq. ID	LIB3166-014-P1-K1-A4
Method	BLASTX
NCBI GI	g2982303
BLAST score	574

E value 2.0e-59
Match length 131
% identity 79
NCBI Description (AF051236) hypothetical protein [Picea mariana]

Seq. No. 224563
Seq. ID LIB3166-014-P1-K1-A8
Method BLASTX
NCBI GI g3264767
BLAST score 500
E value 9.0e-51
Match length 119
% identity 76
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No. 224564
Seq. ID LIB3166-014-P1-K1-B1
Method BLASTX
NCBI GI g4454050
BLAST score 301
E value 2.0e-27
Match length 79
% identity 66
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

Seq. No. 224565
Seq. ID LIB3166-014-P1-K1-B10
Method BLASTX
NCBI GI g2190419
BLAST score 202
E value 8.0e-16
Match length 109
% identity 40
NCBI Description (Y13632) dem [Lycopersicon esculentum]

Seq. No. 224566
Seq. ID LIB3166-014-P1-K1-B2
Method BLASTX
NCBI GI g1432056
BLAST score 184
E value 1.0e-13
Match length 110
% identity 45
NCBI Description (U56834) WRKY3 [Petroselinum crispum]

Seq. No. 224567
Seq. ID LIB3166-014-P1-K1-B5
Method BLASTX
NCBI GI g2318137
BLAST score 590
E value 2.0e-61
Match length 117
% identity 97
NCBI Description (AF014052) Mg protoporphyrin IX chelatase [Nicotiana tabacum]

Seq. No. 224568

Seq. ID	LIB3166-014-P1-K1-B6
Method	BLASTX
NCBI GI	g2970654
BLAST score	184
E value	8.0e-14
Match length	83
% identity	58
NCBI Description	(AF052058) ferritin subunit cowpea2 precursor [Vigna unguiculata]

Seq. No.	224569
Seq. ID	LIB3166-014-P1-K1-B7
Method	BLASTX
NCBI GI	g2970654
BLAST score	215
E value	2.0e-17
Match length	97
% identity	57
NCBI Description	(AF052058) ferritin subunit cowpea2 precursor [Vigna unguiculata]

Seq. No.	224570
Seq. ID	LIB3166-014-P1-K1-B9
Method	BLASTX
NCBI GI	g1814424
BLAST score	575
E value	2.0e-59
Match length	134
% identity	78
NCBI Description	(U85254) homeodomain protein AHDP [Arabidopsis thaliana]

Seq. No.	224571
Seq. ID	LIB3166-014-P1-K1-C12
Method	BLASTX
NCBI GI	g231675
BLAST score	163
E value	1.0e-23
Match length	64
% identity	86
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi_282955_pir__S23525 cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) - common tobacco >gi_19839_emb_CAA44216_ (X62343) cinnamyl-alcohol dehydrogenase [Nicotiana tabacum]

Seq. No.	224572
Seq. ID	LIB3166-014-P1-K1-C2
Method	BLASTX
NCBI GI	g4204293
BLAST score	503
E value	4.0e-51
Match length	125
% identity	76
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	224573
Seq. ID	LIB3166-014-P1-K1-C6

Method	BLASTX
NCBI GI	g2980770
BLAST score	410
E value	3.0e-40
Match length	125
% identity	66
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	224574
Seq. ID	LIB3166-014-P1-K1-C7
Method	BLASTX
NCBI GI	g2980770
BLAST score	420
E value	2.0e-41
Match length	133
% identity	65
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	224575
Seq. ID	LIB3166-014-P1-K1-C8
Method	BLASTX
NCBI GI	g4512651
BLAST score	520
E value	4.0e-53
Match length	133
% identity	68
NCBI Description	(AC007048) putative tyrosine transaminase [Arabidopsis thaliana]

Seq. No.	224576
Seq. ID	LIB3166-014-P1-K1-C9
Method	BLASTX
NCBI GI	g289920
BLAST score	384
E value	3.0e-37
Match length	102
% identity	75
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	224577
Seq. ID	LIB3166-014-P1-K1-D11
Method	BLASTX
NCBI GI	g1652104
BLAST score	330
E value	8.0e-31
Match length	125
% identity	51
NCBI Description	(D90902) hypothetical protein [Synechocystis sp.]

Seq. No.	224578
Seq. ID	LIB3166-014-P1-K1-D12
Method	BLASTX
NCBI GI	g2129921
BLAST score	179
E value	3.0e-13
Match length	48

% identity	73
NCBI Description	hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]

Seq. No.	224579
Seq. ID	LIB3166-014-P1-K1-D3
Method	BLASTX
NCBI GI	g2262111
BLAST score	197
E value	3.0e-15
Match length	75
% identity	55
NCBI Description	(AC002343) ribitol dehydrogenase isolog [Arabidopsis thaliana]

Seq. No.	224580
Seq. ID	LIB3166-014-P1-K1-D4
Method	BLASTX
NCBI GI	g1769887
BLAST score	556
E value	3.0e-57
Match length	129
% identity	85
NCBI Description	(X95736) amino acid permease 6 [Arabidopsis thaliana]

Seq. No.	224581
Seq. ID	LIB3166-014-P1-K1-D9
Method	BLASTX
NCBI GI	g1906828
BLAST score	432
E value	8.0e-43
Match length	104
% identity	84
NCBI Description	(Y11828) heat shock protein [Arabidopsis thaliana]

Seq. No.	224582
Seq. ID	LIB3166-014-P1-K1-E1
Method	BLASTX
NCBI GI	g1370180
BLAST score	233
E value	2.0e-19
Match length	54
% identity	87
NCBI Description	(Z73939) RAB5B [Lotus japonicus]

Seq. No.	224583
Seq. ID	LIB3166-014-P1-K1-E10
Method	BLASTX
NCBI GI	g4008441
BLAST score	379
E value	1.0e-36
Match length	102
% identity	69
NCBI Description	(AL034488) predicted using Genefinder; cDNA EST yk433c6.3 comes from this gene; cDNA EST EMBL:D72601 comes from this gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST yk433c6.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	224584
Seq. ID	LIB3166-014-P1-K1-E11
Method	BLASTX
NCBI GI	g3915847
BLAST score	371
E value	1.0e-35
Match length	81
% identity	86
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	224585
Seq. ID	LIB3166-014-P1-K1-E3
Method	BLASTX
NCBI GI	g3024017
BLAST score	430
E value	2.0e-42
Match length	83
% identity	98
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C) >gi_2565421 (AF026804) eukaryotic translation initiation factor eIF-1A [Onobrychis viciifolia]

Seq. No.	224586
Seq. ID	LIB3166-014-P1-K1-E4
Method	BLASTX
NCBI GI	g2662415
BLAST score	284
E value	2.0e-25
Match length	76
% identity	61
NCBI Description	(U97494) metallothionein-like protein [Prunus armeniaca]

Seq. No.	224587
Seq. ID	LIB3166-014-P1-K1-E5
Method	BLASTX
NCBI GI	g3063396
BLAST score	286
E value	1.0e-42
Match length	110
% identity	82
NCBI Description	(AB012947) vcCyP [Vicia faba]

Seq. No.	224588
Seq. ID	LIB3166-014-P1-K1-E8
Method	BLASTX
NCBI GI	g2244835
BLAST score	298
E value	4.0e-27
Match length	91
% identity	66
NCBI Description	(Z97337) protein kinase homolog [Arabidopsis thaliana]

Seq. No.	224589
Seq. ID	LIB3166-014-P1-K1-E9
Method	BLASTX

NCBI GI	g3738325
BLAST score	403
E value	2.0e-39
Match length	110
% identity	71
NCBI Description	(AC005170) putative CaMB-channel protein [Arabidopsis thaliana]

Seq. No.	224590
Seq. ID	LIB3166-014-P1-K1-F1
Method	BLASTX
NCBI GI	g2924777
BLAST score	376
E value	3.0e-36
Match length	130
% identity	6
NCBI Description	(AC002334) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	224591
Seq. ID	LIB3166-014-P1-K1-F10
Method	BLASTX
NCBI GI	g2662415
BLAST score	173
E value	2.0e-12
Match length	56
% identity	54
NCBI Description	(U97494) metallothionein-like protein [Prunus armeniaca]

Seq. No.	224592
Seq. ID	LIB3166-014-P1-K1-F2
Method	BLASTX
NCBI GI	g1351271
BLAST score	331
E value	6.0e-31
Match length	118
% identity	62
NCBI Description	TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) >gi_1084309_pir__S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi_806312 (L36387) triosephosphate isomerase, chloroplast isozyme [Spinacia oleracea]

Seq. No.	224593
Seq. ID	LIB3166-014-P1-K1-F3
Method	BLASTX
NCBI GI	g1814424
BLAST score	582
E value	2.0e-60
Match length	134
% identity	79
NCBI Description	(U85254) homeodomain protein AHDP [Arabidopsis thaliana]

Seq. No.	224594
Seq. ID	LIB3166-014-P1-K1-F8
Method	BLASTX
NCBI GI	g115484

BLAST score	555
E value	3.0e-57
Match length	108
% identity	59
NCBI Description	CALMODULIN 1 >gi_71684_pir__MCPZDC calmodulin - carrot >gi_478632_pir__S22971 calmodulin - trumpet lily >gi_541839_pir__S40301 calmodulin - Red bryony >gi_2129970_pir__S70768 calmodulin CAM81 - garden petunia >gi_18326_emb_CAA42423_ (X59751) calmodulin [Daucus carota] >gi_19447_emb_CAA78301_ (Z12839) calmodulin [Lilium longiflorum] >gi_169207 (M80836) calmodulin [Petunia hybrida] >gi_308900 (L18912) calmodulin [Lilium longiflorum] >gi_505154_emb_CAA43143_ (X60738) Calmodulin [Malus domestica] >gi_535444 (U13882) calmodulin [Pisum sativum] >gi_445602_prf__1909349A calmodulin [Daucus carota]

Seq. No.	224595
Seq. ID	LIB3166-014-P1-K1-F9
Method	BLASTX
NCBI GI	g1709930
BLAST score	359
E value	2.0e-35
Match length	94
% identity	81
NCBI Description	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE PRECURSOR (AIR CARBOXYLASE) (AIRC) >gi_629656_pir__S43322 phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) - moth bean >gi_349159 (L22584) 5-aminoimidazole ribonucleotide carboxylase [Vigna aconitifolia]

Seq. No.	224596
Seq. ID	LIB3166-014-P1-K1-G1
Method	BLASTX
NCBI GI	g2809251
BLAST score	152
E value	2.0e-10
Match length	34
% identity	74
NCBI Description	(AC002560) F21B7.20 [Arabidopsis thaliana]

Seq. No.	224597
Seq. ID	LIB3166-014-P1-K1-G10
Method	BLASTX
NCBI GI	g2245087
BLAST score	218
E value	1.0e-17
Match length	86
% identity	44
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224598
Seq. ID	LIB3166-014-P1-K1-G5
Method	BLASTX
NCBI GI	g4127456
BLAST score	303
E value	1.0e-27

Match length	114
% identity	59
NCBI Description	(AJ010818) Cpn21 protein [Arabidopsis thaliana]

Seq. No.	224599
Seq. ID	LIB3166-014-P1-K1-G6
Method	BLASTX
NCBI GI	g2088651
BLAST score	482
E value	1.0e-48
Match length	123
% identity	70
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	224600
Seq. ID	LIB3166-014-P1-K1-G7
Method	BLASTX
NCBI GI	g2088651
BLAST score	432
E value	8.0e-43
Match length	118
% identity	66
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	224601
Seq. ID	LIB3166-014-P1-K1-G9
Method	BLASTX
NCBI GI	g3212859
BLAST score	505
E value	2.0e-51
Match length	112
% identity	55
NCBI Description	(AC004005) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224602
Seq. ID	LIB3166-014-P1-K1-H1
Method	BLASTX
NCBI GI	g2191136
BLAST score	312
E value	1.0e-28
Match length	110
% identity	60
NCBI Description	(AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290 [Arabidopsis thaliana]

Seq. No.	224603
Seq. ID	LIB3166-014-P1-K1-H10
Method	BLASTX
NCBI GI	g4510381
BLAST score	219
E value	7.0e-18
Match length	105
% identity	52

NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 224604
Seq. ID LIB3166-014-P1-K1-H11
Method BLASTX
NCBI GI g2760322
BLAST score 356
E value 7.0e-34
Match length 113
% identity 56
NCBI Description (AC002130) F1N21.7 [Arabidopsis thaliana]

Seq. No. 224605
Seq. ID LIB3166-014-P1-K1-H2
Method BLASTX
NCBI GI g4049349
BLAST score 363
E value 1.0e-34
Match length 102
% identity 71
NCBI Description (AL034567) ubiquinol-cytochrome c reductase-like protein [Arabidopsis thaliana]

Seq. No. 224606
Seq. ID LIB3166-014-P1-K1-H6
Method BLASTX
NCBI GI g2209332
BLAST score 365
E value 7.0e-35
Match length 102
% identity 73
NCBI Description (U89272) chloroplast membrane protein ALBINO3 [Arabidopsis thaliana] >gi_3927828 (AC005727) chloroplast membrane protein ALBINO3 [Arabidopsis thaliana]

Seq. No. 224607
Seq. ID LIB3166-014-P1-K1-H8
Method BLASTX
NCBI GI g1237250
BLAST score 545
E value 5.0e-56
Match length 133
% identity 77
NCBI Description (X96784) cytochrome P450 [Nicotiana tabacum]

Seq. No. 224608
Seq. ID LIB3166-014-P1-K1-H9
Method BLASTX
NCBI GI g3269292
BLAST score 231
E value 3.0e-19
Match length 64
% identity 66
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 224609
Seq. ID LIB3166-015-P1-K1-A2

Method	BLASTX
NCBI GI	g3885334
BLAST score	502
E value	7.0e-51
Match length	147
% identity	71
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	224610
Seq. ID	LIB3166-015-P1-K1-A4
Method	BLASTX
NCBI GI	g417103
BLAST score	498
E value	1.0e-50
Match length	111
% identity	94
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	224611
Seq. ID	LIB3166-015-P1-K1-A7
Method	BLASTX
NCBI GI	g4559388
BLAST score	420
E value	3.0e-41
Match length	132
% identity	51
NCBI Description	(AC006526) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224612
Seq. ID	LIB3166-015-P1-K1-B1
Method	BLASTX
NCBI GI	g3759184
BLAST score	351
E value	3.0e-33
Match length	104
% identity	66
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	224613
Seq. ID	LIB3166-015-P1-K1-B2
Method	BLASTX
NCBI GI	g132944
BLAST score	215
E value	5.0e-22
Match length	92
% identity	63
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No.	224614
Seq. ID	LIB3166-015-P1-K1-B4
Method	BLASTX
NCBI GI	g3420049
BLAST score	172
E value	3.0e-12
Match length	131
% identity	40
NCBI Description	(AC004680) putative protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	224615
Seq. ID	LIB3166-015-P1-K1-B5
Method	BLASTX
NCBI GI	g2191136
BLAST score	312
E value	1.0e-28
Match length	110
% identity	60
NCBI Description	(AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290 [Arabidopsis thaliana]

Seq. No.	224616
Seq. ID	LIB3166-015-P1-K1-C10
Method	BLASTX
NCBI GI	g3953463
BLAST score	210
E value	1.0e-16
Match length	60
% identity	60
NCBI Description	(AC002328) F20N2.8 [Arabidopsis thaliana]

Seq. No.	224617
Seq. ID	LIB3166-015-P1-K1-C12
Method	BLASTX
NCBI GI	g728906
BLAST score	330
E value	8.0e-31
Match length	126
% identity	55
NCBI Description	PROBABLE CALCIUM-TRANSPORTING ATPASE 5 >gi_1077722_pir__S50669 hypothetical protein YER166w - yeast (Saccharomyces cerevisiae) >gi_603407 (U18922)

Yer166wp [Saccharomyces cerevisiae]

Seq. No.	224618
Seq. ID	LIB3166-015-P1-K1-C2
Method	BLASTX
NCBI GI	g548852
BLAST score	347
E value	8.0e-33
Match length	82
% identity	79
NCBI Description	40S RIBOSOMAL PROTEIN S21 >gi_481227_pir__S38357 ribosomal protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S subunit ribosomal protein [Oryza sativa]

Seq. No.	224619
Seq. ID	LIB3166-015-P1-K1-C5
Method	BLASTX
NCBI GI	g3249064
BLAST score	325
E value	3.0e-30
Match length	119
% identity	55
NCBI Description	(AC004473) Strong similarity to trehalose-6-phosphate synthase homolog gb_2245136 from A. thaliana chromosome 4 contig gb_Z97344. [Arabidopsis thaliana]

Seq. No.	224620
Seq. ID	LIB3166-015-P1-K1-C6
Method	BLASTX
NCBI GI	g4218116
BLAST score	162
E value	5.0e-11
Match length	53
% identity	58
NCBI Description	(AL035353) putative protein [Arabidopsis thaliana]

Seq. No.	224621
Seq. ID	LIB3166-015-P1-K1-C8
Method	BLASTX
NCBI GI	g1707364
BLAST score	636
E value	1.0e-66
Match length	137
% identity	89
NCBI Description	(X94626) AATP2 [Arabidopsis thaliana]

Seq. No.	224622
Seq. ID	LIB3166-015-P1-K1-D1
Method	BLASTX
NCBI GI	g2911042
BLAST score	304
E value	1.0e-27
Match length	75
% identity	80
NCBI Description	(AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	224623
Seq. ID	LIB3166-015-P1-K1-D2
Method	BLASTX
NCBI GI	g2213425
BLAST score	596
E value	6.0e-62
Match length	143
% identity	43
NCBI Description	(Z97064) hypothetical protein [Citrus x paradisi]

Seq. No.	224624
Seq. ID	LIB3166-015-P1-K1-D3
Method	BLASTX
NCBI GI	g2191135
BLAST score	194
E value	8.0e-15
Match length	92
% identity	38
NCBI Description	(AF007269) A_IG002N01.14 gene product [Arabidopsis thaliana]

Seq. No.	224625
Seq. ID	LIB3166-015-P1-K1-D8
Method	BLASTX
NCBI GI	g2791834
BLAST score	604
E value	7.0e-63
Match length	117
% identity	98
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No.	224626
Seq. ID	LIB3166-015-P1-K1-D9
Method	BLASTX
NCBI GI	g4262236
BLAST score	458
E value	9.0e-46
Match length	123
% identity	69
NCBI Description	(AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	224627
Seq. ID	LIB3166-015-P1-K1-E12
Method	BLASTX
NCBI GI	g3738259
BLAST score	472
E value	4.0e-49
Match length	135
% identity	79
NCBI Description	(AB018411) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	224628
Seq. ID	LIB3166-015-P1-K1-E2
Method	BLASTX
NCBI GI	g2493495

BLAST score	499
E value	1.0e-50
Match length	116
% identity	78
NCBI Description	SERINE CARBOXYPEPTIDASE-LIKE >gi_2129878_pir__S72370 carboxypeptidase - garden pea (fragment) >gi_1089904_emb_CAA92216_ (Z68130) carboxypeptidase [Pisum sativum] >gi_1587217_prf__2206338A Ser carboxypeptidase [Pisum sativum]

Seq. No.	224629
Seq. ID	LIB3166-015-P1-K1-E3
Method	BLASTX
NCBI GI	g4204697
BLAST score	340
E value	6.0e-32
Match length	98
% identity	68
NCBI Description	(AF117063) putative inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana]

Seq. No.	224630
Seq. ID	LIB3166-015-P1-K1-E4
Method	BLASTX
NCBI GI	g4115377
BLAST score	381
E value	9.0e-37
Match length	107
% identity	73
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	224631
Seq. ID	LIB3166-015-P1-K1-E6
Method	BLASTX
NCBI GI	g4337189
BLAST score	472
E value	2.0e-47
Match length	142
% identity	61
NCBI Description	(AC006403) putative calmodulin-binding protein [Arabidopsis thaliana]

Seq. No.	224632
Seq. ID	LIB3166-015-P1-K1-E7
Method	BLASTX
NCBI GI	g4454457
BLAST score	339
E value	8.0e-32
Match length	71
% identity	89
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	224633
Seq. ID	LIB3166-015-P1-K1-E8
Method	BLASTX
NCBI GI	g2739376
BLAST score	262

E value 9.0e-23
Match length 68
% identity 72
NCBI Description (AC002505) putative permease [Arabidopsis thaliana]

Seq. No. 224634
Seq. ID LIB3166-015-P1-K1-E9
Method BLASTX
NCBI GI g4099914
BLAST score 301
E value 2.0e-27
Match length 96
% identity 62
NCBI Description (U91857) ethylene-responsive element binding protein homolog [Stylosanthes hamata]

Seq. No. 224635
Seq. ID LIB3166-015-P1-K1-F1
Method BLASTX
NCBI GI g22240
BLAST score 505
E value 2.0e-51
Match length 126
% identity 80
NCBI Description (X07157) GADPH (383 AA) [Zea mays]

Seq. No. 224636
Seq. ID LIB3166-015-P1-K1-F10
Method BLASTX
NCBI GI g2493318
BLAST score 240
E value 3.0e-20
Match length 90
% identity 51
NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_ (Z25471) blue copper protein [Pisum sativum] >gi_1098264_prf__2115352A blue Cu protein [Pisum sativum]

Seq. No. 224637
Seq. ID LIB3166-015-P1-K1-F11
Method BLASTX
NCBI GI g2388689
BLAST score 246
E value 9.0e-22
Match length 103
% identity 60
NCBI Description (AF016633) GH1 protein [Glycine max]

Seq. No. 224638
Seq. ID LIB3166-015-P1-K1-F12
Method BLASTX
NCBI GI g2440044
BLAST score 450
E value 6.0e-52
Match length 131
% identity 80
NCBI Description (AJ001293) major intrinsic protein PIPB [Craterostigma

plantagineum]

Seq. No.	224639
Seq. ID	LIB3166-015-P1-K1-F3
Method	BLASTX
NCBI GI	g114661
BLAST score	602
E value	1.0e-62
Match length	142
% identity	84
NCBI Description	ATP SYNTHASE A CHAIN PRECURSOR (SUBUNIT IV) >gi_67924_pir__LWNT6 H+-transporting ATP synthase (EC 3.6.1.34) chain a - common tobacco chloroplast >gi_11813_emb_CAA77344_ (Z00044) ATPase sunthase IV subunit [Nicotiana tabacum] >gi_225273_prf__1211235H ATPase a [Nicotiana tabacum]

Seq. No.	224640
Seq. ID	LIB3166-015-P1-K1-F5
Method	BLASTX
NCBI GI	g3342798
BLAST score	386
E value	2.0e-37
Match length	128
% identity	59
NCBI Description	(AF061240) glutamine cyclotransferase precursor [Carica papaya]

Seq. No.	224641
Seq. ID	LIB3166-015-P1-K1-F8
Method	BLASTX
NCBI GI	g3142292
BLAST score	318
E value	8.0e-34
Match length	106
% identity	67
NCBI Description	(AC002411) Contains similarity to tetratricopeptide repeat protein gb_U46571 from home sapiens. EST gb_Z47802 and gb_Z48402 come from this gene. [Arabidopsis thaliana]

Seq. No.	224642
Seq. ID	LIB3166-015-P1-K1-G4
Method	BLASTX
NCBI GI	g2384696
BLAST score	335
E value	2.0e-31
Match length	139
% identity	53
NCBI Description	(AF013216) acyl-CoA oxidase [Myxococcus xanthus]

Seq. No.	224643
Seq. ID	LIB3166-015-P1-K1-G5
Method	BLASTX
NCBI GI	g4510363
BLAST score	510
E value	2.0e-53
Match length	124

% identity	86
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	224644
Seq. ID	LIB3166-015-P1-K1-G8
Method	BLASTX
NCBI GI	g1255951
BLAST score	619
E value	1.0e-64
Match length	143
% identity	81
NCBI Description	(X96932) PS60 [Nicotiana tabacum]

Seq. No.	224645
Seq. ID	LIB3166-015-P1-K1-H1
Method	BLASTX
NCBI GI	g3063396
BLAST score	457
E value	1.0e-45
Match length	116
% identity	77
NCBI Description	(AB012947) vcCyP [Vicia faba]

Seq. No.	224646
Seq. ID	LIB3166-015-P1-K1-H11
Method	BLASTX
NCBI GI	g832876
BLAST score	461
E value	3.0e-46
Match length	96
% identity	94
NCBI Description	(L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi_1097368_prf__2113407A ascorbate free radical reductase [Lycopersicon esculentum]

Seq. No.	224647
Seq. ID	LIB3166-015-P1-K1-H8
Method	BLASTX
NCBI GI	g4539452
BLAST score	349
E value	6.0e-38
Match length	122
% identity	62
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	224648
Seq. ID	LIB3166-016-P1-K1-A1
Method	BLASTX
NCBI GI	g1871185
BLAST score	536
E value	6.0e-55
Match length	132
% identity	72
NCBI Description	(U90439) seven in absentia isolog [Arabidopsis thaliana]

Seq. No.	224649
Seq. ID	LIB3166-016-P1-K1-A10
Method	BLASTX
NCBI GI	g2738949
BLAST score	358
E value	3.0e-34
Match length	80
% identity	85
NCBI Description	(AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa]

Seq. No.	224650
Seq. ID	LIB3166-016-P1-K1-A11
Method	BLASTX
NCBI GI	g1076603
BLAST score	164
E value	1.0e-11
Match length	71
% identity	55
NCBI Description	vsf-1 protein - tomato

Seq. No.	224651
Seq. ID	LIB3166-016-P1-K1-A2
Method	BLASTX
NCBI GI	g3182981
BLAST score	316
E value	3.0e-29
Match length	82
% identity	76
NCBI Description	CELL ELONGATION PROTEIN DIMINUTO >gi_1695692_dbj_BAA13096_ (D86494) diminuto [Pisum sativum]

Seq. No.	224652
Seq. ID	LIB3166-016-P1-K1-A5
Method	BLASTX
NCBI GI	g4220541
BLAST score	139
E value	1.0e-08
Match length	70
% identity	43
NCBI Description	(AL035356) Rab geranylgeranyl transferase like protein [Arabidopsis thaliana]

Seq. No.	224653
Seq. ID	LIB3166-016-P1-K1-A6
Method	BLASTX
NCBI GI	g2815246
BLAST score	223
E value	3.0e-18
Match length	55
% identity	73
NCBI Description	(X95709) class I type 2 metallothionein [Cicer arietinum]

Seq. No.	224654
Seq. ID	LIB3166-016-P1-K1-A7
Method	BLASTX
NCBI GI	g629600

BLAST score	409
E value	3.0e-40
Match length	95
% identity	74
NCBI Description	1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - wild cabbage >gi_562280_emb_CAA57724_ (X82273) 1-aminocyclopropane-1-carboxylate synthase [Brassica oleracea]

Seq. No.	224655
Seq. ID	LIB3166-016-P1-K1-A8
Method	BLASTX
NCBI GI	g1707922
BLAST score	599
E value	2.0e-62
Match length	128
% identity	88
NCBI Description	GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) >gi_1076255_pir__S51944 glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) large chain S1 precursor - beet >gi_556624_emb_CAA55516_ (X78900) glucose-1-phosphate adenylyltransferase [Beta vulgaris]

Seq. No.	224656
Seq. ID	LIB3166-016-P1-K1-A9
Method	BLASTX
NCBI GI	g1707922
BLAST score	322
E value	1.0e-30
Match length	114
% identity	63
NCBI Description	GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) >gi_1076255_pir__S51944 glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) large chain S1 precursor - beet >gi_556624_emb_CAA55516_ (X78900) glucose-1-phosphate adenylyltransferase [Beta vulgaris]

Seq. No.	224657
Seq. ID	LIB3166-016-P1-K1-B10
Method	BLASTX
NCBI GI	g3043428
BLAST score	419
E value	3.0e-41
Match length	92
% identity	85
NCBI Description	(AJ005346) 40S ribosomal protein S5 [Cicer arietinum]

Seq. No.	224658
Seq. ID	LIB3166-016-P1-K1-B11
Method	BLASTX
NCBI GI	g267120
BLAST score	266
E value	2.0e-23

Match length	101
% identity	57
NCBI Description	THIOREDOXIN F-TYPE PRECURSOR (TRX-F) >gi_100070_pir__S20929 thioredoxin f precursor - garden pea >gi_20907_emb_CAA45098_ (X63537) thioredoxin F [Pisum sativum] >gi_1388086 (U35830) thioredoxin f [Pisum sativum]
Seq. No.	224659
Seq. ID	LIB3166-016-P1-K1-B2
Method	BLASTX
NCBI GI	g3297816
BLAST score	550
E value	1.0e-56
Match length	126
% identity	83
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]
Seq. No.	224660
Seq. ID	LIB3166-016-P1-K1-B5
Method	BLASTX
NCBI GI	g1706319
BLAST score	334
E value	2.0e-31
Match length	102
% identity	61
NCBI Description	HISTIDINE DECARBOXYLASE (HDC) (TOM92) >gi_481829_pir__S39554 histidine decarboxylase (EC 4.1.1.22) - tomato >gi_416534_emb_CAA50719_ (X71900) histidine decarboxylase [Lycopersicon esculentum]
Seq. No.	224661
Seq. ID	LIB3166-016-P1-K1-B6
Method	BLASTX
NCBI GI	g113360
BLAST score	375
E value	5.0e-48
Match length	130
% identity	75
NCBI Description	ALCOHOL DEHYDROGENASE 1 >gi_100652_pir__JQ0474 alcohol dehydrogenase (EC 1.1.1.1) 1 - rice >gi_20165_emb_CAA34363_ (X16296) alcohol dehydrogenase 1 [Oryza sativa]
Seq. No.	224662
Seq. ID	LIB3166-016-P1-K1-C1
Method	BLASTX
NCBI GI	g2623309
BLAST score	159
E value	8.0e-11
Match length	107
% identity	37
NCBI Description	(AC002409) similar to tgacg-specific DNA-binding protein [Arabidopsis thaliana]
Seq. No.	224663
Seq. ID	LIB3166-016-P1-K1-C10
Method	BLASTX
NCBI GI	g3249105

BLAST score	318
E value	5.0e-32
Match length	117
% identity	67
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	224664
Seq. ID	LIB3166-016-P1-K1-C11
Method	BLASTX
NCBI GI	g479406
BLAST score	484
E value	2.0e-49
Match length	106
% identity	87
NCBI Description	chlorophyll a/b-binding protein - garden pea >gi_20671_emb_CAA49149_ (X69215) chlorophyll a/b-binding protein [Pisum sativum]

Seq. No.	224665
Seq. ID	LIB3166-016-P1-K1-C12
Method	BLASTX
NCBI GI	g1495804
BLAST score	220
E value	3.0e-18
Match length	90
% identity	53
NCBI Description	(X96406) 13-lipoxygenase [Solanum tuberosum]

Seq. No.	224666
Seq. ID	LIB3166-016-P1-K1-C3
Method	BLASTX
NCBI GI	g488727
BLAST score	381
E value	7.0e-37
Match length	84
% identity	75
NCBI Description	(X72676) 1-aminocyclopropane-1-carboxylate synthase [Brassica juncea]

Seq. No.	224667
Seq. ID	LIB3166-016-P1-K1-C4
Method	BLASTX
NCBI GI	g114682
BLAST score	206
E value	3.0e-16
Match length	71
% identity	63
NCBI Description	ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP) >gi_100471_pir__A35227 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, mitochondrial - sweet potato >gi_168270 (J05397) F-1-ATPase delta subunit precursor (EC 3.6.1.3) [Ipomoea batatas]

Seq. No.	224668
Seq. ID	LIB3166-016-P1-K1-C6

Method	BLASTX
NCBI GI	g2662341
BLAST score	483
E value	2.0e-52
Match length	116
% identity	88
NCBI Description	(D63580) EF-1 alpha [Oryza sativa] >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza sativa] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha [Oryza sativa]

Seq. No.	224669
Seq. ID	LIB3166-016-P1-K1-D11
Method	BLASTX
NCBI GI	g4406777
BLAST score	185
E value	8.0e-14
Match length	85
% identity	47
NCBI Description	(AC006532) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No.	224670
Seq. ID	LIB3166-016-P1-K1-D3
Method	BLASTX
NCBI GI	g4508070
BLAST score	377
E value	2.0e-36
Match length	121
% identity	55
NCBI Description	(AC005882) 24349 [Arabidopsis thaliana]

Seq. No.	224671
Seq. ID	LIB3166-016-P1-K1-D4
Method	BLASTX
NCBI GI	g289920
BLAST score	395
E value	2.0e-38
Match length	84
% identity	89
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	224672
Seq. ID	LIB3166-016-P1-K1-D8
Method	BLASTX
NCBI GI	g3402678
BLAST score	269
E value	7.0e-24
Match length	99
% identity	57
NCBI Description	(AC004697) putative adenylate kinase [Arabidopsis thaliana]

Seq. No.	224673
Seq. ID	LIB3166-016-P1-K1-E1
Method	BLASTX
NCBI GI	g3885334

BLAST score	408
E value	5.0e-40
Match length	119
% identity	62
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	224674
Seq. ID	LIB3166-016-P1-K1-E12
Method	BLASTX
NCBI GI	g544184
BLAST score	305
E value	7.0e-28
Match length	73
% identity	71
NCBI Description	4-ALPHA-GLUCANOTRANSFERASE PRECURSOR (AMYLOMALTASE) (DISPROPORTIONATING ENZYME) (D-ENZYME) >gi_322785_pir__A45049 4-alpha-glucanotransferase (EC 2.4.1.25) - potato >gi_296692_emb_CAA48630_ (X68664) 4-alpha-glucanotransferase [Solanum tuberosum]

Seq. No.	224675
Seq. ID	LIB3166-016-P1-K1-E3
Method	BLASTX
NCBI GI	g1076634
BLAST score	225
E value	2.0e-18
Match length	69
% identity	61
NCBI Description	protein-serine/threonine kinase NPK15 - common tobacco >gi_505146_dbj_BAA06538_ (D31737) protein-serine/threonine kinase [Nicotiana tabacum]

Seq. No.	224676
Seq. ID	LIB3166-016-P1-K1-E5
Method	BLASTX
NCBI GI	g123684
BLAST score	425
E value	5.0e-42
Match length	93
% identity	84
NCBI Description	HEAT SHOCK FACTOR PROTEIN HSF24 (HEAT SHOCK TRANSCRIPTION FACTOR 24) (HSTF 24) (HEAT STRESS TRANSCRIPTION FACTOR) >gi_100267_pir__S12361 heat shock transcription factor HSF24 - Peruvian tomato >gi_19488_emb_CAA39034_ (X55347) heat stress transcription factor [Lycopersicon peruvianum]

Seq. No.	224677
Seq. ID	LIB3166-016-P1-K1-E6
Method	BLASTX
NCBI GI	g1174199
BLAST score	218
E value	9.0e-18
Match length	87
% identity	51
NCBI Description	(U44760) S25-PR6 [Nicotiana tabacum]

Seq. No.	224678
Seq. ID	LIB3166-016-P1-K1-E7
Method	BLASTX
NCBI GI	g3915031
BLAST score	573
E value	2.0e-59
Match length	110
% identity	98
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232_ (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase [Gossypium hirsutum]

Seq. No.	224679
Seq. ID	LIB3166-016-P1-K1-E9
Method	BLASTX
NCBI GI	g585973
BLAST score	496
E value	3.0e-50
Match length	118
% identity	83
NCBI Description	FRUCTOKINASE >gi_626018_pir__S39997 fructokinase (EC 2.7.1.4) - potato >gi_297015_emb_CAA78283_ (Z12823) fructokinase [Solanum tuberosum] >gi_1095321_prf__2108342A fructokinase [Solanum tuberosum]

Seq. No.	224680
Seq. ID	LIB3166-016-P1-K1-F1
Method	BLASTX
NCBI GI	g1263291
BLAST score	544
E value	6.0e-56
Match length	114
% identity	89
NCBI Description	(U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No.	224681
Seq. ID	LIB3166-016-P1-K1-F11
Method	BLASTX
NCBI GI	g3860263
BLAST score	269
E value	1.0e-23
Match length	65
% identity	71
NCBI Description	(AC005824) putative cytochrome p450 protein [Arabidopsis thaliana]

Seq. No.	224682
Seq. ID	LIB3166-016-P1-K1-F12
Method	BLASTX
NCBI GI	g2827712
BLAST score	100
E value	5.0e-12
Match length	102
% identity	44
NCBI Description	(AL021684) endoxyloglucan tranferase-like protein [Arabidopsis thaliana]

Seq. No.	224683
Seq. ID	LIB3166-016-P1-K1-F9
Method	BLASTX
NCBI GI	g117290
BLAST score	382
E value	3.0e-37
Match length	89
% identity	85
NCBI Description	CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT) (P36) (E30) >gi_100071_pir__S23774 triose phosphate/3-phosphoglycerate/phosphate translocator precursor - garden pea >gi_20691_emb_CAA38451_ (X54639) chloroplast import receptor p36 [Pisum sativum] >gi_20853_emb_CAA48210_ (X68077) phosphate translocator [Pisum sativum] >gi_228551_prf__1805409A phosphate translocator [Pisum sativum]

Seq. No.	224684
Seq. ID	LIB3166-016-P1-K1-G1
Method	BLASTX
NCBI GI	g584778
BLAST score	214
E value	3.0e-17
Match length	107
% identity	50
NCBI Description	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 2 PRECURSOR (PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 2) (DAHP SYNTHETASE 2) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE 2) >gi_542033_pir__S40412 2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) 2 precursor - tomato >gi_410488_emb_CAA79856_ (Z21793) phospho-2-dehydro-3-deoxyheptonate aldolase [Lycopersicon esculentum]

Seq. No.	224685
Seq. ID	LIB3166-016-P1-K1-G11
Method	BLASTX
NCBI GI	g4539348
BLAST score	303
E value	1.0e-27
Match length	114
% identity	53
NCBI Description	(AL035539) putative pollen allergen [Arabidopsis thaliana]

Seq. No.	224686
Seq. ID	LIB3166-016-P1-K1-G4
Method	BLASTX
NCBI GI	g2736186
BLAST score	476
E value	6.0e-48
Match length	128
% identity	69
NCBI Description	(AF024623) galactose kinase [Arabidopsis thaliana]

Seq. No.	224687
Seq. ID	LIB3166-016-P1-K1-G9

Method	BLASTX
NCBI GI	g2833375
BLAST score	356
E value	7.0e-34
Match length	71
% identity	93
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 8.2 KD POLYPEPTIDE (RPB10) (RP10) (ABC10) >gi_533690 (U12133) RNA polymerase II subunit RPB10 homolog; similar to yeast RNA polymerase II subunit RPB10, Swiss-Prot Accession Number P22139 [Brassica napus]

Seq. No.	224688
Seq. ID	LIB3166-016-P1-K1-H10
Method	BLASTX
NCBI GI	g4006899
BLAST score	467
E value	7.0e-47
Match length	128
% identity	63
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	224689
Seq. ID	LIB3166-016-P1-K1-H11
Method	BLASTX
NCBI GI	g3776005
BLAST score	337
E value	7.0e-40
Match length	104
% identity	84
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	224690
Seq. ID	LIB3166-016-P1-K1-H12
Method	BLASTX
NCBI GI	g3859659
BLAST score	246
E value	2.0e-21
Match length	65
% identity	78
NCBI Description	(AL031394) putative potassium transporter AtKT5p (AtKT5) [Arabidopsis thaliana]

Seq. No.	224691
Seq. ID	LIB3166-016-P1-K1-H4
Method	BLASTX
NCBI GI	g4538905
BLAST score	437
E value	2.0e-43
Match length	98
% identity	82
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

Seq. No.	224692
Seq. ID	LIB3166-016-P1-K1-H5
Method	BLASTX
NCBI GI	g4102600

BLAST score	594
E value	1.0e-61
Match length	132
% identity	83
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]

Seq. No.	224693
Seq. ID	LIB3166-016-P1-K1-H6
Method	BLASTX
NCBI GI	g3695388
BLAST score	165
E value	2.0e-11
Match length	43
% identity	60
NCBI Description	(AF096371) No definition line found [Arabidopsis thaliana]

Seq. No.	224694
Seq. ID	LIB3166-016-P1-K1-H9
Method	BLASTX
NCBI GI	g2244846
BLAST score	326
E value	2.0e-32
Match length	95
% identity	77
NCBI Description	(Z97337) ferredoxin [Arabidopsis thaliana]

Seq. No.	224695
Seq. ID	LIB3166-017-P1-K1-A1
Method	BLASTX
NCBI GI	g541816
BLAST score	415
E value	7.0e-41
Match length	108
% identity	69
NCBI Description	protein kinase - common ice plant >gi_457689_emb_CAA82990_ (Z30329) protein kinase [Mesembryanthemum crystallinum]

Seq. No.	224696
Seq. ID	LIB3166-017-P1-K1-A10
Method	BLASTX
NCBI GI	g4337175
BLAST score	420
E value	2.0e-41
Match length	118
% identity	67
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	224697
Seq. ID	LIB3166-017-P1-K1-A11
Method	BLASTX
NCBI GI	g3822036
BLAST score	243
E value	1.0e-20
Match length	124

% identity	44
NCBI Description	(AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]
Seq. No.	224698
Seq. ID	LIB3166-017-P1-K1-A2
Method	BLASTX
NCBI GI	g478673
BLAST score	273
E value	4.0e-24
Match length	73
% identity	67
NCBI Description	proline-rich protein precursor - kidney bean >gi_21046_emb_CAA42942_ (X60391) proline-rich protein [Phaseolus vulgaris]
Seq. No.	224699
Seq. ID	LIB3166-017-P1-K1-A5
Method	BLASTX
NCBI GI	g1297359
BLAST score	484
E value	8.0e-49
Match length	130
% identity	71
NCBI Description	(U53701) alcohol dehydrogenase 2d [Gossypium hirsutum]
Seq. No.	224700
Seq. ID	LIB3166-017-P1-K1-A6
Method	BLASTX
NCBI GI	g2243118
BLAST score	382
E value	7.0e-37
Match length	91
% identity	75
NCBI Description	(Y10984) glutathione synthetase [Brassica juncea]
Seq. No.	224701
Seq. ID	LIB3166-017-P1-K1-A7
Method	BLASTX
NCBI GI	g4455199
BLAST score	225
E value	9.0e-19
Match length	95
% identity	59
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]
Seq. No.	224702
Seq. ID	LIB3166-017-P1-K1-A8
Method	BLASTX
NCBI GI	g1762914
BLAST score	174
E value	2.0e-12
Match length	48
% identity	69
NCBI Description	(U65973) alcohol dehydrogenase A [Washingtonia robusta]
Seq. No.	224703
Seq. ID	LIB3166-017-P1-K1-B1

Method	BLASTX
NCBI GI	g2194124
BLAST score	531
E value	2.0e-54
Match length	134
% identity	75
NCBI Description	(AC002062) Similar to Glycine metalloendoproteinase (gb_U63725). [Arabidopsis thaliana]

Seq. No.	224704
Seq. ID	LIB3166-017-P1-K1-B11
Method	BLASTX
NCBI GI	g3927838
BLAST score	212
E value	6.0e-17
Match length	45
% identity	91
NCBI Description	(AC005727) unknown protein [Arabidopsis thaliana]

Seq. No.	224705
Seq. ID	LIB3166-017-P1-K1-B2
Method	BLASTX
NCBI GI	g2980782
BLAST score	142
E value	9.0e-09
Match length	95
% identity	41
NCBI Description	(AL022198) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224706
Seq. ID	LIB3166-017-P1-K1-B3
Method	BLASTX
NCBI GI	g2129771
BLAST score	465
E value	9.0e-47
Match length	100
% identity	82
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-6 - Arabidopsis thaliana >gi_1244758 (U43488) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi_4539299_emb_CAB39602.1_ (AL049480) xyloglucan endo-1, 4-beta-D-glucanase (XTR-6) [Arabidopsis thaliana]

Seq. No.	224707
Seq. ID	LIB3166-017-P1-K1-B7
Method	BLASTX
NCBI GI	g2352492
BLAST score	538
E value	3.0e-55
Match length	125
% identity	78
NCBI Description	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	224708
Seq. ID	LIB3166-017-P1-K1-B9

Method	BLASTX
NCBI GI	g4512625
BLAST score	177
E value	7.0e-13
Match length	106
% identity	31
NCBI Description	(AC004793) ESTs gb_T20423, gb_AA712864, gb_H76323 and gb_Z25560 come from this gene. [Arabidopsis thaliana]

Seq. No.	224709
Seq. ID	LIB3166-017-P1-K1-C1
Method	BLASTX
NCBI GI	g3881507
BLAST score	149
E value	1.0e-09
Match length	46
% identity	52
NCBI Description	(Z47357) cDNA EST yk375c3.5 comes from this gene; cDNA EST yk375c3.3 comes from this gene [Caenorhabditis elegans]

Seq. No.	224710
Seq. ID	LIB3166-017-P1-K1-C10
Method	BLASTX
NCBI GI	g3123264
BLAST score	407
E value	7.0e-40
Match length	85
% identity	87
NCBI Description	60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279_ (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224711
Seq. ID	LIB3166-017-P1-K1-C2
Method	BLASTX
NCBI GI	g4510373
BLAST score	249
E value	3.0e-21
Match length	102
% identity	53
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]

Seq. No.	224712
Seq. ID	LIB3166-017-P1-K1-C3
Method	BLASTX
NCBI GI	g729273
BLAST score	656
E value	5.0e-69
Match length	136
% identity	90
NCBI Description	CYPRO4 PROTEIN >gi_322804_pir__S28592 cypro4 protein - cardoon >gi_17959_emb_CAA49354_ (X69672) cypro4 [Cynara cardunculus]

Seq. No.	224713
Seq. ID	LIB3166-017-P1-K1-C4
Method	BLASTX

NCBI GI	g4455155
BLAST score	307
E value	4.0e-28
Match length	129
% identity	46
NCBI Description	(AL022023) EF-1 alpha - like protein (fragment) [Arabidopsis thaliana]

Seq. No.	224714
Seq. ID	LIB3166-017-P1-K1-C5
Method	BLASTX
NCBI GI	g1679794
BLAST score	306
E value	6.0e-28
Match length	115
% identity	52
NCBI Description	(U77627) Allele: hi2 [Danio rerio]

Seq. No.	224715
Seq. ID	LIB3166-017-P1-K1-C6
Method	BLASTX
NCBI GI	g4567279
BLAST score	336
E value	2.0e-31
Match length	87
% identity	69
NCBI Description	(AC006841) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	224716
Seq. ID	LIB3166-017-P1-K1-C7
Method	BLASTX
NCBI GI	g1362009
BLAST score	463
E value	2.0e-46
Match length	130
% identity	52
NCBI Description	ubiquitin-like protein 7 - Arabidopsis thaliana

Seq. No.	224717
Seq. ID	LIB3166-017-P1-K1-D11
Method	BLASTX
NCBI GI	g3024127
BLAST score	613
E value	5.0e-64
Match length	123
% identity	93
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1655578_emb_CAA95857_ (Z71272) S-adenosyl-L-methionine synthetase 2 [Catharanthus roseus]

Seq. No.	224718
Seq. ID	LIB3166-017-P1-K1-D12
Method	BLASTX
NCBI GI	g4098128
BLAST score	373

E value	6.0e-36
Match length	79
% identity	96
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	224719
Seq. ID	LIB3166-017-P1-K1-D4
Method	BLASTX
NCBI GI	g125606
BLAST score	389
E value	9.0e-38
Match length	84
% identity	87
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir__S12248 pyruvate kinase (EC 2.7.1.40) - potato >gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum tuberosum]

Seq. No.	224720
Seq. ID	LIB3166-017-P1-K1-D8
Method	BLASTX
NCBI GI	g2661840
BLAST score	373
E value	7.0e-36
Match length	98
% identity	69
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]

Seq. No.	224721
Seq. ID	LIB3166-017-P1-K1-D9
Method	BLASTX
NCBI GI	g4454032
BLAST score	140
E value	1.0e-08
Match length	72
% identity	42
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	224722
Seq. ID	LIB3166-017-P1-K1-E1
Method	BLASTX
NCBI GI	g3953471
BLAST score	238
E value	5.0e-20
Match length	68
% identity	68
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No.	224723
Seq. ID	LIB3166-017-P1-K1-E10
Method	BLASTX
NCBI GI	g3834307
BLAST score	434
E value	5.0e-43
Match length	128
% identity	69
NCBI Description	(AC005679) Strong similarity to gene T10I14.120 gi_2832679

putative protein from Arabidopsis thaliana BAC gb_AL021712. ESTs gb_N65887 and gb_N65627 come from this gene. [Arabidopsis thaliana]

Seq. No.	224724
Seq. ID	LIB3166-017-P1-K1-E5
Method	BLASTX
NCBI GI	g1871192
BLAST score	162
E value	4.0e-11
Match length	73
% identity	48
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	224725
Seq. ID	LIB3166-017-P1-K1-E6
Method	BLASTX
NCBI GI	g2160166
BLAST score	493
E value	7.0e-50
Match length	140
% identity	67
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	224726
Seq. ID	LIB3166-017-P1-K1-F10
Method	BLASTX
NCBI GI	g3367568
BLAST score	330
E value	3.0e-33
Match length	108
% identity	64
NCBI Description	(AL031135) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	224727
Seq. ID	LIB3166-017-P1-K1-F12
Method	BLASTX
NCBI GI	g3281846
BLAST score	170
E value	5.0e-12
Match length	59
% identity	59
NCBI Description	(AJ006404) late elongated hypocotyl [Arabidopsis thaliana]

Seq. No.	224728
Seq. ID	LIB3166-017-P1-K1-F2
Method	BLASTX
NCBI GI	g4539408
BLAST score	366
E value	5.0e-35
Match length	135
% identity	60
NCBI Description	(AL049524) putative alpha NAC [Arabidopsis thaliana]

Seq. No.	224729

Seq. ID	LIB3166-017-P1-K1-F3
Method	BLASTX
NCBI GI	g3746069
BLAST score	144
E value	5.0e-09
Match length	104
% identity	30
NCBI Description	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	224730
Seq. ID	LIB3166-017-P1-K1-F7
Method	BLASTX
NCBI GI	g2494111
BLAST score	407
E value	7.0e-40
Match length	105
% identity	74
NCBI Description	(AC002376) Contains similarity to Glycine protein kinase 6 (gb_M67449). [Arabidopsis thaliana]

Seq. No.	224731
Seq. ID	LIB3166-017-P1-K1-F8
Method	BLASTX
NCBI GI	g2961107
BLAST score	186
E value	6.0e-14
Match length	84
% identity	45
NCBI Description	(AF042383) TLS-associated protein with SR repeats [Mus musculus] >gi_2961149 (AF047448) TLS-associated protein TASR [Homo sapiens]

Seq. No.	224732
Seq. ID	LIB3166-017-P1-K1-F9
Method	BLASTX
NCBI GI	g3747050
BLAST score	416
E value	6.0e-41
Match length	106
% identity	76
NCBI Description	(AF093540) ribosomal protein L26 [Zea mays]

Seq. No.	224733
Seq. ID	LIB3166-017-P1-K1-G10
Method	BLASTX
NCBI GI	g1805359
BLAST score	285
E value	1.0e-25
Match length	131
% identity	43
NCBI Description	(AB000623) glucosyl transferase [Nicotiana tabacum]

Seq. No.	224734
Seq. ID	LIB3166-017-P1-K1-G11
Method	BLASTX
NCBI GI	g1172441

BLAST score	239
E value	3.0e-20
Match length	104
% identity	56
NCBI Description	POSSIBLE TRANSCRIPTION FACTOR POSF21 >gi_99685_pir__S21883 DNA-binding protein POSF21 - Arabidopsis thaliana >gi_16429_emb_CAA43366_ (X61031) posF21 [Arabidopsis thaliana]

Seq. No.	224735
Seq. ID	LIB3166-017-P1-K1-G12
Method	BLASTX
NCBI GI	g2160692
BLAST score	225
E value	1.0e-18
Match length	82
% identity	55
NCBI Description	(U73527) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq. No.	224736
Seq. ID	LIB3166-017-P1-K1-G3
Method	BLASTX
NCBI GI	g1469930
BLAST score	379
E value	2.0e-36
Match length	113
% identity	73
NCBI Description	(U48777) fiber-specific acyl carrier protein [Gossypium hirsutum]

Seq. No.	224737
Seq. ID	LIB3166-017-P1-K1-G7
Method	BLASTX
NCBI GI	g1709651
BLAST score	328
E value	1.0e-30
Match length	112
% identity	58
NCBI Description	PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209 plastocyanin a precursor - black poplar >gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus nigra]

Seq. No.	224738
Seq. ID	LIB3166-017-P1-K1-G8
Method	BLASTX
NCBI GI	g445612
BLAST score	507
E value	1.0e-51
Match length	102
% identity	96
NCBI Description	ribosomal protein S19 [Solanum tuberosum]

Seq. No.	224739
Seq. ID	LIB3166-017-P1-K1-H1
Method	BLASTX

NCBI GI	g120669
BLAST score	530
E value	3.0e-54
Match length	113
% identity	88
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	224740
Seq. ID	LIB3166-017-P1-K1-H11
Method	BLASTX
NCBI GI	g1086252
BLAST score	371
E value	1.0e-35
Match length	103
% identity	68
NCBI Description	sucrose cleavage protein - Potato >gi_707001_bbs_157931 (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa] [Solanum tuberosum]

Seq. No.	224741
Seq. ID	LIB3166-017-P1-K1-H12
Method	BLASTX
NCBI GI	g1061040
BLAST score	488
E value	2.0e-49
Match length	96
% identity	92
NCBI Description	(X89867) sterol-C-methyltransferase [Arabidopsis thaliana] >gi_1587694_prf__2207220A sterol C-methyltransferase [Arabidopsis thaliana]

Seq. No.	224742
Seq. ID	LIB3166-017-P1-K1-H2
Method	BLASTX
NCBI GI	g3123271
BLAST score	487
E value	3.0e-49
Match length	100
% identity	88
NCBI Description	40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No.	224743
Seq. ID	LIB3166-017-P1-K1-H4
Method	BLASTX
NCBI GI	g2842689
BLAST score	144
E value	4.0e-09
Match length	107
% identity	36
NCBI Description	HYPOTHETICAL 50.4 KD PROTEIN C1F8.04C IN CHROMOSOME I >gi_1638851_emb_CAB03598_ (Z81312) unknown

[Schizosaccharomyces pombe]

Seq. No.	224744
Seq. ID	LIB3166-017-P1-K1-H6
Method	BLASTX
NCBI GI	g2213884
BLAST score	514
E value	2.0e-52
Match length	134
% identity	71
NCBI Description	(AF004166) 2-isopropylmalate synthase [Lycopersicon pennellii]

Seq. No.	224745
Seq. ID	LIB3166-017-P1-K1-H7
Method	BLASTX
NCBI GI	g2286153
BLAST score	535
E value	6.0e-55
Match length	112
% identity	96
NCBI Description	(AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No.	224746
Seq. ID	LIB3166-018-P1-K1-A10
Method	BLASTX
NCBI GI	g4539348
BLAST score	274
E value	3.0e-24
Match length	104
% identity	52
NCBI Description	(AL035539) putative pollen allergen [Arabidopsis thaliana]

Seq. No.	224747
Seq. ID	LIB3166-018-P1-K1-A2
Method	BLASTX
NCBI GI	g1170312
BLAST score	452
E value	4.0e-45
Match length	111
% identity	87
NCBI Description	HOMEOBOX PROTEIN SBH1 >gi_629614_pir__S42543 hypothetical protein - soybean >gi_485406 (L13663) SBH1 [Glycine max]

Seq. No.	224748
Seq. ID	LIB3166-018-P1-K1-A4
Method	BLASTX
NCBI GI	g2865427
BLAST score	214
E value	2.0e-17
Match length	95
% identity	48
NCBI Description	(AF039372) polyprotein [Arabidopsis thaliana]

Seq. No.	224749
Seq. ID	LIB3166-018-P1-K1-A5
Method	BLASTX

NCBI GI g1220196
BLAST score 540
E value 2.0e-55
Match length 111
% identity 89
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No. 224750
Seq. ID LIB3166-018-P1-K1-A8
Method BLASTX
NCBI GI g2347199
BLAST score 261
E value 7.0e-23
Match length 109
% identity 51
NCBI Description (AC002338) protein kinase isolog [Arabidopsis thaliana]

Seq. No. 224751
Seq. ID LIB3166-018-P1-K1-A9
Method BLASTX
NCBI GI g2961384
BLAST score 238
E value 5.0e-20
Match length 127
% identity 36
NCBI Description (AL022141) aldehyde dehydrogenase like protein [Arabidopsis thaliana]

Seq. No. 224752
Seq. ID LIB3166-018-P1-K1-B1
Method BLASTX
NCBI GI g4580517
BLAST score 396
E value 3.0e-39
Match length 135
% identity 61
NCBI Description (AF036302) scarecrow-like 5 [Arabidopsis thaliana]

Seq. No. 224753
Seq. ID LIB3166-018-P1-K1-B10
Method BLASTX
NCBI GI g2078350
BLAST score 216
E value 1.0e-17
Match length 51
% identity 88
NCBI Description (U95923) transaldolase [Solanum tuberosum]

Seq. No. 224754
Seq. ID LIB3166-018-P1-K1-B12
Method BLASTX
NCBI GI g2129758
BLAST score 292
E value 1.0e-36
Match length 82
% identity 78
NCBI Description ubiquitin conjugating enzyme E2 protein - Arabidopsis

thaliana >gi_992704 (U33757) UBC7 [Arabidopsis thaliana]

Seq. No.	224755
Seq. ID	LIB3166-018-P1-K1-B5
Method	BLASTX
NCBI GI	g2160189
BLAST score	264
E value	4.0e-23
Match length	106
% identity	52
NCBI Description	(AC000132) Similar to A. thaliana receptor-like protein kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb_ATTS4362 come from this gene. [Arabidopsis thaliana]

Seq. No.	224756
Seq. ID	LIB3166-018-P1-K1-B8
Method	BLASTX
NCBI GI	g3758833
BLAST score	216
E value	3.0e-23
Match length	124
% identity	53
NCBI Description	(Y18225) MtN6 [Medicago truncatula]

Seq. No.	224757
Seq. ID	LIB3166-018-P1-K1-C1
Method	BLASTX
NCBI GI	g4455208
BLAST score	487
E value	3.0e-49
Match length	116
% identity	81
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	224758
Seq. ID	LIB3166-018-P1-K1-C10
Method	BLASTX
NCBI GI	g3885329
BLAST score	503
E value	3.0e-51
Match length	96
% identity	98
NCBI Description	(AC005623) alien-like protein [Arabidopsis thaliana]

Seq. No.	224759
Seq. ID	LIB3166-018-P1-K1-C11
Method	BLASTX
NCBI GI	g2498982
BLAST score	221
E value	4.0e-18
Match length	78
% identity	51
NCBI Description	TRANSCRIPTION INITIATION FACTOR TFIID 31 KD SUBUNIT (TAFII-31) (TAFII-32) (TAFII32) (NEURONAL CELL DEATH RELATED GENE IN NEURON -7) (DN-7) >gi_1103900 (U40188) induced upon programmed cell death in neuronally differentiated PC12 cells [Rattus norvegicus]

Seq. No.	224760
Seq. ID	LIB3166-018-P1-K1-C3
Method	BLASTX
NCBI GI	g4210948
BLAST score	545
E value	6.0e-56
Match length	104
% identity	98
NCBI Description	(AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No.	224761
Seq. ID	LIB3166-018-P1-K1-C4
Method	BLASTX
NCBI GI	g3402279
BLAST score	576
E value	1.0e-59
Match length	121
% identity	89
NCBI Description	(AJ000999) putative beta-subunit of K+ channels [Solanum tuberosum]

Seq. No.	224762
Seq. ID	LIB3166-018-P1-K1-C6
Method	BLASTX
NCBI GI	g4103324
BLAST score	583
E value	2.0e-60
Match length	127
% identity	87
NCBI Description	(AF022716) GDP-mannose pyrophosphorylase [Solanum tuberosum]

Seq. No.	224763
Seq. ID	LIB3166-018-P1-K1-C7
Method	BLASTX
NCBI GI	g4218011
BLAST score	142
E value	8.0e-09
Match length	115
% identity	34
NCBI Description	(AC006135) putative protein kinase [Arabidopsis thaliana] >gi_4309721_gb_AAD15491_ (AC006439) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	224764
Seq. ID	LIB3166-018-P1-K1-C8
Method	BLASTX
NCBI GI	g3551983
BLAST score	402
E value	2.0e-39
Match length	117
% identity	71
NCBI Description	(AF085073) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551985 (AF085074) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551987 (AF085075) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551989 (AF085076) alcohol

dehydrogenase A [Gossypium hirsutum] >gi_4140602 (AF090150) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140612 (AF090155) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140614 (AF090156) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140616 (AF090157) alcohol dehydrogenase A [Gossypium hirsutum]

Seq. No.	224765
Seq. ID	LIB3166-018-P1-K1-C9
Method	BLASTX
NCBI GI	g3033395
BLAST score	293
E value	2.0e-26
Match length	75
% identity	69
NCBI Description	(AC004238) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No.	224766
Seq. ID	LIB3166-018-P1-K1-D10
Method	BLASTX
NCBI GI	g3122060
BLAST score	303
E value	7.0e-28
Match length	59
% identity	98
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_2598657_emb_CAA10847_ (AJ222579) elongation factor 1-alpha (EF1-a) [Vicia faba]

Seq. No.	224767
Seq. ID	LIB3166-018-P1-K1-D11
Method	BLASTX
NCBI GI	g4558553
BLAST score	313
E value	7.0e-29
Match length	100
% identity	59
NCBI Description	(AC007138) putative potassium channel [Arabidopsis thaliana]

Seq. No.	224768
Seq. ID	LIB3166-018-P1-K1-D12
Method	BLASTX
NCBI GI	g3334320
BLAST score	452
E value	4.0e-45
Match length	98
% identity	94
NCBI Description	40S RIBOSOMAL PROTEIN SA (P40) >gi_2444420 (AF020553) ribosome-associated protein p40 [Glycine max]

Seq. No.	224769
Seq. ID	LIB3166-018-P1-K1-D3
Method	BLASTX
NCBI GI	g4539335
BLAST score	306

E value	6.0e-28
Match length	123
% identity	50
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	224770
Seq. ID	LIB3166-018-P1-K1-D4
Method	BLASTX
NCBI GI	g1943751
BLAST score	595
E value	7.0e-62
Match length	131
% identity	85
NCBI Description	(U93845) Arabidopsis thaliana ER-type calcium pump protein, complete sequence >gi_2078292 (U96455) ER-type Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]

Seq. No.	224771
Seq. ID	LIB3166-018-P1-K1-D7
Method	BLASTX
NCBI GI	g2980770
BLAST score	329
E value	1.0e-30
Match length	134
% identity	57
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	224772
Seq. ID	LIB3166-018-P1-K1-D9
Method	BLASTX
NCBI GI	g118548
BLAST score	439
E value	1.0e-43
Match length	133
% identity	59
NCBI Description	NADP-SPECIFIC GLUTAMATE DEHYDROGENASE (NADP-GDH) >gi_283447_pir__A42489 glutamate dehydrogenase (NADP+) (EC 1.4.1.4) - Giardia lamblia >gi_159109 (M84604) NADP-dependent glutamate dehydrogenase [Giardia lamblia]

Seq. No.	224773
Seq. ID	LIB3166-018-P1-K1-E1
Method	BLASTX
NCBI GI	g82040
BLAST score	600
E value	2.0e-62
Match length	122
% identity	27
NCBI Description	ubiquitin precursor - flax (fragment) >gi_168304 (M57895) ubiquitin [Linum usitatissimum]

Seq. No.	224774
Seq. ID	LIB3166-018-P1-K1-E10
Method	BLASTX
NCBI GI	g2739365
BLAST score	388
E value	1.0e-37

Match length	81
% identity	83
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	224775
Seq. ID	LIB3166-018-P1-K1-E6
Method	BLASTX
NCBI GI	g2500354
BLAST score	638
E value	7.0e-67
Match length	123
% identity	95
NCBI Description	60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_ (AB001891) QM family protein [Solanum melongena]

Seq. No.	224776
Seq. ID	LIB3166-018-P1-K1-E8
Method	BLASTX
NCBI GI	g119137
BLAST score	532
E value	1.0e-54
Match length	102
% identity	97
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_82771_pir__S06300 translation elongation factor eEF-1 alpha chain, cytosolic (gene TEF2) - Rhizomucor circinelloides f. lusitanicus >gi_2963_emb_CAA35507_ (X17476) EF-1-alpha [Rhizomucor racemosus]

Seq. No.	224777
Seq. ID	LIB3166-018-P1-K1-F1
Method	BLASTX
NCBI GI	g4490732
BLAST score	638
E value	7.0e-67
Match length	123
% identity	93
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	224778
Seq. ID	LIB3166-018-P1-K1-F3
Method	BLASTX
NCBI GI	g2852688
BLAST score	219
E value	7.0e-18
Match length	95
% identity	45
NCBI Description	(AF017753) resistance protein candidate [Lactuca sativa]

Seq. No.	224779
Seq. ID	LIB3166-018-P1-K1-F5
Method	BLASTX
NCBI GI	g4432846
BLAST score	362
E value	2.0e-34
Match length	135

% identity	59
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	224780
Seq. ID	LIB3166-018-P1-K1-F6
Method	BLASTX
NCBI GI	g1173257
BLAST score	172
E value	2.0e-12
Match length	61
% identity	56
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi_1076674_pir__S47642 ribosomal protein S4 - potato >gi_457803_emb_CAA54095_ (X76651) ribosomal protein S4 [Solanum tuberosum]

Seq. No.	224781
Seq. ID	LIB3166-018-P1-K1-F7
Method	BLASTX
NCBI GI	g3775989
BLAST score	149
E value	7.0e-10
Match length	33
% identity	88
NCBI Description	(AJ010458) RNA helicase [Arabidopsis thaliana]

Seq. No.	224782
Seq. ID	LIB3166-018-P1-K1-G1
Method	BLASTX
NCBI GI	g4218535
BLAST score	387
E value	2.0e-37
Match length	96
% identity	68
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]

Seq. No.	224783
Seq. ID	LIB3166-018-P1-K1-G11
Method	BLASTX
NCBI GI	g886116
BLAST score	496
E value	3.0e-50
Match length	123
% identity	71
NCBI Description	(U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473 (AF051338) xyloglucan endotransglycosylase related protein [Arabidopsis thaliana]

Seq. No.	224784
Seq. ID	LIB3166-018-P1-K1-G12
Method	BLASTX
NCBI GI	g1220196
BLAST score	560
E value	9.0e-58
Match length	120
% identity	88
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	224785
Seq. ID	LIB3166-018-P1-K1-G2
Method	BLASTX
NCBI GI	g4468994
BLAST score	334
E value	3.0e-31
Match length	115
% identity	55
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	224786
Seq. ID	LIB3166-018-P1-K1-G3
Method	BLASTX
NCBI GI	g2136258
BLAST score	149
E value	1.0e-09
Match length	66
% identity	44
NCBI Description	template activating factor-I, splice form alpha - human >gi_971272_dbj_BAA08139_ (D45198) template acyivating factor-I alpha [Homo sapiens]

Seq. No.	224787
Seq. ID	LIB3166-018-P1-K1-G5
Method	BLASTX
NCBI GI	g4539333
BLAST score	438
E value	2.0e-43
Match length	131
% identity	64
NCBI Description	(AL035539) putative amino acid transport protein [Arabidopsis thaliana]

Seq. No.	224788
Seq. ID	LIB3166-018-P1-K1-G6
Method	BLASTX
NCBI GI	g4006829
BLAST score	250
E value	2.0e-21
Match length	135
% identity	39
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.	224789
Seq. ID	LIB3166-018-P1-K1-H10
Method	BLASTX
NCBI GI	g2708743
BLAST score	145
E value	2.0e-15
Match length	127
% identity	39
NCBI Description	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]

Seq. No.	224790
Seq. ID	LIB3166-018-P1-K1-H12
Method	BLASTX

NCBI GI	g4262237
BLAST score	279
E value	8.0e-25
Match length	64
% identity	75
NCBI Description	(AC006200) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224791
Seq. ID	LIB3166-018-P1-K1-H2
Method	BLASTX
NCBI GI	g349379
BLAST score	163
E value	3.0e-11
Match length	62
% identity	58
NCBI Description	(L22847) HAHB-1 [Helianthus annuus]

Seq. No.	224792
Seq. ID	LIB3166-018-P1-K1-H3
Method	BLASTX
NCBI GI	g1439609
BLAST score	595
E value	7.0e-62
Match length	123
% identity	61
NCBI Description	(U62778) delta-tonoplast intrinsic protein [Gossypium hirsutum]

Seq. No.	224793
Seq. ID	LIB3166-018-P1-K1-H4
Method	BLASTX
NCBI GI	g2370312
BLAST score	298
E value	4.0e-27
Match length	108
% identity	56
NCBI Description	(AJ000995) DnaJ-like protein [Medicago sativa] >gi_3202020 (AF069507) DnaJ-like protein MsJ1 [Medicago sativa]

Seq. No.	224794
Seq. ID	LIB3166-018-P1-K1-H5
Method	BLASTX
NCBI GI	g1370589
BLAST score	187
E value	5.0e-14
Match length	88
% identity	51
NCBI Description	(X98304) protein induced upon tuberization [Solanum demissum]

Seq. No.	224795
Seq. ID	LIB3166-018-P1-K1-H7
Method	BLASTX
NCBI GI	g4539348
BLAST score	347
E value	6.0e-33
Match length	104

% identity	65
NCBI Description	(AL035539) putative pollen allergen [Arabidopsis thaliana]

Seq. No.	224796
Seq. ID	LIB3166-018-P1-K1-H8
Method	BLASTX
NCBI GI	g3193316
BLAST score	279
E value	6.0e-25
Match length	105
% identity	56
NCBI Description	(AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No.	224797
Seq. ID	LIB3166-018-P1-K1-H9
Method	BLASTX
NCBI GI	g4115337
BLAST score	426
E value	2.0e-42
Match length	88
% identity	17
NCBI Description	(L81141) ubiquitin [Pisum sativum]

Seq. No.	224798
Seq. ID	LIB3166-019-P1-K1-A10
Method	BLASTX
NCBI GI	g2583108
BLAST score	360
E value	3.0e-34
Match length	140
% identity	60
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.	224799
Seq. ID	LIB3166-019-P1-K1-A3
Method	BLASTX
NCBI GI	g82426
BLAST score	570
E value	6.0e-59
Match length	117
% identity	46
NCBI Description	ubiquitin precursor - barley (fragment) >gi_755763_emb_CAA27751_ (X04133) ubiquitin polyprecursor (171 aa) [Hordeum vulgare]

Seq. No.	224800
Seq. ID	LIB3166-019-P1-K1-A8
Method	BLASTX
NCBI GI	g3024126
BLAST score	490
E value	1.0e-49
Match length	98
% identity	95
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine

synthetase 1 [Catharanthus roseus]

Seq. No.	224801
Seq. ID	LIB3166-019-P1-K1-A9
Method	BLASTX
NCBI GI	g2129820
BLAST score	209
E value	7.0e-17
Match length	83
% identity	49
NCBI Description	chitinase (EC 3.2.1.14) class II - peanut >gi_1237025_emb_CAA57773_ (X82329) chitinase (class II) [Arachis hypogaea]

Seq. No.	224802
Seq. ID	LIB3166-019-P1-K1-B1
Method	BLASTX
NCBI GI	g544382
BLAST score	161
E value	5.0e-11
Match length	76
% identity	47
NCBI Description	GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GFAT) >gi_345855_pir__A45055 glutamine--fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) - human >gi_183082 (M90516) glutamine:fructose-6-phosphate amidotransferase [Homo sapiens] >gi_4503981_ref_NP_002047.1_pGFPTa_ glutamine-fructose-6-phosphate transaminase

Seq. No.	224803
Seq. ID	LIB3166-019-P1-K1-B11
Method	BLASTX
NCBI GI	g3789911
BLAST score	295
E value	1.0e-26
Match length	114
% identity	49
NCBI Description	(AF081802) developmental protein DG1118 [Dictyostelium discoideum]

Seq. No.	224804
Seq. ID	LIB3166-019-P1-K1-B3
Method	BLASTX
NCBI GI	g4406780
BLAST score	577
E value	1.0e-59
Match length	139
% identity	81
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	224805
Seq. ID	LIB3166-019-P1-K1-B4
Method	BLASTX
NCBI GI	g1514977

BLAST score	534
E value	1.0e-54
Match length	125
% identity	56
NCBI Description	(D84669) VM23 [Raphanus sativus]

Seq. No.	224806
Seq. ID	LIB3166-019-P1-K1-B6
Method	BLASTX
NCBI GI	g421826
BLAST score	390
E value	8.0e-38
Match length	79
% identity	86
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	224807
Seq. ID	LIB3166-019-P1-K1-B7
Method	BLASTX
NCBI GI	g136636
BLAST score	359
E value	3.0e-34
Match length	72
% identity	92
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	224808
Seq. ID	LIB3166-019-P1-K1-B8
Method	BLASTX
NCBI GI	g1263291
BLAST score	578
E value	7.0e-60
Match length	110
% identity	98
NCBI Description	(U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No.	224809
Seq. ID	LIB3166-019-P1-K1-B9
Method	BLASTX
NCBI GI	g3550454
BLAST score	165
E value	7.0e-20
Match length	69
% identity	81
NCBI Description	(AF085820) alcohol dehydrogenase A [Gossypium barbadense] >gi_3550458 (AF085821) alcohol dehydrogenase A [Gossypium barbadense] >gi_3551965 (AF085064) alcohol dehydrogenase A

[Gossypium hirsutum] >gi_3551967 (AF085065) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551971 (AF085067) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551975 (AF085069) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551977 (AF085070) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140594 (AF090146) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140604 (AF090151) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140606 (AF090152) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140608 (AF090153) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140610 (AF090154) alcohol dehydrogenase A [Gossypium hirsutum]

Seq. No.	224810
Seq. ID	LIB3166-019-P1-K1-C1
Method	BLASTX
NCBI GI	g417073
BLAST score	463
E value	2.0e-46
Match length	120
% identity	78
NCBI Description	GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT) >gi_484529_pir__JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate synthase [Medicago sativa]

Seq. No.	224811
Seq. ID	LIB3166-019-P1-K1-C10
Method	BLASTX
NCBI GI	g2576411
BLAST score	280
E value	6.0e-25
Match length	109
% identity	61
NCBI Description	(AF012833) similar to dynamin-like protein encoded by GenBank Accession Number X99669 [Arabidopsis thaliana]

Seq. No.	224812
Seq. ID	LIB3166-019-P1-K1-C3
Method	BLASTX
NCBI GI	g2129921
BLAST score	195
E value	6.0e-15
Match length	51
% identity	75
NCBI Description	hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]

Seq. No.	224813
Seq. ID	LIB3166-019-P1-K1-C4
Method	BLASTX
NCBI GI	g3548810
BLAST score	200
E value	2.0e-15
Match length	113
% identity	42
NCBI Description	(AC005313) putative chloroplast nucleoid DNA binding

protein [Arabidopsis thaliana]

Seq. No.	224814
Seq. ID	LIB3166-019-P1-K1-C5
Method	BLASTX
NCBI GI	g3924602
BLAST score	262
E value	4.0e-23
Match length	82
% identity	62
NCBI Description	(AF069442) predicted OR23 protein of unknown function [Arabidopsis thaliana]

Seq. No.	224815
Seq. ID	LIB3166-019-P1-K1-D1
Method	BLASTX
NCBI GI	g3046731
BLAST score	236
E value	1.0e-34
Match length	129
% identity	67
NCBI Description	(AJ005373) protein kinase [Craterostigma plantagineum]

Seq. No.	224816
Seq. ID	LIB3166-019-P1-K1-D10
Method	BLASTX
NCBI GI	g2499710
BLAST score	661
E value	1.0e-69
Match length	135
% identity	86
NCBI Description	PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi_1438075 (L33686) phospholipase D [Ricinus communis]

Seq. No.	224817
Seq. ID	LIB3166-019-P1-K1-D11
Method	BLASTX
NCBI GI	g2288981
BLAST score	162
E value	3.0e-11
Match length	97
% identity	25
NCBI Description	(AC002335) calcium binding protein isolog [Arabidopsis thaliana] >gi_3763938 (AC004450) putative calcium binding protein [Arabidopsis thaliana]

Seq. No.	224818
Seq. ID	LIB3166-019-P1-K1-D12
Method	BLASTX
NCBI GI	g556347
BLAST score	269
E value	6.0e-24
Match length	92
% identity	49
NCBI Description	(M92989) protein kinase [Pisum sativum] >gi_445608_prf__1909355A protein kinase [Pisum sativum]

Seq. No.	224819
Seq. ID	LIB3166-019-P1-K1-D2
Method	BLASTX
NCBI GI	g2213592
BLAST score	232
E value	3.0e-19
Match length	72
% identity	33
NCBI Description	(AC000348) T7N9.12 [Arabidopsis thaliana]

Seq. No.	224820
Seq. ID	LIB3166-019-P1-K1-D4
Method	BLASTX
NCBI GI	g2605621
BLAST score	369
E value	2.0e-46
Match length	122
% identity	78
NCBI Description	(D88619) OSMYB3 [Oryza sativa]

Seq. No.	224821
Seq. ID	LIB3166-019-P1-K1-D5
Method	BLASTX
NCBI GI	g1709651
BLAST score	326
E value	2.0e-34
Match length	113
% identity	69
NCBI Description	PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209 plastocyanin a precursor - black poplar >gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus nigra]

Seq. No.	224822
Seq. ID	LIB3166-019-P1-K1-D7
Method	BLASTX
NCBI GI	g4056469
BLAST score	597
E value	4.0e-62
Match length	118
% identity	98
NCBI Description	(AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967, gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t

Seq. No.	224823
Seq. ID	LIB3166-019-P1-K1-D9
Method	BLASTX
NCBI GI	g2160189
BLAST score	508
E value	1.0e-51
Match length	135
% identity	70
NCBI Description	(AC000132) Similar to A. thaliana receptor-like protein

kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb_ATTS4362 come from this gene. [Arabidopsis thaliana]

Seq. No.	224824
Seq. ID	LIB3166-019-P1-K1-E1
Method	BLASTX
NCBI GI	g4371290
BLAST score	273
E value	5.0e-24
Match length	105
% identity	51
NCBI Description	(AC006260) unknown protein [Arabidopsis thaliana]

Seq. No.	224825
Seq. ID	LIB3166-019-P1-K1-E2
Method	BLASTX
NCBI GI	g1871192
BLAST score	224
E value	2.0e-18
Match length	91
% identity	48
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	224826
Seq. ID	LIB3166-019-P1-K1-E3
Method	BLASTX
NCBI GI	g4105794
BLAST score	209
E value	1.0e-16
Match length	67
% identity	52
NCBI Description	(AF049928) PGP224 [Petunia x hybrida]

Seq. No.	224827
Seq. ID	LIB3166-019-P1-K1-E4
Method	BLASTX
NCBI GI	g4371284
BLAST score	647
E value	6.0e-68
Match length	137
% identity	89
NCBI Description	(AC006260) putative plasma membrane intrinsic protein 2B [Arabidopsis thaliana]

Seq. No.	224828
Seq. ID	LIB3166-019-P1-K1-E5
Method	BLASTX
NCBI GI	g1220196
BLAST score	615
E value	3.0e-64
Match length	115
% identity	99
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	224829
Seq. ID	LIB3166-019-P1-K1-E6

Method	BLASTX
NCBI GI	g3461833
BLAST score	466
E value	9.0e-47
Match length	120
% identity	69
NCBI Description	(AC004138) putative expansin [Arabidopsis thaliana]

Seq. No.	224830
Seq. ID	LIB3166-019-P1-K1-E8
Method	BLASTX
NCBI GI	g547683
BLAST score	593
E value	1.0e-61
Match length	126
% identity	91
NCBI Description	HEAT SHOCK COGNATE PROTEIN 80 >gi_170456 (M96549) heat shock cognate protein 80 [Solanum lycopersicum] >gi_445601_prf__1909348A heat shock protein hsp80 [Lycopersicon esculentum]

Seq. No.	224831
Seq. ID	LIB3166-019-P1-K1-F1
Method	BLASTX
NCBI GI	g3953457
BLAST score	238
E value	4.0e-20
Match length	101
% identity	52
NCBI Description	(AC002328) F20N2.2 [Arabidopsis thaliana]

Seq. No.	224832
Seq. ID	LIB3166-019-P1-K1-F12
Method	BLASTX
NCBI GI	g3877723
BLAST score	228
E value	8.0e-19
Match length	118
% identity	42
NCBI Description	(Z69646) similar to Na(+)/H(+) exchanger; cDNA EST yk249c8.5 comes from this gene; cDNA EST yk255a8.5 comes from this gene; cDNA EST EMBL:C12746 comes from this gene; cDNA EST yk471c10.5 comes from this gene [Caenorhabditis ele

Seq. No.	224833
Seq. ID	LIB3166-019-P1-K1-F4
Method	BLASTX
NCBI GI	g4580523
BLAST score	179
E value	4.0e-13
Match length	51
% identity	67
NCBI Description	(AF036305) scarecrow-like 8 [Arabidopsis thaliana]

Seq. No.	224834
Seq. ID	LIB3166-019-P1-K1-F5

Method	BLASTX
NCBI GI	g3451072
BLAST score	314
E value	3.0e-29
Match length	91
% identity	69
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	224835
Seq. ID	LIB3166-019-P1-K1-F7
Method	BLASTX
NCBI GI	g4008159
BLAST score	356
E value	1.0e-39
Match length	99
% identity	84
NCBI Description	(AB015601) DnaJ homolog [Salix gilgiana]

Seq. No.	224836
Seq. ID	LIB3166-019-P1-K1-F8
Method	BLASTX
NCBI GI	g1871577
BLAST score	324
E value	4.0e-30
Match length	111
% identity	55
NCBI Description	(Y11553) putative 21kD protein precursor [Medicago sativa]

Seq. No.	224837
Seq. ID	LIB3166-019-P1-K1-G1
Method	BLASTX
NCBI GI	g4220537
BLAST score	153
E value	4.0e-10
Match length	32
% identity	91
NCBI Description	(AL035356) PsRT17-1 like protein [Arabidopsis thaliana]

Seq. No.	224838
Seq. ID	LIB3166-019-P1-K1-G4
Method	BLASTX
NCBI GI	g3434967
BLAST score	212
E value	6.0e-17
Match length	77
% identity	55
NCBI Description	(AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]

Seq. No.	224839
Seq. ID	LIB3166-019-P1-K1-G5
Method	BLASTX
NCBI GI	g1709358
BLAST score	237
E value	1.0e-31
Match length	134
% identity	57

NCBI Description	NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE PHOSPHOHYDROLASE) (NTPASE) >gi_629638_pir__S48859 nucleoside triphosphatase - garden pea >gi_2129890_pir__S65147 nucleoside triphosphatase precursor, chromatin-associated - garden pea >gi_563612_emb_CAA83655_ (Z32743) nucleoside triphosphatase [Pisum sativum] >gi_4519173_dbj_BAA75506.1_ (AB022319) nucleoside triphosphatase (NTPase) [Pisum sativum]

Seq. No.	224840
Seq. ID	LIB3166-019-P1-K1-G7
Method	BLASTX
NCBI GI	g1220196
BLAST score	268
E value	8.0e-24
Match length	90
% identity	62
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	224841
Seq. ID	LIB3166-019-P1-K1-G8
Method	BLASTX
NCBI GI	g2244732
BLAST score	207
E value	2.0e-16
Match length	65
% identity	71
NCBI Description	(D88413) endo-xyloglucan transferase [Gossypium hirsutum]

Seq. No.	224842
Seq. ID	LIB3166-019-P1-K1-H1
Method	BLASTX
NCBI GI	g2827699
BLAST score	212
E value	6.0e-17
Match length	67
% identity	60
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	224843
Seq. ID	LIB3166-019-P1-K1-H12
Method	BLASTX
NCBI GI	g4545262
BLAST score	241
E value	1.0e-20
Match length	54
% identity	83
NCBI Description	(AF118230) metallothionein-like protein [Gossypium hirsutum]

Seq. No.	224844
Seq. ID	LIB3166-019-P1-K1-H3
Method	BLASTX
NCBI GI	g2129921
BLAST score	194
E value	8.0e-15
Match length	51

% identity	75
NCBI Description	hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]

Seq. No.	224845
Seq. ID	LIB3166-019-P1-K1-H5
Method	BLASTX
NCBI GI	g4510395
BLAST score	520
E value	5.0e-53
Match length	132
% identity	72
NCBI Description	(AC006587) putative beta-galactosidase precursor [Arabidopsis thaliana]

Seq. No.	224846
Seq. ID	LIB3166-019-P1-K1-H7
Method	BLASTX
NCBI GI	g2463569
BLAST score	352
E value	2.0e-33
Match length	75
% identity	87
NCBI Description	(AB007503) squalene synthase [Glycine max]

Seq. No.	224847
Seq. ID	LIB3166-019-P1-K1-H8
Method	BLASTX
NCBI GI	g1362093
BLAST score	181
E value	2.0e-13
Match length	41
% identity	85
NCBI Description	hypothetical protein (clone TPP15) - tomato (fragment) >gi_924632 (U20595) unknown [Solanum lycopersicum]

Seq. No.	224848
Seq. ID	LIB3166-019-P1-K1-H9
Method	BLASTX
NCBI GI	g485518
BLAST score	381
E value	8.0e-37
Match length	104
% identity	75
NCBI Description	ubiquitin / ribosomal protein CEP52 - rice >gi_303857_dbj_BAA02154_ (D12629) ubiquitin/ribosomal polyprotein [Oryza sativa]

Seq. No.	224849
Seq. ID	LIB3166-020-P1-K1-A11
Method	BLASTX
NCBI GI	g1130682
BLAST score	434
E value	4.0e-43
Match length	111
% identity	77
NCBI Description	(Z46959) acetohydroxyacid synthase [Gossypium hirsutum]

Seq. No.	224850
Seq. ID	LIB3166-020-P1-K1-A2
Method	BLASTX
NCBI GI	g419760
BLAST score	606
E value	4.0e-63
Match length	136
% identity	43
NCBI Description	P-glycoprotein atpgp1 - Arabidopsis thaliana >gi_3849833_emb_CAA43646_ (X61370) P-glycoprotein [Arabidopsis thaliana]

Seq. No.	224851
Seq. ID	LIB3166-020-P1-K1-A4
Method	BLASTX
NCBI GI	g3493172
BLAST score	668
E value	2.0e-70
Match length	137
% identity	51
NCBI Description	(U89609) fiber annexin [Gossypium hirsutum]

Seq. No.	224852
Seq. ID	LIB3166-020-P1-K1-A7
Method	BLASTX
NCBI GI	g2129771
BLAST score	469
E value	4.0e-47
Match length	114
% identity	76
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-6 - Arabidopsis thaliana >gi_1244758 (U43488) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi_4539299_emb_CAB39602.1_ (AL049480) xyloglucan endo-1, 4-beta-D-glucanase (XTR-6) [Arabidopsis thaliana]

Seq. No.	224853
Seq. ID	LIB3166-020-P1-K1-B1
Method	BLASTX
NCBI GI	g2827143
BLAST score	614
E value	4.0e-64
Match length	135
% identity	83
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	224854
Seq. ID	LIB3166-020-P1-K1-B12
Method	BLASTX
NCBI GI	g2465008
BLAST score	359
E value	3.0e-34
Match length	135
% identity	52
NCBI Description	(AJ001445) ripening-induced protein [Fragaria vesca]

Seq. No.	224855
Seq. ID	LIB3166-020-P1-K1-B2
Method	BLASTX
NCBI GI	g2281633
BLAST score	317
E value	3.0e-29
Match length	130
% identity	53
NCBI Description	(AF003097) AP2 domain containing protein RAP2.4 [Arabidopsis thaliana]

Seq. No.	224856
Seq. ID	LIB3166-020-P1-K1-B6
Method	BLASTX
NCBI GI	g128194
BLAST score	531
E value	2.0e-54
Match length	129
% identity	79
NCBI Description	NITRATE REDUCTASE (NR) >gi_81572_pir__A41667 nitrate reductase (NADH) (EC 1.6.6.1) - winter squash >gi_167499 (M33154) nitrate reductase [Cucurbita maxima]

Seq. No.	224857
Seq. ID	LIB3166-020-P1-K1-B7
Method	BLASTX
NCBI GI	g4455364
BLAST score	315
E value	5.0e-29
Match length	102
% identity	60
NCBI Description	(AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No.	224858
Seq. ID	LIB3166-020-P1-K1-C11
Method	BLASTX
NCBI GI	g3288883
BLAST score	182
E value	2.0e-29
Match length	113
% identity	64
NCBI Description	(AB015431) SAR DNA binding protein [Oryza sativa]

Seq. No.	224859
Seq. ID	LIB3166-020-P1-K1-C4
Method	BLASTX
NCBI GI	g2262178
BLAST score	149
E value	1.0e-09
Match length	34
% identity	74
NCBI Description	(AC002329) putative Mlo-like protein [Arabidopsis thaliana]

Seq. No.	224860
Seq. ID	LIB3166-020-P1-K1-C9

Method	BLASTX
NCBI GI	g2618723
BLAST score	209
E value	1.0e-16
Match length	89
% identity	55
NCBI Description	(U49073) IAA17 [Arabidopsis thaliana] >gi_2921756 (AF040631) IAA17/AXR3 protein [Arabidopsis thaliana] >gi_4389514_gb_AAB70451_ (AC000104) Identical to Arabidopsis gb_AF040632 and gb_U49073 IAA17/AXR3 gene. ESTs gb_H36782 and gb_F14074 come from this gene. [Arabidopsis thaliana]

Seq. No.	224861
Seq. ID	LIB3166-020-P1-K1-D1
Method	BLASTX
NCBI GI	g3096922
BLAST score	260
E value	1.0e-22
Match length	84
% identity	64
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	224862
Seq. ID	LIB3166-020-P1-K1-D10
Method	BLASTX
NCBI GI	g4572679
BLAST score	339
E value	2.0e-33
Match length	81
% identity	86
NCBI Description	(AC006954) RSZp22 splicing factor; contains RNA recognition motif [Arabidopsis thaliana]

Seq. No.	224863
Seq. ID	LIB3166-020-P1-K1-D11
Method	BLASTX
NCBI GI	g3377843
BLAST score	290
E value	4.0e-26
Match length	120
% identity	53
NCBI Description	(AF076274) contains similarity to rat p47 protein (GB:AB002086) [Arabidopsis thaliana]

Seq. No.	224864
Seq. ID	LIB3166-020-P1-K1-D2
Method	BLASTX
NCBI GI	g128194
BLAST score	523
E value	2.0e-53
Match length	128
% identity	79
NCBI Description	NITRATE REDUCTASE (NR) >gi_81572_pir__A41667 nitrate reductase (NADH) (EC 1.6.6.1) - winter squash >gi_167499 (M33154) nitrate reductase [Cucurbita maxima]

Seq. No.	224865
Seq. ID	LIB3166-020-P1-K1-D4
Method	BLASTX
NCBI GI	g3676071
BLAST score	402
E value	2.0e-39
Match length	108
% identity	69
NCBI Description	(Y17969) ERG protein [Arabidopsis thaliana]

Seq. No.	224866
Seq. ID	LIB3166-020-P1-K1-D6
Method	BLASTX
NCBI GI	g3377843
BLAST score	198
E value	2.0e-19
Match length	122
% identity	48
NCBI Description	(AF076274) contains similarity to rat p47 protein (GB:AB002086) [Arabidopsis thaliana]

Seq. No.	224867
Seq. ID	LIB3166-020-P1-K1-D9
Method	BLASTX
NCBI GI	g3252866
BLAST score	181
E value	6.0e-16
Match length	132
% identity	45
NCBI Description	(AF033535) putative zinc transporter [Arabidopsis thaliana]

Seq. No.	224868
Seq. ID	LIB3166-020-P1-K1-E10
Method	BLASTX
NCBI GI	g2257598
BLAST score	539
E value	3.0e-55
Match length	135
% identity	79
NCBI Description	(AB005551) phosphoglycerate kinase [Robinia pseudoacacia]

Seq. No.	224869
Seq. ID	LIB3166-020-P1-K1-E11
Method	BLASTX
NCBI GI	g289920
BLAST score	672
E value	6.0e-71
Match length	128
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	224870
Seq. ID	LIB3166-020-P1-K1-E3
Method	BLASTX
NCBI GI	g4512670
BLAST score	148

E value 2.0e-09
Match length 115
% identity 31
NCBI Description (AC006931) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 224871
Seq. ID LIB3166-020-P1-K1-E4
Method BLASTX
NCBI GI g4539348
BLAST score 331
E value 7.0e-31
Match length 133
% identity 51
NCBI Description (AL035539) putative pollen allergen [Arabidopsis thaliana]

Seq. No. 224872
Seq. ID LIB3166-020-P1-K1-E5
Method BLASTX
NCBI GI g2811028
BLAST score 278
E value 7.0e-25
Match length 88
% identity 66
NCBI Description HYPOTHETICAL 47.9 KD PROTEIN M021B04.12 >gi_2191188 (AF007271) similar to S. cerevisiae SIK1P (PID:g984964) [Arabidopsis thaliana]

Seq. No. 224873
Seq. ID LIB3166-020-P1-K1-E7
Method BLASTX
NCBI GI g2981167
BLAST score 119
E value 3.0e-10
Match length 52
% identity 71
NCBI Description (AF053076) late embryogenis abundant protein 5 [Nicotiana tabacum]

Seq. No. 224874
Seq. ID LIB3166-020-P1-K1-E8
Method BLASTX
NCBI GI g3341687
BLAST score 207
E value 2.0e-16
Match length 69
% identity 62
NCBI Description (AC003672) putative ras protein [Arabidopsis thaliana]

Seq. No. 224875
Seq. ID LIB3166-020-P1-K1-E9
Method BLASTX
NCBI GI g1771160
BLAST score 457
E value 1.0e-45
Match length 131
% identity 71
NCBI Description (X98929) SBT1 [Lycopersicon esculentum]

>gi_3687305_emb_CAA06999_ (AJ006378) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	224876
Seq. ID	LIB3166-020-P1-K1-F1
Method	BLASTX
NCBI GI	g4190952
BLAST score	314
E value	6.0e-29
Match length	102
% identity	62
NCBI Description	(AB022689) similar to hsr203J [Lycopersicon esculentum]

Seq. No.	224877
Seq. ID	LIB3166-020-P1-K1-F12
Method	BLASTX
NCBI GI	g2065013
BLAST score	398
E value	9.0e-39
Match length	118
% identity	65
NCBI Description	(Y11650) cyclic phosphodiesterase [Arabidopsis thaliana] >gi_2832621_emb_CAA16750_ (AL021711) cyclic phosphodiesterase [Arabidopsis thaliana]

Seq. No.	224878
Seq. ID	LIB3166-020-P1-K1-F2
Method	BLASTX
NCBI GI	g1706323
BLAST score	248
E value	3.0e-21
Match length	85
% identity	56
NCBI Description	ORNITHINE DECARBOXYLASE (ODC) >gi_2118242_pir__S64704 ornithine decarboxylase (EC 4.1.1.17) - jimsonweed >gi_871008_emb_CAA61121_ (X87847) ornithine decarboxylase [Datura stramonium]

Seq. No.	224879
Seq. ID	LIB3166-020-P1-K1-F4
Method	BLASTX
NCBI GI	g3036951
BLAST score	368
E value	2.0e-35
Match length	74
% identity	96
NCBI Description	(AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	224880
Seq. ID	LIB3166-020-P1-K1-F6
Method	BLASTX
NCBI GI	g4406819
BLAST score	226
E value	1.0e-32
Match length	133
% identity	64

NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]

Seq. No. 224881
Seq. ID LIB3166-020-P1-K1-F9
Method BLASTX
NCBI GI g3334115
BLAST score 670
E value 1.0e-70
Match length 136
% identity 63
NCBI Description ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

Seq. No. 224882
Seq. ID LIB3166-020-P1-K1-G1
Method BLASTX
NCBI GI g3600061
BLAST score 389
E value 1.0e-37
Match length 117
% identity 63
NCBI Description (AF080120) contains similarity to DNA binding proteins [Arabidopsis thaliana]

Seq. No. 224883
Seq. ID LIB3166-020-P1-K1-G12
Method BLASTX
NCBI GI g3757523
BLAST score 202
E value 9.0e-16
Match length 81
% identity 57
NCBI Description (AC005167) putative transportin [Arabidopsis thaliana]

Seq. No. 224884
Seq. ID LIB3166-020-P1-K1-G2
Method BLASTX
NCBI GI g2618721
BLAST score 292
E value 2.0e-26
Match length 96
% identity 65
NCBI Description (U49072) IAA16 [Arabidopsis thaliana]

Seq. No. 224885
Seq. ID LIB3166-020-P1-K1-G3
Method BLASTX
NCBI GI g4567228
BLAST score 248
E value 2.0e-26
Match length 83
% identity 77
NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]

Seq. No. 224886

Seq. ID	LIB3166-020-P1-K1-G4
Method	BLASTX
NCBI GI	g1944216
BLAST score	479
E value	3.0e-48
Match length	105
% identity	86
NCBI Description	(D84246) alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	224887
Seq. ID	LIB3166-020-P1-K1-G5
Method	BLASTX
NCBI GI	g3901012
BLAST score	184
E value	4.0e-14
Match length	72
% identity	53
NCBI Description	(AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]

Seq. No.	224888
Seq. ID	LIB3166-020-P1-K1-G6
Method	BLASTX
NCBI GI	g3212871
BLAST score	240
E value	3.0e-20
Match length	54
% identity	78
NCBI Description	(AC004005) putative translation initiation factor [Arabidopsis thaliana]

Seq. No.	224889
Seq. ID	LIB3166-020-P1-K1-G7
Method	BLASTX
NCBI GI	g172215
BLAST score	200
E value	1.0e-15
Match length	84
% identity	49
NCBI Description	(J03530) RNA polymerase A(I) large subunit [Saccharomyces cerevisiae]

Seq. No.	224890
Seq. ID	LIB3166-020-P1-K1-G8
Method	BLASTX
NCBI GI	g585053
BLAST score	208
E value	1.0e-16
Match length	122
% identity	38
NCBI Description	MITOTIC CONTROL PROTEIN DIS3 >gi_283075_pir__A41944 mitotic control protein dis3+ - fission yeast (Schizosaccharomyces pombe) >gi_173381 (M74094) mitotic control protein [Schizosaccharomyces pombe] >gi_3650393_emb_CAA21102_ (AL031743) mitotic control protein dis3. [Schizosaccharomyces pombe]

Seq. No.	224891
Seq. ID	LIB3166-020-P1-K1-H10
Method	BLASTX
NCBI GI	g4539414
BLAST score	236
E value	9.0e-20
Match length	103
% identity	50
NCBI Description	(AL049524) putative subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	224892
Seq. ID	LIB3166-020-P1-K1-H11
Method	BLASTX
NCBI GI	g132805
BLAST score	114
E value	5.0e-14
Match length	95
% identity	52
NCBI Description	60S RIBOSOMAL PROTEIN L17 (L23) (AMINO ACID STARVATION-INDUCED PROTEIN) (ASI) >gi_71282_pir__R5RT17 ribosomal protein L17 - rat >gi_57111_emb_CAA42765_ (X60212) ribosomal protein L22 [Rattus norvegicus] >gi_57682_emb_CAA41278_ (X58389) ribosomal protein L17 [Rattus rattus]

Seq. No.	224893
Seq. ID	LIB3166-020-P1-K1-H3
Method	BLASTX
NCBI GI	g4210948
BLAST score	236
E value	1.0e-24
Match length	78
% identity	78
NCBI Description	(AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No.	224894
Seq. ID	LIB3166-020-P1-K1-H4
Method	BLASTX
NCBI GI	g1439609
BLAST score	587
E value	6.0e-61
Match length	123
% identity	96
NCBI Description	(U62778) delta-tonoplast intrinsic protein [Gossypium hirsutum]

Seq. No.	224895
Seq. ID	LIB3166-020-P1-K1-H8
Method	BLASTX
NCBI GI	g4490297
BLAST score	401
E value	4.0e-39
Match length	134
% identity	57
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	224896
Seq. ID	LIB3166-021-P1-K1-A1
Method	BLASTX
NCBI GI	g2827548
BLAST score	309
E value	2.0e-28
Match length	120
% identity	52
NCBI Description	(AL021635) cytochrome P450 - like protein [Arabidopsis thaliana]

Seq. No.	224897
Seq. ID	LIB3166-021-P1-K1-A12
Method	BLASTX
NCBI GI	g485514
BLAST score	197
E value	3.0e-15
Match length	44
% identity	86
NCBI Description	ADR11-2 protein - soybean (fragment) >gi_296443_emb_CAA49341_ (X69640) auxin down regulated [Glycine max]

Seq. No.	224898
Seq. ID	LIB3166-021-P1-K1-A5
Method	BLASTX
NCBI GI	g3256035
BLAST score	231
E value	3.0e-19
Match length	124
% identity	44
NCBI Description	(Y14274) putative serine/threonine protein kinase [Sorghum bicolor]

Seq. No.	224899
Seq. ID	LIB3166-021-P1-K1-A6
Method	BLASTX
NCBI GI	g1063415
BLAST score	603
E value	7.0e-63
Match length	120
% identity	93
NCBI Description	(L40948) K+ channel protein [Arabidopsis thaliana]

Seq. No.	224900
Seq. ID	LIB3166-021-P1-K1-A8
Method	BLASTX
NCBI GI	g2213599
BLAST score	346
E value	9.0e-33
Match length	120
% identity	57
NCBI Description	(AC000348) T7N9.19 [Arabidopsis thaliana]

Seq. No.	224901
Seq. ID	LIB3166-021-P1-K1-A9
Method	BLASTX

09604504 - 100700

NCBI GI g602076
BLAST score 527
E value 5.0e-54
Match length 107
% identity 23
NCBI Description (X77456) pentameric polyubiquitin [Nicotiana tabacum]

Seq. No. 224902
Seq. ID LIB3166-021-P1-K1-B10
Method BLASTX
NCBI GI g3269289
BLAST score 315
E value 4.0e-29
Match length 89
% identity 70
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 224903
Seq. ID LIB3166-021-P1-K1-B11
Method BLASTX
NCBI GI g2829863
BLAST score 320
E value 1.0e-29
Match length 103
% identity 57
NCBI Description (AC002396) Putative peroxidase [Arabidopsis thaliana]

Seq. No. 224904
Seq. ID LIB3166-021-P1-K1-B3
Method BLASTX
NCBI GI g4126399
BLAST score 469
E value 4.0e-47
Match length 114
% identity 81
NCBI Description (AB011794) chalcone isomerase [Citrus sinensis]

Seq. No. 224905
Seq. ID LIB3166-021-P1-K1-B4
Method BLASTX
NCBI GI g2407639
BLAST score 231
E value 3.0e-19
Match length 126
% identity 38
NCBI Description (AF018263) protein phosphatase 5; PP5 [Xenopus laevis]

Seq. No. 224906
Seq. ID LIB3166-021-P1-K1-B5
Method BLASTX
NCBI GI g3242702
BLAST score 510
E value 6.0e-52
Match length 117
% identity 78
NCBI Description (AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224907
Seq. ID	LIB3166-021-P1-K1-B6
Method	BLASTX
NCBI GI	g4559331
BLAST score	400
E value	4.0e-39
Match length	83
% identity	83
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	224908
Seq. ID	LIB3166-021-P1-K1-B7
Method	BLASTX
NCBI GI	g2736186
BLAST score	454
E value	2.0e-45
Match length	122
% identity	70
NCBI Description	(AF024623) galactose kinase [Arabidopsis thaliana]

Seq. No.	224909
Seq. ID	LIB3166-021-P1-K1-B9
Method	BLASTX
NCBI GI	g2980770
BLAST score	615
E value	3.0e-64
Match length	126
% identity	90
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	224910
Seq. ID	LIB3166-021-P1-K1-C3
Method	BLASTX
NCBI GI	g2947063
BLAST score	181
E value	2.0e-13
Match length	77
% identity	44
NCBI Description	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	224911
Seq. ID	LIB3166-021-P1-K1-C5
Method	BLASTX
NCBI GI	g2459431
BLAST score	387
E value	2.0e-37
Match length	110
% identity	73
NCBI Description	(AC002332) unknown protein [Arabidopsis thaliana]

Seq. No.	224912
Seq. ID	LIB3166-021-P1-K1-C6
Method	BLASTX
NCBI GI	g3434969
BLAST score	342
E value	3.0e-32

Match length	80
% identity	81
NCBI Description	(AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]

Seq. No.	224913
Seq. ID	LIB3166-021-P1-K1-C8
Method	BLASTX
NCBI GI	g3860274
BLAST score	209
E value	1.0e-16
Match length	53
% identity	72
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana] >gi_4314397_gb_AAD15607_ (AC006232) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	224914
Seq. ID	LIB3166-021-P1-K1-D1
Method	BLASTX
NCBI GI	g1777443
BLAST score	242
E value	1.0e-20
Match length	106
% identity	53
NCBI Description	(U28422) CCA1 [Arabidopsis thaliana] >gi_3510263 (AC005310) DNA-binding protein CCA1 [Arabidopsis thaliana] >gi_4090569 (U79156) CCA1 [Arabidopsis thaliana]

Seq. No.	224915
Seq. ID	LIB3166-021-P1-K1-D10
Method	BLASTX
NCBI GI	g4263821
BLAST score	321
E value	8.0e-30
Match length	116
% identity	63
NCBI Description	(AC006067) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224916
Seq. ID	LIB3166-021-P1-K1-D2
Method	BLASTX
NCBI GI	g2281645
BLAST score	228
E value	6.0e-19
Match length	70
% identity	61
NCBI Description	(AF003103) AP2 domain containing protein RAP2.10 [Arabidopsis thaliana] >gi_2632063_emb_CAA05630_ (AJ002598) TINY-like protein [Arabidopsis thaliana]

Seq. No.	224917
Seq. ID	LIB3166-021-P1-K1-D3
Method	BLASTX
NCBI GI	g730645
BLAST score	430
E value	1.0e-42

Match length	111
% identity	79
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]
Seq. No.	224918
Seq. ID	LIB3166-021-P1-K1-D9
Method	BLASTX
NCBI GI	g116343
BLAST score	248
E value	3.0e-21
Match length	122
% identity	41
NCBI Description	BASIC ENDOCHITINASE PRECURSOR
Seq. No.	224919
Seq. ID	LIB3166-021-P1-K1-E10
Method	BLASTX
NCBI GI	g2618721
BLAST score	292
E value	2.0e-26
Match length	57
% identity	89
NCBI Description	(U49072) IAA16 [Arabidopsis thaliana]
Seq. No.	224920
Seq. ID	LIB3166-021-P1-K1-E11
Method	BLASTX
NCBI GI	g3080423
BLAST score	193
E value	8.0e-15
Match length	85
% identity	51
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]
Seq. No.	224921
Seq. ID	LIB3166-021-P1-K1-E12
Method	BLASTX
NCBI GI	g3434967
BLAST score	197
E value	3.0e-15
Match length	70
% identity	57
NCBI Description	(AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]
Seq. No.	224922
Seq. ID	LIB3166-021-P1-K1-E2
Method	BLASTX
NCBI GI	g3335337
BLAST score	147

E value	2.0e-09
Match length	34
% identity	85
NCBI Description	(AC004512) Similar to acyl carrier protein, mitochondrial precursor (ACP) NADH-ubiquinone oxidoreductase 9.6 KD subunit (MYACP-1), gb_L23574 from A. thaliana. ESTs gb_Z30712, gb_Z30713, gb_Z26204, gb_N37975 and gb_N96330 come from this gene

Seq. No.	224923
Seq. ID	LIB3166-021-P1-K1-E3
Method	BLASTX
NCBI GI	g2507300
BLAST score	467
E value	2.0e-47
Match length	123
% identity	79
NCBI Description	ACTIVATOR 1 40 KD SUBUNIT (REPLICATION FACTOR C 40 KD SUBUNIT) (A1 40 KD SUBUNIT) (RF-C 40 KD SUBUNIT) (RFC40) >gi_1590811 (M87338) replication factor C, 40-kDa subunit [Homo sapiens] >gi_2914760 (AF045555) replication factor C subunit 2 [Homo sapiens] >gi_4506487_ref_NP_002905.1_pRFC2_ replication factor C (activator 1) 2 (40kD)

Seq. No.	224924
Seq. ID	LIB3166-021-P1-K1-E6
Method	BLASTX
NCBI GI	g729470
BLAST score	415
E value	8.0e-41
Match length	104
% identity	76
NCBI Description	MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH) >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2) precursor, mitochondrial - potato >gi_297798_emb_CAA79702_ (Z21493) mitochondrial formate dehydrogenase precursor [Solanum tuberosum]

Seq. No.	224925
Seq. ID	LIB3166-021-P1-K1-E7
Method	BLASTX
NCBI GI	g4375833
BLAST score	430
E value	1.0e-42
Match length	119
% identity	66
NCBI Description	(AL021713) receptor serine/threonine kinase-like protein [Arabidopsis thaliana]

Seq. No.	224926
Seq. ID	LIB3166-021-P1-K1-E9
Method	BLASTX
NCBI GI	g3434973
BLAST score	196
E value	3.0e-15
Match length	73

% identity	53
NCBI Description	(AB008106) ethylene responsive element binding factor 4 [Arabidopsis thaliana]

Seq. No.	224927
Seq. ID	LIB3166-021-P1-K1-F10
Method	BLASTX
NCBI GI	g1170745
BLAST score	595
E value	6.0e-62
Match length	116
% identity	100
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA14-A >gi_167326 (M88321) Group 4 late embryogenesis-abundant protein [Gossypium hirsutum] >gi_167328 (M88322) Group 4 late embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No.	224928
Seq. ID	LIB3166-021-P1-K1-F5
Method	BLASTX
NCBI GI	g2660676
BLAST score	534
E value	9.0e-55
Match length	125
% identity	78
NCBI Description	(AC002342) Dreg-2 like protein [Arabidopsis thaliana]

Seq. No.	224929
Seq. ID	LIB3166-021-P1-K1-F7
Method	BLASTX
NCBI GI	g464621
BLAST score	339
E value	6.0e-32
Match length	118
% identity	58
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	224930
Seq. ID	LIB3166-021-P1-K1-F8
Method	BLASTX
NCBI GI	g4454042
BLAST score	381
E value	7.0e-37
Match length	86
% identity	79
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	224931
Seq. ID	LIB3166-021-P1-K1-F9
Method	BLASTX
NCBI GI	g1129145
BLAST score	465
E value	1.0e-46
Match length	122

% identity	79
NCBI Description	(X75329) acetyl-CoA C-acyltransferase [Mangifera indica]

Seq. No.	224932
Seq. ID	LIB3166-021-P1-K1-G10
Method	BLASTX
NCBI GI	g2507421
BLAST score	247
E value	1.0e-21
Match length	58
% identity	81
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi_1800277 (U81042) translation initiation factor [Arabidopsis thaliana] >gi_4490709_emb_CAB38843.1_ (AL035680) translation initiation factor [Arabidopsis thaliana]

Seq. No.	224933
Seq. ID	LIB3166-021-P1-K1-G11
Method	BLASTX
NCBI GI	g2352492
BLAST score	290
E value	4.0e-26
Match length	121
% identity	49
NCBI Description	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	224934
Seq. ID	LIB3166-021-P1-K1-G12
Method	BLASTX
NCBI GI	g466160
BLAST score	198
E value	1.0e-15
Match length	63
% identity	60
NCBI Description	HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III >gi_630771_pir__S44903 ZK652.3 protein - Caenorhabditis elegans >gi_289769 (L14429) putative [Caenorhabditis elegans]

Seq. No.	224935
Seq. ID	LIB3166-021-P1-K1-G2
Method	BLASTX
NCBI GI	g2498291
BLAST score	243
E value	1.0e-20
Match length	120
% identity	45
NCBI Description	DIHYDRODIPICOLINATE REDUCTASE >gi_1651716_dbj_BAA16644_ (D90899) dihydrodipicolinate reductase [Synechocystis sp.]

Seq. No.	224936
Seq. ID	LIB3166-021-P1-K1-G4
Method	BLASTX
NCBI GI	g3335378
BLAST score	439

E value	1.0e-43
Match length	90
% identity	88
NCBI Description	(AC003028) Myb-related transcription activator [Arabidopsis thaliana]

Seq. No.	224937
Seq. ID	LIB3166-021-P1-K1-G5
Method	BLASTX
NCBI GI	g462195
BLAST score	412
E value	2.0e-40
Match length	86
% identity	93
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir__S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No.	224938
Seq. ID	LIB3166-021-P1-K1-G6
Method	BLASTX
NCBI GI	g466160
BLAST score	366
E value	5.0e-35
Match length	84
% identity	85
NCBI Description	HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III >gi_630771_pir__S44903 ZK652.3 protein - Caenorhabditis elegans >gi_289769 (L14429) putative [Caenorhabditis elegans]

Seq. No.	224939
Seq. ID	LIB3166-021-P1-K1-G7
Method	BLASTX
NCBI GI	g3080371
BLAST score	233
E value	2.0e-19
Match length	62
% identity	63
NCBI Description	(AL022580) putative pectinacetylesterase protein [Arabidopsis thaliana]

Seq. No.	224940
Seq. ID	LIB3166-021-P1-K1-G8
Method	BLASTX
NCBI GI	g4220481
BLAST score	186
E value	5.0e-14
Match length	71
% identity	55
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	224941
Seq. ID	LIB3166-021-P1-K1-G9
Method	BLASTX

NCBI GI	g3335375
BLAST score	428
E value	2.0e-42
Match length	83
% identity	93
NCBI Description	(AC003028) putative amidase [Arabidopsis thaliana]

Seq. No.	224942
Seq. ID	LIB3166-021-P1-K1-H1
Method	BLASTX
NCBI GI	g480669
BLAST score	454
E value	2.0e-45
Match length	107
% identity	80
NCBI Description	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Jerusalem artichoke (fragment) >gi_1359894_emb_CAA81210_ (Z26251) NADPH-ferrihemoprotein reductase [Helianthus tuberosus]

Seq. No.	224943
Seq. ID	LIB3166-021-P1-K1-H3
Method	BLASTX
NCBI GI	g2245005
BLAST score	190
E value	2.0e-14
Match length	76
% identity	58
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224944
Seq. ID	LIB3166-021-P1-K1-H4
Method	BLASTX
NCBI GI	g4490702
BLAST score	290
E value	4.0e-26
Match length	127
% identity	57
NCBI Description	(AL035680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224945
Seq. ID	LIB3166-021-P1-K1-H5
Method	BLASTX
NCBI GI	g100200
BLAST score	362
E value	1.0e-34
Match length	100
% identity	71
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	224946
Seq. ID	LIB3166-021-P1-K1-H6
Method	BLASTX
NCBI GI	g2213583
BLAST score	320
E value	1.0e-29
Match length	114
% identity	54

NCBI Description	(AC000348) T7N9.3 [Arabidopsis thaliana]

Seq. No.	224947
Seq. ID	LIB3166-021-P1-K1-H7
Method	BLASTX
NCBI GI	g2980788
BLAST score	189
E value	2.0e-14
Match length	124
% identity	39
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	224948
Seq. ID	LIB3166-021-P1-K1-H8
Method	BLASTX
NCBI GI	g2462925
BLAST score	428
E value	1.0e-42
Match length	92
% identity	87
NCBI Description	(AJ000053) GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis thaliana]

Seq. No.	224949
Seq. ID	LIB3166-022-P1-K1-A10
Method	BLASTX
NCBI GI	g1800147
BLAST score	351
E value	3.0e-33
Match length	84
% identity	77
NCBI Description	(U83655) membrane associated protein [Arabidopsis thaliana]

Seq. No.	224950
Seq. ID	LIB3166-022-P1-K1-A11
Method	BLASTX
NCBI GI	g4371290
BLAST score	282
E value	3.0e-25
Match length	91
% identity	59
NCBI Description	(AC006260) unknown protein [Arabidopsis thaliana]

Seq. No.	224951
Seq. ID	LIB3166-022-P1-K1-A12
Method	BLASTX
NCBI GI	g2642153
BLAST score	168
E value	7.0e-12
Match length	90
% identity	38
NCBI Description	(AC003000) unknown protein [Arabidopsis thaliana] >gi_2795810 (AC003674) unknown protein [Arabidopsis thaliana]

Seq. No.	224952

Seq. ID	LIB3166-022-P1-K1-A2
Method	BLASTX
NCBI GI	g1363484
BLAST score	263
E value	5.0e-23
Match length	121
% identity	52
NCBI Description	IAA13 protein - Arabidopsis thaliana >gi_972929 (U18415) IAA13 [Arabidopsis thaliana] >gi_2459414 (AC002332) auxin inducible protein, IAA13 [Arabidopsis thaliana]

Seq. No.	224953
Seq. ID	LIB3166-022-P1-K1-A5
Method	BLASTX
NCBI GI	g1206005
BLAST score	295
E value	1.0e-26
Match length	65
% identity	89
NCBI Description	(U42400) putative MADS-box family transcription factor [Pinus radiata]

Seq. No.	224954
Seq. ID	LIB3166-022-P1-K1-A7
Method	BLASTX
NCBI GI	g99737
BLAST score	566
E value	2.0e-58
Match length	128
% identity	84
NCBI Description	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Arabidopsis thaliana >gi_16189_emb_CAA46815_ (X66017) NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]

Seq. No.	224955
Seq. ID	LIB3166-022-P1-K1-B1
Method	BLASTX
NCBI GI	g2811029
BLAST score	587
E value	6.0e-61
Match length	129
% identity	84
NCBI Description	ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT) (ACETYLORNITHINE TRANSAMINASE) (AOTA) >gi_1944511_emb_CAA69936_ (Y08680) acetylornithine aminotransferase [Alnus glutinosa]

Seq. No.	224956
Seq. ID	LIB3166-022-P1-K1-B10
Method	BLASTX
NCBI GI	g1345919
BLAST score	307
E value	1.0e-28
Match length	66
% identity	92
NCBI Description	APOCYTOCHROME F PRECURSOR >gi_984315 (U26948) cytochrome f precursor [Glycine max]

Seq. No.	224957
Seq. ID	LIB3166-022-P1-K1-B4
Method	BLASTX
NCBI GI	g1363483
BLAST score	243
E value	1.0e-20
Match length	63
% identity	76
NCBI Description	IAA12 protein - Arabidopsis thaliana >gi_972927 (U18414) IAA12 [Arabidopsis thaliana] >gi_2494122 (AC002376) Match to Arabidopsis IAA12 (gb_U18414). [Arabidopsis thaliana]

Seq. No.	224958
Seq. ID	LIB3166-022-P1-K1-B5
Method	BLASTX
NCBI GI	g3834323
BLAST score	149
E value	1.0e-09
Match length	50
% identity	58
NCBI Description	(AC005679) F9K20.25 [Arabidopsis thaliana]

Seq. No.	224959
Seq. ID	LIB3166-022-P1-K1-B7
Method	BLASTX
NCBI GI	g2997755
BLAST score	173
E value	2.0e-12
Match length	98
% identity	38
NCBI Description	(AF054823) TFIIH transcription/DNA repair factor p52 subunit [Mus musculus]

Seq. No.	224960
Seq. ID	LIB3166-022-P1-K1-B8
Method	BLASTX
NCBI GI	g1439609
BLAST score	559
E value	1.0e-57
Match length	115
% identity	53
NCBI Description	(U62778) delta-tonoplast intrinsic protein [Gossypium hirsutum]

Seq. No.	224961
Seq. ID	LIB3166-022-P1-K1-B9
Method	BLASTX
NCBI GI	g1351974
BLAST score	502
E value	5.0e-51
Match length	97
% identity	100
NCBI Description	ADP-RIBOSYLATION FACTOR >gi_1076788_pir__S49325 ADP-ribosylation factor - maize >gi_1076789_pir__S53486 ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_ (X80042) ADP-ribosylation factor [Zea mays]

Seq. No.	224962
Seq. ID	LIB3166-022-P1-K1-C12
Method	BLASTX
NCBI GI	g4468979
BLAST score	345
E value	1.0e-32
Match length	79
% identity	81
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	224963
Seq. ID	LIB3166-022-P1-K1-C3
Method	BLASTX
NCBI GI	g1220196
BLAST score	410
E value	4.0e-54
Match length	107
% identity	99
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	224964
Seq. ID	LIB3166-022-P1-K1-C6
Method	BLASTX
NCBI GI	g3107905
BLAST score	440
E value	9.0e-44
Match length	117
% identity	12
NCBI Description	(D85101) leaf protein [Ipomoea nil]

Seq. No.	224965
Seq. ID	LIB3166-022-P1-K1-C7
Method	BLASTX
NCBI GI	g4512122
BLAST score	219
E value	7.0e-18
Match length	120
% identity	47
NCBI Description	(AF131219) chorismate mutase 3 [Arabidopsis thaliana]

Seq. No.	224966
Seq. ID	LIB3166-022-P1-K1-C8
Method	BLASTX
NCBI GI	g4249382
BLAST score	437
E value	2.0e-43
Match length	126
% identity	67
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	224967
Seq. ID	LIB3166-022-P1-K1-C9
Method	BLASTX
NCBI GI	g584778

BLAST score	221
E value	5.0e-18
Match length	115
% identity	45
NCBI Description	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 2 PRECURSOR (PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 2) (DAHP SYNTHETASE 2) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE 2) >gi_542033_pir__S40412 2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) 2 precursor - tomato >gi_410488_emb_CAA79856_ (Z21793) phospho-2-dehydro-3-deoxyheptonate aldolase [Lycopersicon esculentum]

Seq. No.	224968
Seq. ID	LIB3166-022-P1-K1-D10
Method	BLASTX
NCBI GI	g2618731
BLAST score	584
E value	1.0e-60
Match length	124
% identity	88
NCBI Description	(U49077) IAA21 [Arabidopsis thaliana]

Seq. No.	224969
Seq. ID	LIB3166-022-P1-K1-D12
Method	BLASTX
NCBI GI	g68200
BLAST score	470
E value	3.0e-47
Match length	118
% identity	81
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No.	224970
Seq. ID	LIB3166-022-P1-K1-D4
Method	BLASTX
NCBI GI	g3434967
BLAST score	344
E value	2.0e-32
Match length	123
% identity	62
NCBI Description	(AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]

Seq. No.	224971
Seq. ID	LIB3166-022-P1-K1-D5
Method	BLASTX
NCBI GI	g421867
BLAST score	203
E value	1.0e-18
Match length	115
% identity	45
NCBI Description	ubiquitin / ribosomal protein CEP52 - turnip >gi_347064 (L21898) ubiquitin/ribosomal protein [Brassica rapa] >gi_395079_emb_CAA80863_ (Z24738) ubiquitin/ribosomal

protein [Brassica rapa]

Seq. No.	224972
Seq. ID	LIB3166-022-P1-K1-D8
Method	BLASTX
NCBI GI	g3885884
BLAST score	580
E value	4.0e-60
Match length	117
% identity	91
NCBI Description	(AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No.	224973
Seq. ID	LIB3166-022-P1-K1-E1
Method	BLASTX
NCBI GI	g553107
BLAST score	286
E value	1.0e-25
Match length	105
% identity	57
NCBI Description	(L04967) triosephosphate isomerase [Oryza sativa]

Seq. No.	224974
Seq. ID	LIB3166-022-P1-K1-E11
Method	BLASTX
NCBI GI	g3059095
BLAST score	471
E value	2.0e-47
Match length	97
% identity	92
NCBI Description	(AJ001091) magnesium chelatase subunit [Glycine max]

Seq. No.	224975
Seq. ID	LIB3166-022-P1-K1-E3
Method	BLASTX
NCBI GI	g3334261
BLAST score	232
E value	2.0e-19
Match length	54
% identity	74
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi_1655851 (U61973) metallothionein-like protein [Malus domestica]

Seq. No.	224976
Seq. ID	LIB3166-022-P1-K1-E6
Method	BLASTX
NCBI GI	g3608412
BLAST score	324
E value	4.0e-30
Match length	122
% identity	51
NCBI Description	(AF079355) protein phosphatase-2c [Mesembryanthemum crystallinum]

Seq. No.	224977
Seq. ID	LIB3166-022-P1-K1-E8
Method	BLASTX

NCBI GI	g2244781
BLAST score	242
E value	2.0e-20
Match length	126
% identity	31
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224978
Seq. ID	LIB3166-022-P1-K1-F10
Method	BLASTX
NCBI GI	g1403522
BLAST score	263
E value	5.0e-23
Match length	88
% identity	59
NCBI Description	(X57187) chitinase [Phaseolus vulgaris]

Seq. No.	224979
Seq. ID	LIB3166-022-P1-K1-F11
Method	BLASTX
NCBI GI	g1161575
BLAST score	161
E value	5.0e-11
Match length	84
% identity	50
NCBI Description	(X94947) homeobox [Lycopersicon esculentum]

Seq. No.	224980
Seq. ID	LIB3166-022-P1-K1-F12
Method	BLASTX
NCBI GI	g2914709
BLAST score	339
E value	7.0e-32
Match length	87
% identity	75
NCBI Description	(AC003974) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224981
Seq. ID	LIB3166-022-P1-K1-F2
Method	BLASTX
NCBI GI	g2160161
BLAST score	189
E value	3.0e-14
Match length	120
% identity	4
NCBI Description	(AC000132) F21M12.7 gene product [Arabidopsis thaliana]

Seq. No.	224982
Seq. ID	LIB3166-022-P1-K1-F9
Method	BLASTX
NCBI GI	g2462825
BLAST score	405
E value	1.0e-39
Match length	90
% identity	86
NCBI Description	(AF000657) contains Procite 'RNP1' putative RNA-binding region [Arabidopsis thaliana]

Seq. No.	224983
Seq. ID	LIB3166-022-P1-K1-G1
Method	BLASTX
NCBI GI	g4539383
BLAST score	195
E value	5.0e-15
Match length	86
% identity	43
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	224984
Seq. ID	LIB3166-022-P1-K1-G11
Method	BLASTX
NCBI GI	g541951
BLAST score	320
E value	1.0e-29
Match length	107
% identity	60
NCBI Description	SPCP2 protein - soybean >gi_310578 (L12258) nodulin-26 [Glycine max]

Seq. No.	224985
Seq. ID	LIB3166-022-P1-K1-G2
Method	BLASTX
NCBI GI	g3935170
BLAST score	192
E value	1.0e-14
Match length	132
% identity	47
NCBI Description	(AC004557) F17L21.13 [Arabidopsis thaliana]

Seq. No.	224986
Seq. ID	LIB3166-022-P1-K1-G3
Method	BLASTX
NCBI GI	g1255954
BLAST score	453
E value	3.0e-45
Match length	105
% identity	77
NCBI Description	(Z70677) thioredoxin [Ricinus communis]

Seq. No.	224987
Seq. ID	LIB3166-022-P1-K1-G4
Method	BLASTX
NCBI GI	g3451411
BLAST score	504
E value	3.0e-51
Match length	140
% identity	69
NCBI Description	(Z98761) seryl-tRNA synthetase [Helianthus annuus]

Seq. No.	224988
Seq. ID	LIB3166-022-P1-K1-G6
Method	BLASTX
NCBI GI	g2443878

BLAST score	177
E value	8.0e-13
Match length	128
% identity	38
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No.	224989
Seq. ID	LIB3166-022-P1-K1-G7
Method	BLASTX
NCBI GI	g2146739
BLAST score	373
E value	7.0e-36
Match length	112
% identity	65
NCBI Description	hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521 (U28214) hexokinase 1 [Arabidopsis thaliana]

Seq. No.	224990
Seq. ID	LIB3166-022-P1-K1-G8
Method	BLASTX
NCBI GI	g3582333
BLAST score	199
E value	2.0e-15
Match length	92
% identity	47
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224991
Seq. ID	LIB3166-022-P1-K1-G9
Method	BLASTX
NCBI GI	g2829863
BLAST score	306
E value	5.0e-28
Match length	101
% identity	56
NCBI Description	(AC002396) Putative peroxidase [Arabidopsis thaliana]

Seq. No.	224992
Seq. ID	LIB3166-022-P1-K1-H1
Method	BLASTX
NCBI GI	g4544443
BLAST score	159
E value	8.0e-11
Match length	34
% identity	91
NCBI Description	(AC006592) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	224993
Seq. ID	LIB3166-022-P1-K1-H10
Method	BLASTX
NCBI GI	g4210948
BLAST score	522
E value	2.0e-53
Match length	99
% identity	99
NCBI Description	(AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No.	224994
Seq. ID	LIB3166-022-P1-K1-H2
Method	BLASTX
NCBI GI	g1842140
BLAST score	164
E value	2.0e-11
Match length	103
% identity	31
NCBI Description	(AB001024) similar to Saccharomyces cerevisiae ORM1 gene: EMBL Accession Number Y08687 [Schizosaccharomyces pombe]

Seq. No.	224995
Seq. ID	LIB3166-022-P1-K1-H3
Method	BLASTX
NCBI GI	g3892054
BLAST score	498
E value	2.0e-50
Match length	121
% identity	69
NCBI Description	(AC002330) putative glycosyltransferase [Arabidopsis thaliana]

Seq. No.	224996
Seq. ID	LIB3166-022-P1-K1-H4
Method	BLASTX
NCBI GI	g4006890
BLAST score	563
E value	4.0e-58
Match length	124
% identity	84
NCBI Description	(Z99708) ubiquitin--protein ligase-like protein [Arabidopsis thaliana]

Seq. No.	224997
Seq. ID	LIB3166-022-P1-K1-H5
Method	BLASTX
NCBI GI	g3482967
BLAST score	168
E value	9.0e-12
Match length	46
% identity	70
NCBI Description	(AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	224998
Seq. ID	LIB3166-022-P1-K1-H7
Method	BLASTX
NCBI GI	g1107526
BLAST score	345
E value	1.0e-32
Match length	128
% identity	53
NCBI Description	(X87931) SIEP1L protein [Beta vulgaris]

Seq. No. 224999

Seq. ID	LIB3166-023-P1-K1-A10
Method	BLASTX
NCBI GI	g2129739
BLAST score	299
E value	3.0e-27
Match length	65
% identity	91
NCBI Description	shaggy-like kinase etha - Arabidopsis thaliana >gi_1161512_emb_CAA64409_ (X94939) shaggy-like kinase etha [Arabidopsis thaliana] >gi_1627516_emb_CAA70144_ (Y08947) shaggy-like kinase etha [Arabidopsis thaliana]

Seq. No.	225000
Seq. ID	LIB3166-023-P1-K1-A11
Method	BLASTX
NCBI GI	g2829911
BLAST score	435
E value	4.0e-43
Match length	110
% identity	45
NCBI Description	(AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No.	225001
Seq. ID	LIB3166-023-P1-K1-A7
Method	BLASTX
NCBI GI	g2980760
BLAST score	246
E value	6.0e-21
Match length	76
% identity	62
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	225002
Seq. ID	LIB3166-023-P1-K1-B10
Method	BLASTX
NCBI GI	g2662310
BLAST score	412
E value	2.0e-40
Match length	110
% identity	70
NCBI Description	(AB009307) bpw1 [Hordeum vulgare]

Seq. No.	225003
Seq. ID	LIB3166-023-P1-K1-B3
Method	BLASTX
NCBI GI	g3249084
BLAST score	435
E value	4.0e-43
Match length	127
% identity	22
NCBI Description	(AC004473) Similar to red-1 (related to thioredoxin) gene gb_X92750 from Mus musculus. ESTs gb_AA712687 and gb_Z37223 come from this gene [Arabidopsis thaliana]

Seq. No.	225004
Seq. ID	LIB3166-023-P1-K1-B4
Method	BLASTX

NCBI GI	g2865623
BLAST score	434
E value	5.0e-43
Match length	105
% identity	80
NCBI Description	(AF045286) GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase [Arabidopsis thaliana]

Seq. No.	225005
Seq. ID	LIB3166-023-P1-K1-B6
Method	BLASTX
NCBI GI	g3493172
BLAST score	278
E value	9.0e-25
Match length	70
% identity	80
NCBI Description	(U89609) fiber annexin [Gossypium hirsutum]

Seq. No.	225006
Seq. ID	LIB3166-023-P1-K1-B7
Method	BLASTX
NCBI GI	g3355474
BLAST score	109
E value	1.0e-12
Match length	51
% identity	58
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.	225007
Seq. ID	LIB3166-023-P1-K1-B9
Method	BLASTX
NCBI GI	g3249084
BLAST score	235
E value	7.0e-20
Match length	97
% identity	20
NCBI Description	(AC004473) Similar to red-1 (related to thioredoxin) gene gb_X92750 from Mus musculus. ESTs gb_AA712687 and gb_Z37223 come from this gene [Arabidopsis thaliana]

Seq. No.	225008
Seq. ID	LIB3166-023-P1-K1-C1
Method	BLASTX
NCBI GI	g3785972
BLAST score	130
E value	2.0e-18
Match length	83
% identity	75
NCBI Description	(AC005560) putative auxin transport protein [Arabidopsis thaliana] >gi_4262249_gb_AAD14542_ (AC006200) putative auxin transport protein [Arabidopsis thaliana]

Seq. No.	225009
Seq. ID	LIB3166-023-P1-K1-C3
Method	BLASTX
NCBI GI	g100454

BLAST score 395
E value 2.0e-38
Match length 88
% identity 86
NCBI Description photosystem II oxygen-evolving complex protein 1 - potato >gi_809113_emb_CAA35601_ (X17578) 33kDa precursor protein of oxygen-evolving complex [Solanum tuberosum]

Seq. No. 225010
Seq. ID LIB3166-023-P1-K1-C4
Method BLASTX
NCBI GI g3150402
BLAST score 189
E value 3.0e-14
Match length 90
% identity 56
NCBI Description (AC004165) putative malonyl-CoA:Acyl carrier protein transacylase [Arabidopsis thaliana]

Seq. No. 225011
Seq. ID LIB3166-023-P1-K1-C5
Method BLASTX
NCBI GI g445613
BLAST score 305
E value 7.0e-28
Match length 113
% identity 58
NCBI Description ribosomal protein L7 [Solanum tuberosum]

Seq. No. 225012
Seq. ID LIB3166-023-P1-K1-C7
Method BLASTX
NCBI GI g3377509
BLAST score 348
E value 6.0e-33
Match length 88
% identity 83
NCBI Description (AF056027) auxin transport protein REH1 [Oryza sativa]

Seq. No. 225013
Seq. ID LIB3166-023-P1-K1-C8
Method BLASTX
NCBI GI g571519
BLAST score 146
E value 2.0e-09
Match length 62
% identity 9
NCBI Description (U16852) polyubiquitin [Gracilaria verrucosa] >gi_1095488_prf__2109223A poly-ubiquitin [Gracilaria verrucosa]

Seq. No. 225014
Seq. ID LIB3166-023-P1-K1-C9
Method BLASTX
NCBI GI g2244811
BLAST score 164
E value 2.0e-11

Match length	77
% identity	53
NCBI Description	(Z97336) unnamed protein product [Arabidopsis thaliana]

Seq. No.	225015
Seq. ID	LIB3166-023-P1-K1-D1
Method	BLASTX
NCBI GI	g544134
BLAST score	157
E value	1.0e-10
Match length	49
% identity	61
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR >gi_99720_pir__S22863 hypothetical protein - Arabidopsis thaliana >gi_421844_pir__A46260 RecA functional analog DRT100 - Arabidopsis thaliana (fragment)

Seq. No.	225016
Seq. ID	LIB3166-023-P1-K1-D11
Method	BLASTX
NCBI GI	g1169476
BLAST score	268
E value	9.0e-25
Match length	123
% identity	67
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632) vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No.	225017
Seq. ID	LIB3166-023-P1-K1-D12
Method	BLASTX
NCBI GI	g1531758
BLAST score	259
E value	2.0e-22
Match length	55
% identity	84
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	225018
Seq. ID	LIB3166-023-P1-K1-D6
Method	BLASTX
NCBI GI	g3928150
BLAST score	236
E value	1.0e-40
Match length	125
% identity	72
NCBI Description	(AJ131049) hypothetical protein [Cicer arietinum]

Seq. No.	225019
Seq. ID	LIB3166-023-P1-K1-D7
Method	BLASTX
NCBI GI	g4379369
BLAST score	179
E value	2.0e-13
Match length	77

% identity	28
NCBI Description	(X90560) Calmodulin [Cloning vector pBluescript]

Seq. No.	225020
Seq. ID	LIB3166-023-P1-K1-D8
Method	BLASTX
NCBI GI	g3643598
BLAST score	532
E value	2.0e-54
Match length	126
% identity	72
NCBI Description	(AC005395) putative poly(A) polymerase [Arabidopsis thaliana]

Seq. No.	225021
Seq. ID	LIB3166-023-P1-K1-D9
Method	BLASTX
NCBI GI	g3885338
BLAST score	215
E value	2.0e-17
Match length	109
% identity	36
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	225022
Seq. ID	LIB3166-023-P1-K1-E11
Method	BLASTX
NCBI GI	g1076621
BLAST score	487
E value	3.0e-49
Match length	110
% identity	78
NCBI Description	cytochrome b5 - common tobacco >gi_296386_emb_CAA50575_ (X71441) cytochrome b5 [Nicotiana tabacum]

Seq. No.	225023
Seq. ID	LIB3166-023-P1-K1-E4
Method	BLASTX
NCBI GI	g4490705
BLAST score	471
E value	2.0e-47
Match length	108
% identity	86
NCBI Description	(AL035680) ribosomal protein L14-like protein [Arabidopsis thaliana]

Seq. No.	225024
Seq. ID	LIB3166-023-P1-K1-E5
Method	BLASTX
NCBI GI	g1458245
BLAST score	270
E value	8.0e-24
Match length	128
% identity	46
NCBI Description	(U64834) coded for by C. elegans cDNA cm17a1; coded for by C. elegans cDNA cm7g1; coded for by C. elegans cDNA CEMSE26F; similar to methyltransferases [Caenorhabditis

elegans]

Seq. No.	225025
Seq. ID	LIB3166-023-P1-K1-E6
Method	BLASTX
NCBI GI	g4508068
BLAST score	155
E value	3.0e-10
Match length	38
% identity	68
NCBI Description	(AC005882) 3063 [Arabidopsis thaliana]

Seq. No.	225026
Seq. ID	LIB3166-023-P1-K1-E7
Method	BLASTX
NCBI GI	g2335098
BLAST score	245
E value	7.0e-21
Match length	108
% identity	44
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]

Seq. No.	225027
Seq. ID	LIB3166-023-P1-K1-E8
Method	BLASTX
NCBI GI	g2245106
BLAST score	180
E value	2.0e-24
Match length	87
% identity	58
NCBI Description	(Z97343) thioesterase homolog [Arabidopsis thaliana]

Seq. No.	225028
Seq. ID	LIB3166-023-P1-K1-F5
Method	BLASTX
NCBI GI	g2827549
BLAST score	431
E value	1.0e-42
Match length	88
% identity	88
NCBI Description	(AL021635) glycoprotein endopeptidase - like protein [Arabidopsis thaliana]

Seq. No.	225029
Seq. ID	LIB3166-023-P1-K1-G1
Method	BLASTX
NCBI GI	g3832512
BLAST score	146
E value	2.0e-20
Match length	64
% identity	84
NCBI Description	(AF097922) granule-bound glycogen (starch) synthase [Astragalus membranaceus]

Seq. No.	225030
Seq. ID	LIB3166-023-P1-K1-G10
Method	BLASTX

NCBI GI	g4455177
BLAST score	434
E value	5.0e-43
Match length	120
% identity	70
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	225031
Seq. ID	LIB3166-023-P1-K1-G8
Method	BLASTX
NCBI GI	g2459419
BLAST score	216
E value	2.0e-17
Match length	126
% identity	46
NCBI Description	(AC002332) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225032
Seq. ID	LIB3166-023-P1-K1-G9
Method	BLASTX
NCBI GI	g3451075
BLAST score	536
E value	4.0e-58
Match length	128
% identity	86
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	225033
Seq. ID	LIB3166-023-P1-K1-H1
Method	BLASTX
NCBI GI	g4580523
BLAST score	279
E value	7.0e-25
Match length	126
% identity	39
NCBI Description	(AF036305) scarecrow-like 8 [Arabidopsis thaliana]

Seq. No.	225034
Seq. ID	LIB3166-023-P1-K1-H10
Method	BLASTX
NCBI GI	g417154
BLAST score	668
E value	2.0e-70
Match length	130
% identity	98
NCBI Description	HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

Seq. No.	225035
Seq. ID	LIB3166-023-P1-K1-H11
Method	BLASTX
NCBI GI	g3402678
BLAST score	191
E value	2.0e-14
Match length	53

% identity	74
NCBI Description	(AC004697) putative adenylate kinase [Arabidopsis thaliana]
Seq. No.	225036
Seq. ID	LIB3166-023-P1-K1-H12
Method	BLASTX
NCBI GI	g2833389
BLAST score	350
E value	2.0e-33
Match length	86
% identity	41
NCBI Description	SOLUBLE GLYCOGEN (STARCH) SYNTHASE PRECURSOR (SS III) >gi_1200154_emb_CAA65065_ (X95759) glycogen (starch) synthase [Solanum tuberosum]
Seq. No.	225037
Seq. ID	LIB3166-023-P1-K1-H4
Method	BLASTX
NCBI GI	g1353352
BLAST score	272
E value	5.0e-32
Match length	115
% identity	57
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]
Seq. No.	225038
Seq. ID	LIB3166-023-P1-K1-H5
Method	BLASTX
NCBI GI	g2982458
BLAST score	272
E value	5.0e-24
Match length	81
% identity	67
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]
Seq. No.	225039
Seq. ID	LIB3166-023-P1-K1-H6
Method	BLASTX
NCBI GI	g1171579
BLAST score	173
E value	3.0e-15
Match length	83
% identity	60
NCBI Description	(X95342) cytochrome P450 [Nicotiana tabacum]
Seq. No.	225040
Seq. ID	LIB3166-023-P1-K1-H7
Method	BLASTX
NCBI GI	g3046821
BLAST score	311
E value	1.0e-28
Match length	56
% identity	96
NCBI Description	(AB004785) homeobox gene [Nicotiana tabacum]
Seq. No.	225041

Seq. ID	LIB3166-023-P1-K1-H8
Method	BLASTX
NCBI GI	g136251
BLAST score	172
E value	2.0e-12
Match length	63
% identity	60
NCBI Description	TRYPTOPHAN SYNTHASE BETA CHAIN 1 PRECURSOR >gi_99767_pir__A31393 tryptophan synthase (EC 4.2.1.20) beta chain - Arabidopsis thaliana >gi_166892 (M23872) tryptophan synthase beta subunit [Arabidopsis thaliana]

Seq. No.	225042
Seq. ID	LIB3166-023-P1-K1-H9
Method	BLASTX
NCBI GI	g3434967
BLAST score	225
E value	1.0e-18
Match length	77
% identity	58
NCBI Description	(AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]

Seq. No.	225043
Seq. ID	LIB3166-024-P1-K1-A1
Method	BLASTX
NCBI GI	g2147165
BLAST score	477
E value	5.0e-48
Match length	113
% identity	52
NCBI Description	calmodulin - Bidens pilosa >gi_939860_emb_CAA61980_ (X89890) Calmodulin [Bidens pilosa]

Seq. No.	225044
Seq. ID	LIB3166-024-P1-K1-A3
Method	BLASTX
NCBI GI	g2880043
BLAST score	159
E value	8.0e-11
Match length	62
% identity	48
NCBI Description	(AC002340) putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]

Seq. No.	225045
Seq. ID	LIB3166-024-P1-K1-A4
Method	BLASTX
NCBI GI	g3513745
BLAST score	193
E value	6.0e-19
Match length	112
% identity	44
NCBI Description	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]

Seq. No.	225046

Seq. ID LIB3166-024-P1-K1-A6
Method BLASTX
NCBI GI g3269293
BLAST score 249
E value 2.0e-21
Match length 88
% identity 64
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 225047
Seq. ID LIB3166-024-P1-K1-A8
Method BLASTX
NCBI GI g1815759
BLAST score 194
E value 7.0e-15
Match length 105
% identity 40
NCBI Description (U85499) pollen-specific protein [Phalaris coerulescens]

Seq. No. 225048
Seq. ID LIB3166-024-P1-K1-B1
Method BLASTX
NCBI GI g3600032
BLAST score 174
E value 1.0e-12
Match length 38
% identity 87
NCBI Description (AF080119) contains similarity to tropomyosin (Pfam: Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam: ATP-synt_B.hmm, score: 10.89) [Arabidopsis thaliana]

Seq. No. 225049
Seq. ID LIB3166-024-P1-K1-B10
Method BLASTX
NCBI GI g2879867
BLAST score 396
E value 1.0e-38
Match length 110
% identity 68
NCBI Description (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces pombe]

Seq. No. 225050
Seq. ID LIB3166-024-P1-K1-B11
Method BLASTX
NCBI GI g4455199
BLAST score 435
E value 3.0e-43
Match length 116
% identity 74
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 225051
Seq. ID LIB3166-024-P1-K1-B12
Method BLASTX
NCBI GI g3063396
BLAST score 542

E value	1.0e-55
Match length	126
% identity	81
NCBI Description	(AB012947) vcCyP [Vicia faba]

Seq. No.	225052
Seq. ID	LIB3166-024-P1-K1-B2
Method	BLASTX
NCBI GI	g2959767
BLAST score	423
E value	1.0e-41
Match length	108
% identity	77
NCBI Description	(AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292 (AC005309) glutathione-conjugate transporter AtMRP4 [Arabidopsis thaliana]

Seq. No.	225053
Seq. ID	LIB3166-024-P1-K1-B3
Method	BLASTX
NCBI GI	g586004
BLAST score	530
E value	3.0e-54
Match length	109
% identity	89
NCBI Description	SUPEROXIDE DISMUTASE [CU-ZN] >gi_421962_pir__S34267 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato >gi_542090_pir__S40404 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato >gi_311971_emb_CAA51654_ (X73139) superoxide dismutase [Ipomoea batatas]

Seq. No.	225054
Seq. ID	LIB3166-024-P1-K1-B4
Method	BLASTX
NCBI GI	g3776005
BLAST score	213
E value	4.0e-17
Match length	42
% identity	98
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	225055
Seq. ID	LIB3166-024-P1-K1-B5
Method	BLASTX
NCBI GI	g4567253
BLAST score	230
E value	4.0e-19
Match length	118
% identity	47
NCBI Description	(AC007070) putative serpin protein [Arabidopsis thaliana]

Seq. No.	225056
Seq. ID	LIB3166-024-P1-K1-B7
Method	BLASTX
NCBI GI	g3355475
BLAST score	298
E value	4.0e-27

Match length	66
% identity	92
NCBI Description	(AC004218) ribosomal protein L23a [Arabidopsis thaliana]

Seq. No.	225057
Seq. ID	LIB3166-024-P1-K1-B8
Method	BLASTX
NCBI GI	g2078561
BLAST score	186
E value	7.0e-21
Match length	106
% identity	67
NCBI Description	(U96661) naringenin-chalcone synthase [Chrysosplenium americanum]

Seq. No.	225058
Seq. ID	LIB3166-024-P1-K1-C11
Method	BLASTX
NCBI GI	g2618721
BLAST score	139
E value	1.0e-08
Match length	45
% identity	62
NCBI Description	(U49072) IAA16 [Arabidopsis thaliana]

Seq. No.	225059
Seq. ID	LIB3166-024-P1-K1-C12
Method	BLASTX
NCBI GI	g4262226
BLAST score	155
E value	3.0e-10
Match length	31
% identity	87
NCBI Description	(AC006200) putative protein kinase [Arabidopsis thaliana]

Seq. No.	225060
Seq. ID	LIB3166-024-P1-K1-C2
Method	BLASTX
NCBI GI	g4210948
BLAST score	565
E value	2.0e-58
Match length	109
% identity	96
NCBI Description	(AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No.	225061
Seq. ID	LIB3166-024-P1-K1-C3
Method	BLASTX
NCBI GI	g3757527
BLAST score	178
E value	5.0e-13
Match length	43
% identity	84
NCBI Description	(AC005167) putative ribosomal protein L27 [Arabidopsis thaliana]

Seq. No.	225062

Seq. ID	LIB3166-024-P1-K1-C5
Method	BLASTX
NCBI GI	g3355468
BLAST score	261
E value	3.0e-23
Match length	63
% identity	87
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No.	225063
Seq. ID	LIB3166-024-P1-K1-C6
Method	BLASTX
NCBI GI	g2194142
BLAST score	500
E value	8.0e-51
Match length	109
% identity	84
NCBI Description	(AC002062) ESTs gb_N38288,gb_T43486,gb_AA395242 come from this gene. [Arabidopsis thaliana]

Seq. No.	225064
Seq. ID	LIB3166-024-P1-K1-C8
Method	BLASTX
NCBI GI	g2289003
BLAST score	241
E value	2.0e-20
Match length	55
% identity	82
NCBI Description	(AC002335) membrane transporter D1 isolog [Arabidopsis thaliana]

Seq. No.	225065
Seq. ID	LIB3166-024-P1-K1-D12
Method	BLASTX
NCBI GI	g3582342
BLAST score	221
E value	5.0e-18
Match length	125
% identity	41
NCBI Description	(AC005496) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	225066
Seq. ID	LIB3166-024-P1-K1-D4
Method	BLASTX
NCBI GI	g3033386
BLAST score	165
E value	2.0e-11
Match length	72
% identity	46
NCBI Description	(AC004238) RING3-like protein [Arabidopsis thaliana]

Seq. No.	225067
Seq. ID	LIB3166-024-P1-K1-D5
Method	BLASTX
NCBI GI	g2245082

BLAST score 518
E value 7.0e-53
Match length 115
% identity 84
NCBI Description (Z97343) SCARECROW homolog [Arabidopsis thaliana]

Seq. No. 225068
Seq. ID LIB3166-024-P1-K1-E1
Method BLASTX
NCBI GI g3947735
BLAST score 280
E value 6.0e-25
Match length 107
% identity 51
NCBI Description (AJ009720) NL27 [Solanum tuberosum]

Seq. No. 225069
Seq. ID LIB3166-024-P1-K1-E10
Method BLASTX
NCBI GI g2289002
BLAST score 350
E value 3.0e-33
Match length 110
% identity 65
NCBI Description (AC002335) unknown protein [Arabidopsis thaliana]

Seq. No. 225070
Seq. ID LIB3166-024-P1-K1-E12
Method BLASTX
NCBI GI g1346524
BLAST score 601
E value 1.0e-62
Match length 126
% identity 90
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi_497900 (M73430) S-adenosyl methionine synthetase [Populus deltoides]

Seq. No. 225071
Seq. ID LIB3166-024-P1-K1-E4
Method BLASTX
NCBI GI g2342685
BLAST score 424
E value 7.0e-42
Match length 127
% identity 65
NCBI Description (AC000106) Contains similarity to Rhodococcus amidase (gb_D16207). ESTs gb_T20504,gb_H36650,gb_N97423,gb_H36595 come from this gene. [Arabidopsis thaliana]

Seq. No. 225072
Seq. ID LIB3166-024-P1-K1-E6
Method BLASTX
NCBI GI g1871192
BLAST score 156
E value 2.0e-10

0004074 - 0004950

Match length	116
% identity	41
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	225073
Seq. ID	LIB3166-024-P1-K1-E7
Method	BLASTX
NCBI GI	g3135013
BLAST score	154
E value	3.0e-10
Match length	103
% identity	40
NCBI Description	(AJ005963) 100 kDa protein [Ajellomyces capsulatus]

Seq. No.	225074
Seq. ID	LIB3166-024-P1-K1-E9
Method	BLASTX
NCBI GI	g3334322
BLAST score	451
E value	5.0e-45
Match length	109
% identity	81
NCBI Description	GTP-BINDING PROTEIN SAR1B >gi_2108347 (U55036) small GTP-binding protein Bsar1b [Brassica rapa]

Seq. No.	225075
Seq. ID	LIB3166-024-P1-K1-F12
Method	BLASTX
NCBI GI	g886116
BLAST score	428
E value	2.0e-42
Match length	119
% identity	66
NCBI Description	(U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473 (AF051338) xyloglucan endotransglycosylase related protein [Arabidopsis thaliana]

Seq. No.	225076
Seq. ID	LIB3166-024-P1-K1-F4
Method	BLASTX
NCBI GI	g1351408
BLAST score	419
E value	3.0e-41
Match length	96
% identity	81
NCBI Description	VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) >gi_1076563_pir__S51117 cystein proteinase - sweet orange >gi_633185_emb_CAA87720_ (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi_1588548_prf__2208463A vascular processing protease [Citrus sinensis]

Seq. No.	225077
Seq. ID	LIB3166-024-P1-K1-F5
Method	BLASTX
NCBI GI	g1518540
BLAST score	574

E value	2.0e-59
Match length	133
% identity	86
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	225078
Seq. ID	LIB3166-024-P1-K1-F7
Method	BLASTX
NCBI GI	g4567279
BLAST score	409
E value	4.0e-40
Match length	112
% identity	71
NCBI Description	(AC006841) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	225079
Seq. ID	LIB3166-024-P1-K1-F9
Method	BLASTX
NCBI GI	g2342682
BLAST score	448
E value	1.0e-44
Match length	114
% identity	75
NCBI Description	(AC000106) Contains similarity to Rattus AMP-activated protein kinase (gb_X95577). [Arabidopsis thaliana]

Seq. No.	225080
Seq. ID	LIB3166-024-P1-K1-G11
Method	BLASTX
NCBI GI	g4580460
BLAST score	293
E value	1.0e-26
Match length	88
% identity	69
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No.	225081
Seq. ID	LIB3166-024-P1-K1-G2
Method	BLASTX
NCBI GI	g1486472
BLAST score	405
E value	1.0e-39
Match length	92
% identity	86
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]

Seq. No.	225082
Seq. ID	LIB3166-024-P1-K1-G3
Method	BLASTX
NCBI GI	g2864622
BLAST score	228
E value	7.0e-19
Match length	100
% identity	49

NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]
Seq. No.	225083
Seq. ID	LIB3166-024-P1-K1-G5
Method	BLASTX
NCBI GI	g4539370
BLAST score	337
E value	1.0e-31
Match length	86
% identity	73
NCBI Description	(AL049525) UDP-galactose 4-epimerase-like protein [Arabidopsis thaliana]
Seq. No.	225084
Seq. ID	LIB3166-024-P1-K1-G7
Method	BLASTX
NCBI GI	g3142303
BLAST score	522
E value	2.0e-53
Match length	127
% identity	83
NCBI Description	(AC002411) Strong similarity to MRP-like ABC transporter gb_U92650 from A. thaliana and canalicular multi-drug resistance protein gb_L49379 from Rattus norvegicus. [Arabidopsis thaliana]
Seq. No.	225085
Seq. ID	LIB3166-024-P1-K1-G8
Method	BLASTX
NCBI GI	g3650030
BLAST score	217
E value	1.0e-17
Match length	74
% identity	53
NCBI Description	(AC005396) unknown protein [Arabidopsis thaliana]
Seq. No.	225086
Seq. ID	LIB3166-024-P1-K1-G9
Method	BLASTX
NCBI GI	g464981
BLAST score	354
E value	1.0e-33
Match length	65
% identity	98
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]
Seq. No.	225087
Seq. ID	LIB3166-024-P1-K1-H1
Method	BLASTX
NCBI GI	g4099914
BLAST score	279
E value	7.0e-25
Match length	79
% identity	71
NCBI Description	(U91857) ethylene-responsive element binding protein

	homolog [Stylosanthes hamata]
Seq. No.	225088
Seq. ID	LIB3166-024-P1-K1-H10
Method	BLASTX
NCBI GI	g3660471
BLAST score	590
E value	2.0e-61
Match length	124
% identity	91
NCBI Description	(AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]
Seq. No.	225089
Seq. ID	LIB3166-024-P1-K1-H12
Method	BLASTX
NCBI GI	g125887
BLAST score	196
E value	4.0e-15
Match length	101
% identity	45
NCBI Description	ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR >gi_82092_pir__S04765 LAT52 protein precursor - tomato >gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon esculentum]
Seq. No.	225090
Seq. ID	LIB3166-024-P1-K1-H2
Method	BLASTX
NCBI GI	g2702270
BLAST score	302
E value	1.0e-27
Match length	85
% identity	66
NCBI Description	(AC003033) unknown protein [Arabidopsis thaliana]
Seq. No.	225091
Seq. ID	LIB3166-024-P1-K1-H3
Method	BLASTX
NCBI GI	g1173256
BLAST score	572
E value	3.0e-59
Match length	129
% identity	88
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal protein S4 - upland cotton >gi_488739_emb_CAA55882_ (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]
Seq. No.	225092
Seq. ID	LIB3166-024-P1-K1-H4
Method	BLASTX
NCBI GI	g3894190
BLAST score	208
E value	2.0e-16
Match length	71
% identity	54

NCBI Description	(AC005662) putative RNA polymerase [Arabidopsis thaliana]

Seq. No.	225093
Seq. ID	LIB3166-024-P1-K1-H7
Method	BLASTX
NCBI GI	g1353193
BLAST score	157
E value	1.0e-10
Match length	71
% identity	49
NCBI Description	O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir__JQ2268 O-methyltransferase (EC 2.1.1.-) - maize >gi_404070 (L14063) O-methyltransferase [Zea mays]

Seq. No.	225094
Seq. ID	LIB3166-024-P1-K1-H8
Method	BLASTX
NCBI GI	g2529342
BLAST score	587
E value	5.0e-61
Match length	112
% identity	94
NCBI Description	(L76554) transketolase [Spinacia oleracea]

Seq. No.	225095
Seq. ID	LIB3166-024-P1-K1-H9
Method	BLASTX
NCBI GI	g4115914
BLAST score	319
E value	2.0e-29
Match length	117
% identity	52
NCBI Description	(AF118222) contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=297.8, E=1.3e-85, N=1) [Arabidopsis thaliana] >gi_4539410_emb_CAB40043.1_ (AL049524) putative Fe(II)/ascorbate oxidase [Arabidopsis thaliana]

Seq. No.	225096
Seq. ID	LIB3166-025-P1-K1-A11
Method	BLASTX
NCBI GI	g3789911
BLAST score	266
E value	2.0e-23
Match length	117
% identity	43
NCBI Description	(AF081802) developmental protein DG1118 [Dictyostelium discoideum]

Seq. No.	225097
Seq. ID	LIB3166-025-P1-K1-A2
Method	BLASTX
NCBI GI	g289920
BLAST score	507
E value	1.0e-51
Match length	104
% identity	90

NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]
Seq. No.	225098
Seq. ID	LIB3166-025-P1-K1-A4
Method	BLASTX
NCBI GI	g3273243
BLAST score	582
E value	2.0e-60
Match length	127
% identity	23
NCBI Description	(AB004660) NLS receptor [Oryza sativa] >gi_3273245_dbj_BAA31166_ (AB004814) NLS receptor [Oryza sativa]
Seq. No.	225099
Seq. ID	LIB3166-025-P1-K1-A5
Method	BLASTX
NCBI GI	g2660670
BLAST score	370
E value	1.0e-35
Match length	103
% identity	74
NCBI Description	(AC002342) putative Cu2+-transporting ATPase [Arabidopsis thaliana]
Seq. No.	225100
Seq. ID	LIB3166-025-P1-K1-A6
Method	BLASTX
NCBI GI	g2827559
BLAST score	162
E value	3.0e-11
Match length	42
% identity	71
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana] >gi_3292808_emb_CAA19798_ (AL031018) putative protein [Arabidopsis thaliana]
Seq. No.	225101
Seq. ID	LIB3166-025-P1-K1-A7
Method	BLASTX
NCBI GI	g4454026
BLAST score	166
E value	1.0e-11
Match length	53
% identity	62
NCBI Description	(AL035394) phosphatase like protein [Arabidopsis thaliana]
Seq. No.	225102
Seq. ID	LIB3166-025-P1-K1-A8
Method	BLASTX
NCBI GI	g4335739
BLAST score	173
E value	2.0e-12
Match length	71
% identity	48
NCBI Description	(AC006248) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225103
Seq. ID	LIB3166-025-P1-K1-A9
Method	BLASTX
NCBI GI	g3552003
BLAST score	666
E value	3.0e-70
Match length	129
% identity	97
NCBI Description	(AF085083) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3552005 (AF085084) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3552007 (AF085085) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140632 (AF090165) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140634 (AF090166) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140636 (AF090167) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140638 (AF090168) alcohol dehydrogenase A [Gossypium hirsutum]

Seq. No.	225104
Seq. ID	LIB3166-025-P1-K1-B11
Method	BLASTX
NCBI GI	g2462745
BLAST score	288
E value	4.0e-26
Match length	85
% identity	60
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	225105
Seq. ID	LIB3166-025-P1-K1-B2
Method	BLASTX
NCBI GI	g1843527
BLAST score	444
E value	3.0e-44
Match length	118
% identity	76
NCBI Description	(U73747) annexin [Gossypium hirsutum]

Seq. No.	225106
Seq. ID	LIB3166-025-P1-K1-B3
Method	BLASTX
NCBI GI	g4469023
BLAST score	229
E value	6.0e-19
Match length	66
% identity	83
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	225107
Seq. ID	LIB3166-025-P1-K1-B4
Method	BLASTX
NCBI GI	g3395429
BLAST score	318
E value	2.0e-29
Match length	127
% identity	50

NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]
Seq. No.	225108
Seq. ID	LIB3166-025-P1-K1-C11
Method	BLASTX
NCBI GI	g2462762
BLAST score	278
E value	8.0e-25
Match length	105
% identity	55
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.	225109
Seq. ID	LIB3166-025-P1-K1-C12
Method	BLASTX
NCBI GI	g4510407
BLAST score	142
E value	8.0e-09
Match length	122
% identity	35
NCBI Description	(AC006587) unknown protein [Arabidopsis thaliana]
Seq. No.	225110
Seq. ID	LIB3166-025-P1-K1-C3
Method	BLASTX
NCBI GI	g2144271
BLAST score	597
E value	4.0e-62
Match length	127
% identity	91
NCBI Description	trans-cinnamate 4-monooxygenase (EC 1.14.13.11) C - Populus kitakamiensis (fragment) >gi_1777372_dbj_BAA11578_ (D82814) cinnamic acid 4-hydroxylase [Populus kitakamiensis]
Seq. No.	225111
Seq. ID	LIB3166-025-P1-K1-C5
Method	BLASTX
NCBI GI	g1220196
BLAST score	537
E value	4.0e-55
Match length	115
% identity	87
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.	225112
Seq. ID	LIB3166-025-P1-K1-C6
Method	BLASTX
NCBI GI	g3805845
BLAST score	463
E value	2.0e-46
Match length	118
% identity	73
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]
Seq. No.	225113
Seq. ID	LIB3166-025-P1-K1-C7

Method	BLASTX
NCBI GI	g131392
BLAST score	331
E value	6.0e-31
Match length	104
% identity	68
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_81479_pir__S00005 photosystem II oxygen-evolving complex protein 2 precursor - spinach >gi_21265_emb_CAA29055_ (X05511) 23 kDa OEC protein [Spinacia oleracea] >gi_225596_prf__1307179A luminal protein 23kD [Spinacia oleracea]

Seq. No.	225114
Seq. ID	LIB3166-025-P1-K1-C8
Method	BLASTX
NCBI GI	g4097579
BLAST score	441
E value	7.0e-44
Match length	92
% identity	89
NCBI Description	(U64922) NTGP1 [Nicotiana tabacum]

Seq. No.	225115
Seq. ID	LIB3166-025-P1-K1-D1
Method	BLASTX
NCBI GI	g3738293
BLAST score	410
E value	3.0e-40
Match length	95
% identity	78
NCBI Description	(AC005309) putative CCAAT-binding transcription factor subunit A (CBF-A) [Arabidopsis thaliana]

Seq. No.	225116
Seq. ID	LIB3166-025-P1-K1-D2
Method	BLASTX
NCBI GI	g509163
BLAST score	336
E value	2.0e-35
Match length	102
% identity	69
NCBI Description	(X69193) cyprosin [Cynara cardunculus]

Seq. No.	225117
Seq. ID	LIB3166-025-P1-K1-D5
Method	BLASTX
NCBI GI	g3080401
BLAST score	438
E value	2.0e-43
Match length	112
% identity	77
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana] >gi_4455265_emb_CAB36801.1_ (AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	225118
Seq. ID	LIB3166-025-P1-K1-D6
Method	BLASTX
NCBI GI	g4510376
BLAST score	371
E value	1.0e-35
Match length	83
% identity	78
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	225119
Seq. ID	LIB3166-025-P1-K1-D7
Method	BLASTX
NCBI GI	g3763916
BLAST score	200
E value	1.0e-15
Match length	103
% identity	45
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana] >gi_4531439_gb_AAD22124.1_AC006224_6 (AC006224) unknown protein [Arabidopsis thaliana]

Seq. No.	225120
Seq. ID	LIB3166-025-P1-K1-E1
Method	BLASTX
NCBI GI	g3367523
BLAST score	340
E value	4.0e-32
Match length	88
% identity	74
NCBI Description	(AC004392) ESTs gb_AA728658 and gb_N95943 come from this gene. [Arabidopsis thaliana]

Seq. No.	225121
Seq. ID	LIB3166-025-P1-K1-E10
Method	BLASTX
NCBI GI	g118564
BLAST score	531
E value	2.0e-54
Match length	125
% identity	82
NCBI Description	GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE REDUCTASE) (HPR) (GDH) >gi_65955_pir__DEKVG glycerate dehydrogenase (EC 1.1.1.29) - cucumber >gi_18264_emb_CAA41434_ (X58542) NADH-dependent hydroxypyruvate reductase [Cucumis sativus] >gi_18275_emb_CAA32764_ (X14609) NAPH-dependent hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

Seq. No.	225122
Seq. ID	LIB3166-025-P1-K1-E3
Method	BLASTX
NCBI GI	g1352821
BLAST score	537
E value	4.0e-55
Match length	107
% identity	95

NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	225123
Seq. ID	LIB3166-025-P1-K1-E4
Method	BLASTX
NCBI GI	g3421096
BLAST score	516
E value	1.0e-52
Match length	114
% identity	89
NCBI Description	(AF043528) 20S proteasome subunit PAG1 [Arabidopsis thaliana] >gi_3885332 (AC005623) proteasome component [Arabidopsis thaliana]
Seq. No.	225124
Seq. ID	LIB3166-025-P1-K1-E5
Method	BLASTX
NCBI GI	g4567319
BLAST score	558
E value	1.0e-57
Match length	124
% identity	87
NCBI Description	(AC005956) putative copper amine oxidase [Arabidopsis thaliana]
Seq. No.	225125
Seq. ID	LIB3166-025-P1-K1-E8
Method	BLASTX
NCBI GI	g1706318
BLAST score	268
E value	1.0e-23
Match length	106
% identity	55
NCBI Description	GLUTAMATE DECARBOXYLASE (GAD) (ERT D1) >gi_1362098_pir__S56177 probable glutamate decarboxylase - tomato >gi_995555_emb_CAA56812_ (X80840) homology to pyroxidal-5'-phosphate-dependant glutamate decarboxylases; putative start codon [Lycopersicon esculentum]
Seq. No.	225126
Seq. ID	LIB3166-025-P1-K1-F10
Method	BLASTX
NCBI GI	g1220196
BLAST score	538
E value	3.0e-55
Match length	114
% identity	89
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.	225127
Seq. ID	LIB3166-025-P1-K1-F11
Method	BLASTX
NCBI GI	g2894306

BLAST score	471
E value	2.0e-47
Match length	122
% identity	80
NCBI Description	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]

Seq. No.	225128
Seq. ID	LIB3166-025-P1-K1-F3
Method	BLASTX
NCBI GI	g477280
BLAST score	230
E value	4.0e-19
Match length	57
% identity	70
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) 55K protein precursor - potato >gi_410633_bbs_136740 cytochrome c reductase-processing peptidase subunit I, MPP subunit I, P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 534 aa]

Seq. No.	225129
Seq. ID	LIB3166-025-P1-K1-F5
Method	BLASTX
NCBI GI	g118564
BLAST score	215
E value	1.0e-23
Match length	82
% identity	78
NCBI Description	GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE REDUCTASE) (HPR) (GDH) >gi_65955_pir__DEKVG glycerate dehydrogenase (EC 1.1.1.29) - cucumber >gi_18264_emb_CAA41434_ (X58542) NADH-dependent hydroxypyruvate reductase [Cucumis sativus] >gi_18275_emb_CAA32764_ (X14609) NAPH-dependent hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

Seq. No.	225130
Seq. ID	LIB3166-025-P1-K1-F6
Method	BLASTX
NCBI GI	g2286153
BLAST score	614
E value	4.0e-64
Match length	126
% identity	95
NCBI Description	(AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No.	225131
Seq. ID	LIB3166-025-P1-K1-F9
Method	BLASTX
NCBI GI	g1143427
BLAST score	548
E value	2.0e-56
Match length	127
% identity	88
NCBI Description	(X73961) heat shock protein 70 [Cucumis sativus]

Seq. No. 225132

Seq. ID	LIB3166-025-P1-K1-G3
Method	BLASTX
NCBI GI	g3367522
BLAST score	323
E value	5.0e-30
Match length	105
% identity	61
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	225133
Seq. ID	LIB3166-025-P1-K1-G4
Method	BLASTX
NCBI GI	g82519
BLAST score	215
E value	2.0e-17
Match length	68
% identity	69
NCBI Description	hypothetical 15K protein (trnH-trnV intergenic region) - rice chloroplast >gi_12029_emb_CAA33937_ (X15901) ORF137 [Oryza sativa] >gi_12073_emb_CAA33925_ (X15901) ORF137 [Oryza sativa] >gi_226651_prf__1603356CB ORF 137 [Oryza sativa]

Seq. No.	225134
Seq. ID	LIB3166-025-P1-K1-G5
Method	BLASTX
NCBI GI	g2435511
BLAST score	172
E value	2.0e-12
Match length	59
% identity	58
NCBI Description	(AF024504) contains similarity to prolyl 4-hydroxylase alpha subunit [Arabidopsis thaliana]

Seq. No.	225135
Seq. ID	LIB3166-025-P1-K1-G6
Method	BLASTX
NCBI GI	g1173137
BLAST score	498
E value	1.0e-50
Match length	98
% identity	94
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 19 KD POLYPEPTIDE (RNA POLYMERASE II SUBUNIT 5) >gi_322700_pir__B44457 RNA polymerase II fifth largest subunit - Glycine max=soybeans >gi_170052 (M90504) RNA polymerase II [Glycine max]

Seq. No.	225136
Seq. ID	LIB3166-025-P1-K1-G8
Method	BLASTX
NCBI GI	g3935147
BLAST score	373
E value	7.0e-36
Match length	117
% identity	62
NCBI Description	(AC005106) T25N20.11 [Arabidopsis thaliana]

Seq. No.	225137
Seq. ID	LIB3166-025-P1-K1-H10
Method	BLASTX
NCBI GI	g3128228
BLAST score	146
E value	3.0e-09
Match length	32
% identity	84
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	225138
Seq. ID	LIB3166-025-P1-K1-H6
Method	BLASTX
NCBI GI	g4544443
BLAST score	166
E value	1.0e-11
Match length	34
% identity	94
NCBI Description	(AC006592) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	225139
Seq. ID	LIB3166-025-P1-K1-H8
Method	BLASTX
NCBI GI	g3004560
BLAST score	433
E value	6.0e-43
Match length	97
% identity	81
NCBI Description	(AC003673) putative ATP binding protein [Arabidopsis thaliana]

Seq. No.	225140
Seq. ID	LIB3166-026-P1-K1-A1
Method	BLASTX
NCBI GI	g2462762
BLAST score	325
E value	3.0e-30
Match length	120
% identity	57
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	225141
Seq. ID	LIB3166-026-P1-K1-A10
Method	BLASTX
NCBI GI	g2213624
BLAST score	378
E value	2.0e-36
Match length	126
% identity	60
NCBI Description	(AC000103) F21J9.16 [Arabidopsis thaliana]

Seq. No.	225142

Seq. ID	LIB3166-026-P1-K1-A11
Method	BLASTX
NCBI GI	g2463569
BLAST score	318
E value	2.0e-29
Match length	68
% identity	85
NCBI Description	(AB007503) squalene synthase [Glycine max]

Seq. No.	225143
Seq. ID	LIB3166-026-P1-K1-A5
Method	BLASTX
NCBI GI	g1076626
BLAST score	452
E value	3.0e-45
Match length	120
% identity	72
NCBI Description	glycine rich protein - common tobacco >gi_790473_emb_CAA58702_ (X83731) soluble, glycine rich protein [Nicotiana tabacum]

Seq. No.	225144
Seq. ID	LIB3166-026-P1-K1-A6
Method	BLASTX
NCBI GI	g4056432
BLAST score	560
E value	8.0e-58
Match length	124
% identity	81
NCBI Description	(AC005990) Similar to gi_2245014 glucosyltransferase homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97341. ESTs gb_T20778 and gb_AA586281 come from this gene. [Arabidopsis thaliana]

Seq. No.	225145
Seq. ID	LIB3166-026-P1-K1-A8
Method	BLASTX
NCBI GI	g3955021
BLAST score	214
E value	4.0e-31
Match length	106
% identity	72
NCBI Description	(AJ010811) HB2 homeodomain protein [Populus tremula x Populus tremuloides]

Seq. No.	225146
Seq. ID	LIB3166-026-P1-K1-A9
Method	BLASTX
NCBI GI	g2980801
BLAST score	154
E value	4.0e-18
Match length	83
% identity	59
NCBI Description	(AL022197) transcriptional activator CBF1 [Arabidopsis thaliana] >gi_3660550_dbj_BAA33435_ (AB013816) DREB1B [Arabidopsis thaliana] >gi_3738226_dbj_BAA33792_ (AB007788) DREB1B [Arabidopsis thaliana]

Seq. No.	225147
Seq. ID	LIB3166-026-P1-K1-B11
Method	BLASTX
NCBI GI	g3183640
BLAST score	542
E value	1.0e-55
Match length	107
% identity	97
NCBI Description	(AJ005869) transmembrane channel protein [Cicer arietinum]

Seq. No.	225148
Seq. ID	LIB3166-026-P1-K1-B2
Method	BLASTX
NCBI GI	g886116
BLAST score	495
E value	3.0e-50
Match length	129
% identity	69
NCBI Description	(U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473 (AF051338) xyloglucan endotransglycosylase related protein [Arabidopsis thaliana]

Seq. No.	225149
Seq. ID	LIB3166-026-P1-K1-B6
Method	BLASTX
NCBI GI	g1946359
BLAST score	149
E value	1.0e-09
Match length	31
% identity	87
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	225150
Seq. ID	LIB3166-026-P1-K1-B8
Method	BLASTX
NCBI GI	g2760830
BLAST score	399
E value	6.0e-39
Match length	122
% identity	60
NCBI Description	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	225151
Seq. ID	LIB3166-026-P1-K1-C1
Method	BLASTX
NCBI GI	g4490732
BLAST score	631
E value	4.0e-66
Match length	124
% identity	96
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	225152
Seq. ID	LIB3166-026-P1-K1-C3

Method	BLASTX
NCBI GI	g2815246
BLAST score	215
E value	2.0e-17
Match length	53
% identity	72
NCBI Description	(X95709) class I type 2 metallothionein [Cicer arietinum]

Seq. No.	225153
Seq. ID	LIB3166-026-P1-K1-C5
Method	BLASTX
NCBI GI	g4309744
BLAST score	209
E value	1.0e-16
Match length	115
% identity	37
NCBI Description	(AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225154
Seq. ID	LIB3166-026-P1-K1-C6
Method	BLASTX
NCBI GI	g2129583
BLAST score	283
E value	2.0e-25
Match length	78
% identity	73
NCBI Description	ferritin - Arabidopsis thaliana >gi_1246401_emb_CAA63932_ (X94248) ferritin [Arabidopsis thaliana]

Seq. No.	225155
Seq. ID	LIB3166-026-P1-K1-C7
Method	BLASTX
NCBI GI	g2829862
BLAST score	255
E value	4.0e-22
Match length	95
% identity	53
NCBI Description	(AC002396) Similar to glucosyltransferases [Arabidopsis thaliana]

Seq. No.	225156
Seq. ID	LIB3166-026-P1-K1-D10
Method	BLASTX
NCBI GI	g2496731
BLAST score	228
E value	3.0e-39
Match length	123
% identity	72
NCBI Description	HYPOTHETICAL 30.2 KD PROTEIN Y4OV >gi_2182566 (AE000089) Y4oV [Rhizobium sp. NGR234]

Seq. No.	225157
Seq. ID	LIB3166-026-P1-K1-D12
Method	BLASTX
NCBI GI	g439493
BLAST score	188
E value	3.0e-14

Match length	74
% identity	61
NCBI Description	(D26086) zinc-finger protein [Petunia x hybrida]

Seq. No.	225158
Seq. ID	LIB3166-026-P1-K1-D2
Method	BLASTX
NCBI GI	g2306917
BLAST score	387
E value	2.0e-37
Match length	96
% identity	81
NCBI Description	(AF003728) plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	225159
Seq. ID	LIB3166-026-P1-K1-D4
Method	BLASTX
NCBI GI	g232202
BLAST score	350
E value	3.0e-33
Match length	91
% identity	73
NCBI Description	GLUTATHIONE S-TRANSFERASE PARB (CLASS-PHI) >gi_285295_pir__A41789 glutathione transferase (EC 2.5.1.18) - common tobacco >gi_218294_dbj_BAA01394_ (D10524) glutathione S-transferase [Nicotiana tabacum]

Seq. No.	225160
Seq. ID	LIB3166-026-P1-K1-D7
Method	BLASTX
NCBI GI	g3355468
BLAST score	509
E value	8.0e-52
Match length	123
% identity	86
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No.	225161
Seq. ID	LIB3166-026-P1-K1-D8
Method	BLASTX
NCBI GI	g1666234
BLAST score	540
E value	2.0e-55
Match length	103
% identity	99
NCBI Description	(U76193) actin [Pisum sativum] >gi_1724143 (U81049) actin [Pisum sativum]

Seq. No.	225162
Seq. ID	LIB3166-026-P1-K1-E10
Method	BLASTX
NCBI GI	g4544409
BLAST score	416
E value	7.0e-41
Match length	114

% identity	69
NCBI Description	(AC006955) putative transcription factor [Arabidopsis thaliana]
Seq. No.	225163
Seq. ID	LIB3166-026-P1-K1-F10
Method	BLASTX
NCBI GI	g1762428
BLAST score	417
E value	5.0e-41
Match length	123
% identity	14
NCBI Description	(U59467) aromatic rich glycoprotein JP630 [Arabidopsis thaliana]
Seq. No.	225164
Seq. ID	LIB3166-026-P1-K1-F3
Method	BLASTX
NCBI GI	g2583117
BLAST score	161
E value	5.0e-11
Match length	54
% identity	61
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana]
Seq. No.	225165
Seq. ID	LIB3166-026-P1-K1-F6
Method	BLASTX
NCBI GI	g2529668
BLAST score	538
E value	3.0e-55
Match length	124
% identity	83
NCBI Description	(AC002535) putative photolyase/blue-light receptor [Arabidopsis thaliana] >gi_3319288 (AF053366) photolyase/blue light photoreceptor PHR2 [Arabidopsis thaliana]
Seq. No.	225166
Seq. ID	LIB3166-026-P1-K1-G1
Method	BLASTX
NCBI GI	g4204302
BLAST score	150
E value	1.0e-09
Match length	41
% identity	68
NCBI Description	(AC003027) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	225167
Seq. ID	LIB3166-026-P1-K1-G10
Method	BLASTX
NCBI GI	g3236259
BLAST score	378
E value	2.0e-36
Match length	112
% identity	63
NCBI Description	(AC004684) putative alcohol dehydrogenase [Arabidopsis

thaliana]

Seq. No.	225168
Seq. ID	LIB3166-026-P1-K1-G11
Method	BLASTX
NCBI GI	g3360289
BLAST score	491
E value	9.0e-50
Match length	120
% identity	72
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	225169
Seq. ID	LIB3166-026-P1-K1-G12
Method	BLASTX
NCBI GI	g2677828
BLAST score	311
E value	1.0e-28
Match length	100
% identity	57
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	225170
Seq. ID	LIB3166-026-P1-K1-G3
Method	BLASTX
NCBI GI	g4098129
BLAST score	659
E value	2.0e-69
Match length	128
% identity	96
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	225171
Seq. ID	LIB3166-026-P1-K1-G6
Method	BLASTX
NCBI GI	g1172664
BLAST score	167
E value	9.0e-12
Match length	37
% identity	89
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_419791_pir__S31165 photosystem I chain III precursor - Flaveria trinervia >gi_298482_bbs_127083 photosystem I reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem I subunit III [Flaveria trinervia]

Seq. No.	225172
Seq. ID	LIB3166-026-P1-K1-G8
Method	BLASTX
NCBI GI	g417103
BLAST score	565
E value	2.0e-58
Match length	114
% identity	98

NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	225173
Seq. ID	LIB3166-026-P1-K1-G9
Method	BLASTX
NCBI GI	g4220534
BLAST score	163
E value	2.0e-11
Match length	60
% identity	58
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	225174
Seq. ID	LIB3166-026-P1-K1-H1
Method	BLASTX
NCBI GI	g4220534
BLAST score	274
E value	3.0e-24
Match length	122
% identity	54
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	225175
Seq. ID	LIB3166-026-P1-K1-H12
Method	BLASTX
NCBI GI	g728949
BLAST score	139
E value	1.0e-08
Match length	49
% identity	53
NCBI Description	BLUE COPPER PROTEIN PRECURSOR >gi_99665_pir__S25555 blue copper protein - Arabidopsis thaliana >gi_2147156_pir__I39698 blue copper-binding protein - Arabidopsis thaliana >gi_16203_emb_CAA78771_ (Z15058) blue copper-binding protein [unidentified bacterium] >gi_739987_prf__2004275A blue copper-binding protein [Arabidopsis thaliana]

Seq. No.	225176

Seq. ID	LIB3166-026-P1-K1-H3
Method	BLASTX
NCBI GI	g2244898
BLAST score	190
E value	2.0e-14
Match length	55
% identity	69
NCBI Description	(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]

Seq. No.	225177
Seq. ID	LIB3166-026-P1-K1-H4
Method	BLASTX
NCBI GI	g2459435
BLAST score	184
E value	1.0e-13
Match length	83
% identity	52
NCBI Description	(AC002332) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No.	225178
Seq. ID	LIB3166-026-P1-K1-H5
Method	BLASTX
NCBI GI	g3643603
BLAST score	516
E value	1.0e-52
Match length	123
% identity	77
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	225179
Seq. ID	LIB3166-026-P1-K1-H6
Method	BLASTX
NCBI GI	g3885338
BLAST score	204
E value	2.0e-16
Match length	68
% identity	50
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	225180
Seq. ID	LIB3166-027-P1-K1-A1
Method	BLASTX
NCBI GI	g3860323
BLAST score	322
E value	3.0e-30
Match length	69
% identity	86
NCBI Description	(AJ012688) hypothetical protein [Cicer arietinum]

Seq. No.	225181
Seq. ID	LIB3166-027-P1-K1-A11
Method	BLASTX
NCBI GI	g1263291
BLAST score	157
E value	4.0e-12

Match length	85
% identity	49
NCBI Description	(U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No.	225182
Seq. ID	LIB3166-027-P1-K1-A2
Method	BLASTX
NCBI GI	g3928519
BLAST score	160
E value	5.0e-11
Match length	60
% identity	50
NCBI Description	(AB011670) wpk4 protein kinase [Triticum aestivum]

Seq. No.	225183
Seq. ID	LIB3166-027-P1-K1-A3
Method	BLASTX
NCBI GI	g1513180
BLAST score	146
E value	2.0e-09
Match length	61
% identity	46
NCBI Description	(U65511) stellacyanin [Cucumis sativus]

Seq. No.	225184
Seq. ID	LIB3166-027-P1-K1-A4
Method	BLASTX
NCBI GI	g2281631
BLAST score	280
E value	6.0e-25
Match length	128
% identity	54
NCBI Description	(AF003096) AP2 domain containing protein RAP2.3 [Arabidopsis thaliana]

Seq. No.	225185
Seq. ID	LIB3166-027-P1-K1-B1
Method	BLASTX
NCBI GI	g4567245
BLAST score	260
E value	1.0e-22
Match length	125
% identity	51
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.	225186
Seq. ID	LIB3166-027-P1-K1-B11
Method	BLASTX
NCBI GI	g4164408
BLAST score	347
E value	6.0e-33
Match length	89
% identity	73
NCBI Description	(AJ132228) amino acid carrier [Ricinus communis]

Seq. No.	225187
Seq. ID	LIB3166-027-P1-K1-B3

Method	BLASTX
NCBI GI	g3549679
BLAST score	159
E value	7.0e-11
Match length	41
% identity	83
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	225188
Seq. ID	LIB3166-027-P1-K1-B4
Method	BLASTX
NCBI GI	g1326338
BLAST score	168
E value	8.0e-12
Match length	73
% identity	49
NCBI Description	(U58746) R05G6.4 gene product [Caenorhabditis elegans]

Seq. No.	225189
Seq. ID	LIB3166-027-P1-K1-B5
Method	BLASTX
NCBI GI	g3135693
BLAST score	170
E value	4.0e-12
Match length	52
% identity	60
NCBI Description	(AF064201) glutathione S-transferase [Gossypium hirsutum]

Seq. No.	225190
Seq. ID	LIB3166-027-P1-K1-B6
Method	BLASTX
NCBI GI	g2443836
BLAST score	180
E value	3.0e-13
Match length	51
% identity	57
NCBI Description	(AF020793) tonoplast intrinsic protein homolog MSMCP1 [Medicago sativa]

Seq. No.	225191
Seq. ID	LIB3166-027-P1-K1-B7
Method	BLASTX
NCBI GI	g2341034
BLAST score	406
E value	7.0e-40
Match length	83
% identity	96
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	225192
Seq. ID	LIB3166-027-P1-K1-B9
Method	BLASTX
NCBI GI	g3264767
BLAST score	308
E value	2.0e-28
Match length	94
% identity	64

NCBI Description	(AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No.	225193
Seq. ID	LIB3166-027-P1-K1-C12
Method	BLASTX
NCBI GI	g4406771
BLAST score	205
E value	3.0e-16
Match length	79
% identity	54
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225194
Seq. ID	LIB3166-027-P1-K1-C2
Method	BLASTX
NCBI GI	g2351580
BLAST score	347
E value	5.0e-44
Match length	120
% identity	73
NCBI Description	(U82433) thymidine diphospho-glucose 4-6-dehydratase homolog [Prunus armeniaca]

Seq. No.	225195
Seq. ID	LIB3166-027-P1-K1-C4
Method	BLASTX
NCBI GI	g4158232
BLAST score	535
E value	7.0e-55
Match length	110
% identity	92
NCBI Description	(Y18626) reversibly glycosylated polypeptide [Triticum aestivum]

Seq. No.	225196
Seq. ID	LIB3166-027-P1-K1-C5
Method	BLASTX
NCBI GI	g4235430
BLAST score	470
E value	3.0e-47
Match length	100
% identity	87
NCBI Description	(AF098458) latex-abundant protein [Hevea brasiliensis]

Seq. No.	225197
Seq. ID	LIB3166-027-P1-K1-C6
Method	BLASTX
NCBI GI	g1352821
BLAST score	506
E value	2.0e-51
Match length	97
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	225198
Seq. ID	LIB3166-027-P1-K1-D10
Method	BLASTX
NCBI GI	g4220527
BLAST score	168
E value	6.0e-12
Match length	51
% identity	59
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	225199
Seq. ID	LIB3166-027-P1-K1-D11
Method	BLASTX
NCBI GI	g2827528
BLAST score	424
E value	6.0e-42
Match length	103
% identity	78
NCBI Description	(AL021633) predicted protein [Arabidopsis thaliana]

Seq. No.	225200
Seq. ID	LIB3166-027-P1-K1-D2
Method	BLASTX
NCBI GI	g4455180
BLAST score	276
E value	1.0e-24
Match length	105
% identity	58
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	225201
Seq. ID	LIB3166-027-P1-K1-E1
Method	BLASTX
NCBI GI	g1708924
BLAST score	318
E value	2.0e-29
Match length	86
% identity	71
NCBI Description	MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME) >gi_515759 (L34836) malate dehydrogenase (NADP+) [Vitis vinifera]

Seq. No.	225202
Seq. ID	LIB3166-027-P1-K1-E11
Method	BLASTX
NCBI GI	g1001253
BLAST score	124
E value	2.0e-09
Match length	110
% identity	42
NCBI Description	(D64003) hypothetical protein [Synechocystis sp.]

Seq. No.	225203
Seq. ID	LIB3166-027-P1-K1-E2
Method	BLASTX
NCBI GI	g728949

BLAST score	237
E value	5.0e-20
Match length	112
% identity	44
NCBI Description	BLUE COPPER PROTEIN PRECURSOR >gi_99665_pir__S25555 blue copper protein - Arabidopsis thaliana >gi_2147156_pir__I39698 blue copper-binding protein - Arabidopsis thaliana >gi_16203_emb_CAA78771_ (Z15058) blue copper-binding protein [unidentified bacterium] >gi_739987_prf__2004275A blue copper-binding protein [Arabidopsis thaliana]

Seq. No.	225204
Seq. ID	LIB3166-027-P1-K1-E3
Method	BLASTX
NCBI GI	g3158476
BLAST score	511
E value	4.0e-52
Match length	116
% identity	84
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	225205
Seq. ID	LIB3166-027-P1-K1-E4
Method	BLASTX
NCBI GI	g2662343
BLAST score	577
E value	8.0e-60
Match length	110
% identity	100
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	225206
Seq. ID	LIB3166-027-P1-K1-F1
Method	BLASTX
NCBI GI	g2369714
BLAST score	639
E value	4.0e-67
Match length	122
% identity	98
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	225207
Seq. ID	LIB3166-027-P1-K1-F10
Method	BLASTX
NCBI GI	g3434973
BLAST score	237
E value	4.0e-20
Match length	60
% identity	75
NCBI Description	(AB008106) ethylene responsive element binding factor 4 [Arabidopsis thaliana]

Seq. No.	225208
Seq. ID	LIB3166-027-P1-K1-F11
Method	BLASTX
NCBI GI	g4539423

BLAST score	465
E value	8.0e-47
Match length	107
% identity	81
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	225209
Seq. ID	LIB3166-027-P1-K1-F5
Method	BLASTX
NCBI GI	g3912923
BLAST score	152
E value	6.0e-10
Match length	69
% identity	61
NCBI Description	(AF001308) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225210
Seq. ID	LIB3166-027-P1-K1-F6
Method	BLASTX
NCBI GI	g125887
BLAST score	182
E value	2.0e-13
Match length	95
% identity	44
NCBI Description	ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR >gi_82092_pir__S04765 LAT52 protein precursor - tomato >gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon esculentum]

Seq. No.	225211
Seq. ID	LIB3166-027-P1-K1-G6
Method	BLASTX
NCBI GI	g3747044
BLAST score	175
E value	1.0e-12
Match length	75
% identity	47
NCBI Description	(AF093537) blue copper protein [Zea mays]

Seq. No.	225212
Seq. ID	LIB3166-027-P1-K1-G9
Method	BLASTX
NCBI GI	g3334245
BLAST score	325
E value	2.0e-30
Match length	74
% identity	84
NCBI Description	LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi_2909424_emb_CAA12028_ (AJ224520) Glyoxalase I [Cicer arietinum]

Seq. No.	225213
Seq. ID	LIB3166-027-P1-K1-H1
Method	BLASTX

NCBI GI	g3702368
BLAST score	267
E value	2.0e-23
Match length	86
% identity	63
NCBI Description	(AJ001855) alpha subunit of F-actin capping protein [Arabidopsis thaliana]

Seq. No.	225214
Seq. ID	LIB3166-027-P1-K1-H10
Method	BLASTX
NCBI GI	g4388826
BLAST score	238
E value	3.0e-20
Match length	91
% identity	49
NCBI Description	(AC006528) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225215
Seq. ID	LIB3166-027-P1-K1-H2
Method	BLASTX
NCBI GI	g456568
BLAST score	282
E value	2.0e-40
Match length	90
% identity	93
NCBI Description	(L29077) ubiquitin conjugating enzyme [Pisum sativum]

Seq. No.	225216
Seq. ID	LIB3166-027-P1-K1-H3
Method	BLASTX
NCBI GI	g1703380
BLAST score	313
E value	8.0e-29
Match length	87
% identity	71
NCBI Description	ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607_ (D17760) ADP-ribosylation factor [Oryza sativa]

Seq. No.	225217
Seq. ID	LIB3166-027-P1-K1-H7
Method	BLASTX
NCBI GI	g4090259
BLAST score	345
E value	2.0e-41
Match length	91
% identity	78
NCBI Description	(AJ131733) ubiquitin-conjugating enzyme E2 [Pseudotsuga menziesii]

Seq. No.	225218
Seq. ID	LIB3166-028-P1-K1-A10
Method	BLASTX
NCBI GI	g543813
BLAST score	413
E value	1.0e-40
Match length	84

% identity	95
NCBI Description	FLORAL HOMEOTIC PROTEIN APETALA1 (AGL7 PROTEIN) >gi_16162_emb_CAA78909_ (Z16421) AP1 [Arabidopsis thaliana]

Seq. No.	225219
Seq. ID	LIB3166-028-P1-K1-A12
Method	BLASTX
NCBI GI	g602586
BLAST score	181
E value	1.0e-13
Match length	99
% identity	47
NCBI Description	(X83229) 1-amniocyclopropane-1-carboxylate oxidase [Nicotiana tabacum]

Seq. No.	225220
Seq. ID	LIB3166-028-P1-K1-A6
Method	BLASTX
NCBI GI	g4218535
BLAST score	244
E value	5.0e-28
Match length	85
% identity	66
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]

Seq. No.	225221
Seq. ID	LIB3166-028-P1-K1-A9
Method	BLASTX
NCBI GI	g1076746
BLAST score	418
E value	2.0e-41
Match length	82
% identity	99
NCBI Description	heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]

Seq. No.	225222
Seq. ID	LIB3166-028-P1-K1-B11
Method	BLASTX
NCBI GI	g3250691
BLAST score	191
E value	1.0e-14
Match length	89
% identity	47
NCBI Description	(AL024486) putative chitinase [Arabidopsis thaliana]

Seq. No.	225223
Seq. ID	LIB3166-028-P1-K1-B12
Method	BLASTX
NCBI GI	g3551999
BLAST score	272
E value	4.0e-24
Match length	110
% identity	55
NCBI Description	(AF085081) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3552001 (AF085082) alcohol dehydrogenase A [Gossypium

hirsutum] >gi_4140628 (AF090163) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140630 (AF090164) alcohol dehydrogenase A [Gossypium hirsutum]

Seq. No.	225224
Seq. ID	LIB3166-028-P1-K1-B2
Method	BLASTX
NCBI GI	g2244955
BLAST score	271
E value	6.0e-24
Match length	114
% identity	44
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225225
Seq. ID	LIB3166-028-P1-K1-B3
Method	BLASTX
NCBI GI	g2809243
BLAST score	210
E value	5.0e-17
Match length	75
% identity	53
NCBI Description	(AC002560) F21B7.12 [Arabidopsis thaliana]

Seq. No.	225226
Seq. ID	LIB3166-028-P1-K1-B4
Method	BLASTX
NCBI GI	g1399380
BLAST score	510
E value	6.0e-52
Match length	102
% identity	90
NCBI Description	(U43683) S-adenosyl-L-methionine:delta24-sterol-C-methyltransferase [Glycine max]

Seq. No.	225227
Seq. ID	LIB3166-028-P1-K1-B6
Method	BLASTX
NCBI GI	g3785990
BLAST score	228
E value	6.0e-19
Match length	91
% identity	56
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana] >gi_4220487 (AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225228
Seq. ID	LIB3166-028-P1-K1-B9
Method	BLASTX
NCBI GI	g3193316
BLAST score	184
E value	3.0e-14
Match length	48
% identity	71
NCBI Description	(AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No.	225229
Seq. ID	LIB3166-028-P1-K1-C10
Method	BLASTX
NCBI GI	g3461820
BLAST score	178
E value	5.0e-13
Match length	93
% identity	46
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	225230
Seq. ID	LIB3166-028-P1-K1-C11
Method	BLASTX
NCBI GI	g585564
BLAST score	561
E value	6.0e-58
Match length	122
% identity	87
NCBI Description	FERREDOXIN--NITRITE REDUCTASE PRECURSOR >gi_81443_pir__S20495 ferredoxin--nitrite reductase (EC 1.7.7.1) precursor - European white birch >gi_17927_emb_CAA42690_ (X60093) ferredoxin--nitrite reductase [Betula pendula]

Seq. No.	225231
Seq. ID	LIB3166-028-P1-K1-C2
Method	BLASTX
NCBI GI	g2760320
BLAST score	146
E value	3.0e-09
Match length	87
% identity	43
NCBI Description	(AC002130) F1N21.4 [Arabidopsis thaliana]

Seq. No.	225232
Seq. ID	LIB3166-028-P1-K1-C5
Method	BLASTX
NCBI GI	g1498053
BLAST score	417
E value	5.0e-41
Match length	104
% identity	82
NCBI Description	(U64436) ribosomal protein S8 [Zea mays]

Seq. No.	225233
Seq. ID	LIB3166-028-P1-K1-C6
Method	BLASTX
NCBI GI	g2500115
BLAST score	555
E value	3.0e-57
Match length	124
% identity	85
NCBI Description	GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE) >gi_529375_dbj_BAA07108_ (D37870) Glutathione Reductase precursor [Spinacia oleracea]

Seq. No.	225234
Seq. ID	LIB3166-028-P1-K1-C7
Method	BLASTX
NCBI GI	g126896
BLAST score	450
E value	6.0e-45
Match length	112
% identity	79
NCBI Description	MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR >gi_319831_pir__DEPUMW malate dehydrogenase (EC 1.1.1.37) precursor, mitochondrial - watermelon >gi_18297_emb_CAA35239_ (X17362) precursor protein (AA -27 to 320) [Citrullus lanatus]

Seq. No.	225235
Seq. ID	LIB3166-028-P1-K1-C8
Method	BLASTX
NCBI GI	g1871192
BLAST score	282
E value	3.0e-25
Match length	116
% identity	56
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	225236
Seq. ID	LIB3166-028-P1-K1-C9
Method	BLASTX
NCBI GI	g2791834
BLAST score	400
E value	4.0e-39
Match length	93
% identity	85
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No.	225237
Seq. ID	LIB3166-028-P1-K1-D10
Method	BLASTX
NCBI GI	g1762945
BLAST score	230
E value	4.0e-19
Match length	58
% identity	72
NCBI Description	(U66269) ORF; able to induce HR-like lesions [Nicotiana tabacum]

Seq. No.	225238
Seq. ID	LIB3166-028-P1-K1-D11
Method	BLASTX
NCBI GI	g3212877
BLAST score	382
E value	6.0e-37
Match length	86
% identity	80
NCBI Description	(AC004005) Lea-like protein [Arabidopsis thaliana]

Seq. No.	225239

Seq. ID	LIB3166-028-P1-K1-D3
Method	BLASTX
NCBI GI	g529707
BLAST score	253
E value	7.0e-22
Match length	110
% identity	44
NCBI Description	(U13070) No definition line found [Caenorhabditis elegans]

Seq. No.	225240
Seq. ID	LIB3166-028-P1-K1-D4
Method	BLASTX
NCBI GI	g1707032
BLAST score	232
E value	2.0e-19
Match length	116
% identity	42
NCBI Description	(U80445) coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA yk65h8

Seq. No.	225241
Seq. ID	LIB3166-028-P1-K1-D5
Method	BLASTX
NCBI GI	g3617741
BLAST score	547
E value	2.0e-56
Match length	115
% identity	90
NCBI Description	(AC005687) L3 cytoplasmic ribosomal protein [Arabidopsis thaliana]

Seq. No.	225242
Seq. ID	LIB3166-028-P1-K1-D6
Method	BLASTX
NCBI GI	g3297816
BLAST score	241
E value	2.0e-20
Match length	63
% identity	75
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	225243
Seq. ID	LIB3166-028-P1-K1-D9
Method	BLASTX
NCBI GI	g2245066
BLAST score	329
E value	9.0e-31
Match length	118
% identity	54
NCBI Description	(Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No.	225244
Seq. ID	LIB3166-028-P1-K1-E1
Method	BLASTX

NCBI GI	g1922242
BLAST score	186
E value	5.0e-14
Match length	99
% identity	44
NCBI Description	(Y10084) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225245
Seq. ID	LIB3166-028-P1-K1-E2
Method	BLASTX
NCBI GI	g4220481
BLAST score	142
E value	8.0e-09
Match length	59
% identity	56
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	225246
Seq. ID	LIB3166-028-P1-K1-E3
Method	BLASTX
NCBI GI	g4101568
BLAST score	317
E value	2.0e-29
Match length	102
% identity	60
NCBI Description	(AF004816) unknown [Triticum aestivum]

Seq. No.	225247
Seq. ID	LIB3166-028-P1-K1-E5
Method	BLASTX
NCBI GI	g1621268
BLAST score	292
E value	2.0e-26
Match length	63
% identity	89
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	225248
Seq. ID	LIB3166-028-P1-K1-E6
Method	BLASTX
NCBI GI	g462013
BLAST score	575
E value	1.0e-59
Match length	125
% identity	90
NCBI Description	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) >gi_542022_pir__S39558 HSP90 homolog - Madagascar periwinkle >gi_348696 (L14594) heat shock protein 90 [Catharanthus roseus]

Seq. No.	225249
Seq. ID	LIB3166-028-P1-K1-E7
Method	BLASTX.
NCBI GI	g1345698
BLAST score	527
E value	5.0e-54
Match length	105

% identity	93
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR (CAB-151) (LHCP) >gi_99601_pir__S20917 chlorophyll a/b-binding protein - upland cotton >gi_452314_emb_CAA38025_ (X54090) chlorophyll ab binding protein [Gossypium hirsutum]
Seq. No.	225250
Seq. ID	LIB3166-028-P1-K1-F12
Method	BLASTX
NCBI GI	g267073
BLAST score	404
E value	1.0e-39
Match length	78
% identity	95
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]
Seq. No.	225251
Seq. ID	LIB3166-028-P1-K1-F2
Method	BLASTX
NCBI GI	g2980801
BLAST score	314
E value	5.0e-29
Match length	90
% identity	69
NCBI Description	(AL022197) transcriptional activator CBF1 [Arabidopsis thaliana] >gi_3660550_dbj_BAA33435_ (AB013816) DREB1B [Arabidopsis thaliana] >gi_3738226_dbj_BAA33792_ (AB007788) DREB1B [Arabidopsis thaliana]
Seq. No.	225252
Seq. ID	LIB3166-028-P1-K1-F3
Method	BLASTX
NCBI GI	g4454484
BLAST score	284
E value	2.0e-25
Match length	97
% identity	61
NCBI Description	(AC006234) putative diacylglycerol kinase [Arabidopsis thaliana]
Seq. No.	225253
Seq. ID	LIB3166-028-P1-K1-F7
Method	BLASTX
NCBI GI	g2317906
BLAST score	344
E value	2.0e-32
Match length	67
% identity	99
NCBI Description	(U89959) ARA-5 [Arabidopsis thaliana]
Seq. No.	225254
Seq. ID	LIB3166-028-P1-K1-F8
Method	BLASTX

NCBI GI	g2352492
BLAST score	268
E value	1.0e-23
Match length	61
% identity	75
NCBI Description	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	225255
Seq. ID	LIB3166-028-P1-K1-F9
Method	BLASTX
NCBI GI	g232202
BLAST score	352
E value	2.0e-33
Match length	91
% identity	73
NCBI Description	GLUTATHIONE S-TRANSFERASE PARB (CLASS-PHI) >gi_285295_pir__A41789 glutathione transferase (EC 2.5.1.18) - common tobacco >gi_218294_dbj_BAA01394_ (D10524) glutathione S-transferase [Nicotiana tabacum]

Seq. No.	225256
Seq. ID	LIB3166-028-P1-K1-G1
Method	BLASTX
NCBI GI	g1723536
BLAST score	362
E value	1.0e-34
Match length	117
% identity	58
NCBI Description	PROBABLE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 BETA SUBUNIT (EIF-3 BETA) >gi_1256531_emb_CAA94637_ (Z70691) eukaryotic translation initiation factor 3 beta subunit [Schizosaccharomyces pombe]

Seq. No.	225257
Seq. ID	LIB3166-028-P1-K1-G10
Method	BLASTX
NCBI GI	g3402684
BLAST score	418
E value	3.0e-41
Match length	111
% identity	75
NCBI Description	(AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225258
Seq. ID	LIB3166-028-P1-K1-G11
Method	BLASTX
NCBI GI	g4006891
BLAST score	155
E value	3.0e-10
Match length	38
% identity	76
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	225259
Seq. ID	LIB3166-028-P1-K1-G2

Method	BLASTX
NCBI GI	g3080418
BLAST score	213
E value	4.0e-17
Match length	57
% identity	56
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	225260
Seq. ID	LIB3166-028-P1-K1-G5
Method	BLASTX
NCBI GI	g3158474
BLAST score	286
E value	1.0e-25
Match length	73
% identity	79
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]

Seq. No.	225261
Seq. ID	LIB3166-028-P1-K1-G8
Method	BLASTX
NCBI GI	g2760830
BLAST score	603
E value	7.0e-63
Match length	122
% identity	93
NCBI Description	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	225262
Seq. ID	LIB3166-028-P1-K1-G9
Method	BLASTX
NCBI GI	g3158474
BLAST score	181
E value	2.0e-13
Match length	70
% identity	60
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]

Seq. No.	225263
Seq. ID	LIB3166-028-P1-K1-H10
Method	BLASTX
NCBI GI	g115764
BLAST score	262
E value	7.0e-23
Match length	93
% identity	59
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE I PRECURSOR (CAB-6A) (LIGHT-HARVESTING COMPLEX I 26 KD PROTEIN) >gi_170494 (J03558) chlorophyll a/b binding protein precursor [Lycopersicon esculentum]

Seq. No.	225264
Seq. ID	LIB3166-028-P1-K1-H11
Method	BLASTX
NCBI GI	g2459445
BLAST score	279

E value	7.0e-25
Match length	72
% identity	36
NCBI Description	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	225265
Seq. ID	LIB3166-028-P1-K1-H12
Method	BLASTX
NCBI GI	g2459445
BLAST score	259
E value	1.0e-22
Match length	70
% identity	37
NCBI Description	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	225266
Seq. ID	LIB3166-028-P1-K1-H2
Method	BLASTX
NCBI GI	g3212877
BLAST score	380
E value	1.0e-36
Match length	85
% identity	81
NCBI Description	(AC004005) Lea-like protein [Arabidopsis thaliana]

Seq. No.	225267
Seq. ID	LIB3166-028-P1-K1-H5
Method	BLASTX
NCBI GI	g2760322
BLAST score	449
E value	8.0e-45
Match length	123
% identity	65
NCBI Description	(AC002130) F1N21.7 [Arabidopsis thaliana]

Seq. No.	225268
Seq. ID	LIB3166-028-P1-K1-H6
Method	BLASTX
NCBI GI	g2459445
BLAST score	292
E value	2.0e-26
Match length	76
% identity	36
NCBI Description	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	225269
Seq. ID	LIB3166-028-P1-K1-H7
Method	BLASTX
NCBI GI	g1737222
BLAST score	216
E value	5.0e-18
Match length	56
% identity	75
NCBI Description	(U79958) BP-80 vacuolar sorting receptor [Pisum sativum]

Seq. No.	225270
Seq. ID	LIB3166-029-P1-K1-A12
Method	BLASTX
NCBI GI	g729668
BLAST score	246
E value	4.0e-21
Match length	61
% identity	79
NCBI Description	HISTONE H1 >gi_2147479_pir__S65059 histone H1, drought-inducible - Lycopersicon pennellii >gi_436823 (U01890) Solanum pennellii histone H1 [Solanum pennellii]

Seq. No.	225271
Seq. ID	LIB3166-029-P1-K1-A2
Method	BLASTX
NCBI GI	g3377841
BLAST score	273
E value	1.0e-24
Match length	59
% identity	90
NCBI Description	(AF075598) contains similarity to phosphofructokinases (Pfam; PFK.hmm, score; 36.60) [Arabidopsis thaliana]

Seq. No.	225272
Seq. ID	LIB3166-029-P1-K1-A6
Method	BLASTX
NCBI GI	g1531756
BLAST score	182
E value	2.0e-13
Match length	38
% identity	84
NCBI Description	(X82413) proline-rich-like protein [Asparagus officinalis]

Seq. No.	225273
Seq. ID	LIB3166-029-P1-K1-B1
Method	BLASTX
NCBI GI	g2145358
BLAST score	313
E value	6.0e-29
Match length	108
% identity	56
NCBI Description	(Y10922) HD-Zip protein [Arabidopsis thaliana]

Seq. No.	225274
Seq. ID	LIB3166-029-P1-K1-B12
Method	BLASTX
NCBI GI	g2982262
BLAST score	327
E value	2.0e-30
Match length	107
% identity	60
NCBI Description	(AF051214) probable glutathione S-transferase [Picea mariana]

Seq. No.	225275
Seq. ID	LIB3166-029-P1-K1-B4

Method	BLASTX
NCBI GI	g3047125
BLAST score	274
E value	2.0e-24
Match length	105
% identity	52
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	225276
Seq. ID	LIB3166-029-P1-K1-B5
Method	BLASTX
NCBI GI	g289920
BLAST score	474
E value	6.0e-48
Match length	89
% identity	99
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	225277
Seq. ID	LIB3166-029-P1-K1-B9
Method	BLASTX
NCBI GI	g4530585
BLAST score	355
E value	8.0e-34
Match length	85
% identity	74
NCBI Description	(AF130978) B12D protein [Ipomoea batatas]

Seq. No.	225278
Seq. ID	LIB3166-029-P1-K1-C11
Method	BLASTX
NCBI GI	g466172
BLAST score	279
E value	5.0e-25
Match length	64
% identity	83
NCBI Description	GTP-BINDING PROTEIN YPTM2 >gi_283056_pir__B38202 ypt family - maize >gi_287835_emb_CAA44919_ (X63278) yptm2 [Zea mays]

Seq. No.	225279
Seq. ID	LIB3166-029-P1-K1-C9
Method	BLASTX
NCBI GI	g1431629
BLAST score	291
E value	3.0e-26
Match length	82
% identity	66
NCBI Description	(X99348) pectinacetylesterase precursor [Vigna radiata]

Seq. No.	225280
Seq. ID	LIB3166-029-P1-K1-D1
Method	BLASTX
NCBI GI	g1840425
BLAST score	127
E value	8.0e-12
Match length	70

% identity	60
NCBI Description	(U36586) alcohol dehydrogenase [Vitis vinifera]

Seq. No.	225281
Seq. ID	LIB3166-029-P1-K1-D4
Method	BLASTX
NCBI GI	g3080389
BLAST score	310
E value	1.0e-47
Match length	125
% identity	81
NCBI Description	(AL022603) putative membrane associated protein [Arabidopsis thaliana]

Seq. No.	225282
Seq. ID	LIB3166-029-P1-K1-D8
Method	BLASTX
NCBI GI	g3047092
BLAST score	216
E value	2.0e-17
Match length	115
% identity	49
NCBI Description	(AF058826) No definition line found [Arabidopsis thaliana]

Seq. No.	225283
Seq. ID	LIB3166-029-P1-K1-D9
Method	BLASTX
NCBI GI	g2661840
BLAST score	367
E value	3.0e-35
Match length	96
% identity	70
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]

Seq. No.	225284
Seq. ID	LIB3166-029-P1-K1-E5
Method	BLASTX
NCBI GI	g3297816
BLAST score	151
E value	9.0e-10
Match length	46
% identity	70
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	225285
Seq. ID	LIB3166-029-P1-K1-E6
Method	BLASTX
NCBI GI	g4056507
BLAST score	156
E value	2.0e-10
Match length	47
% identity	64
NCBI Description	(AC005896) putative RNA binding protein [Arabidopsis thaliana]

Seq. No.	225286
Seq. ID	LIB3166-029-P1-K1-E8

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Method	BLASTX
NCBI GI	g2088651
BLAST score	294
E value	1.0e-26
Match length	112
% identity	54
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	225287
Seq. ID	LIB3166-029-P1-K1-F4
Method	BLASTX
NCBI GI	g1922242
BLAST score	144
E value	4.0e-09
Match length	57
% identity	58
NCBI Description	(Y10084) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225288
Seq. ID	LIB3166-029-P1-K1-F6
Method	BLASTX
NCBI GI	g100203
BLAST score	302
E value	1.0e-27
Match length	102
% identity	62
NCBI Description	cysteine proteinase (EC 3.4.22.-) precursor - tomato >gi_19195_emb_CAA78403_ (Z14028) pre-pro-cysteine proteinase [Lycopersicon esculentum]

Seq. No.	225289
Seq. ID	LIB3166-029-P1-K1-F7
Method	BLASTX
NCBI GI	g833835
BLAST score	360
E value	1.0e-34
Match length	81
% identity	74
NCBI Description	(U26025) amygdalin hydrolase isoform AH I precursor [Prunus serotina]

Seq. No.	225290
Seq. ID	LIB3166-029-P1-K1-F9
Method	BLASTX
NCBI GI	g1076746
BLAST score	207
E value	2.0e-16
Match length	86
% identity	59
NCBI Description	heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]

Seq. No.	225291
Seq. ID	LIB3166-029-P1-K1-G12
Method	BLASTX

NCBI GI	g4544443
BLAST score	373
E value	5.0e-36
Match length	115
% identity	33
NCBI Description	(AC006592) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	225292
Seq. ID	LIB3166-029-P1-K1-G6
Method	BLASTX
NCBI GI	g267069
BLAST score	501
E value	7.0e-51
Match length	97
% identity	96
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	225293
Seq. ID	LIB3166-029-P1-K1-G7
Method	BLASTX
NCBI GI	g4006911
BLAST score	302
E value	1.0e-28
Match length	71
% identity	93
NCBI Description	(Z99708) trichohyalin like protein [Arabidopsis thaliana]

Seq. No.	225294
Seq. ID	LIB3166-029-P1-K1-G8
Method	BLASTX
NCBI GI	g136057
BLAST score	295
E value	8.0e-27
Match length	85
% identity	67
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase - Coptis japonica >gi_556171 (J04121) triosephosphate isomerase [Coptis japonica]

Seq. No.	225295
Seq. ID	LIB3166-029-P1-K1-G9
Method	BLASTX
NCBI GI	g3877580
BLAST score	177
E value	6.0e-13
Match length	108
% identity	42
NCBI Description	(Z67755) F54F7.1 [Caenorhabditis elegans]

Seq. No.	225296
Seq. ID	LIB3166-029-P1-K1-H1
Method	BLASTX

NCBI GI	g2832703
BLAST score	316
E value	3.0e-29
Match length	97
% identity	56
NCBI Description	(AL021713) potassium channel protein KAT2 [Arabidopsis thaliana]

Seq. No.	225297
Seq. ID	LIB3166-029-P1-K1-H5
Method	BLASTX
NCBI GI	g2347199
BLAST score	355
E value	9.0e-34
Match length	105
% identity	70
NCBI Description	(AC002338) protein kinase isolog [Arabidopsis thaliana]

Seq. No.	225298
Seq. ID	LIB3166-029-P1-K1-H6
Method	BLASTX
NCBI GI	g228210
BLAST score	405
E value	1.0e-39
Match length	101
% identity	77
NCBI Description	granule-bound starch synthase [Solanum tuberosum]

Seq. No.	225299
Seq. ID	LIB3166-030-P1-K1-A12
Method	BLASTX
NCBI GI	g729051
BLAST score	247
E value	3.0e-21
Match length	89
% identity	63
NCBI Description	CALTRACTIN (CENTRIN) >gi_444342_prf__1906390A caltractin-like protein [Atriplex nummularia]

Seq. No.	225300
Seq. ID	LIB3166-030-P1-K1-A2
Method	BLASTX
NCBI GI	g1172001
BLAST score	439
E value	9.0e-44
Match length	102
% identity	83
NCBI Description	PHENYLALANINE AMMONIA-LYASE >gi_541843_pir__JQ2265 phenylalanine ammonia-lyase (EC 4.3.1.5) - western balsam poplar x cottonwood >gi_169454 (L11747) phenylalanine ammonia lyase [Populus trichocarpa x Populus deltoides]

Seq. No.	225301
Seq. ID	LIB3166-030-P1-K1-A3
Method	BLASTX
NCBI GI	g3080372
BLAST score	145

E value	3.0e-09
Match length	93
% identity	41
NCBI Description	(AL022580) putative pectinacetylesterase [Arabidopsis thaliana]

Seq. No.	225302
Seq. ID	LIB3166-030-P1-K1-A5
Method	BLASTX
NCBI GI	g2661179
BLAST score	317
E value	2.0e-29
Match length	106
% identity	58
NCBI Description	(U80984) AtZW10 [Arabidopsis thaliana]

Seq. No.	225303
Seq. ID	LIB3166-030-P1-K1-A6
Method	BLASTX
NCBI GI	g3298443
BLAST score	282
E value	3.0e-25
Match length	101
% identity	59
NCBI Description	(AB010880) chloroplast ribosomal protein L17 [Nicotiana tabacum]

Seq. No.	225304
Seq. ID	LIB3166-030-P1-K1-B10
Method	BLASTX
NCBI GI	g3193316
BLAST score	536
E value	5.0e-55
Match length	115
% identity	89
NCBI Description	(AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No.	225305
Seq. ID	LIB3166-030-P1-K1-B11
Method	BLASTX
NCBI GI	g2218152
BLAST score	620
E value	7.0e-65
Match length	122
% identity	89
NCBI Description	(AF005279) type IIIa membrane protein cp-wap13 [Vigna unguiculata]

Seq. No.	225306
Seq. ID	LIB3166-030-P1-K1-B12
Method	BLASTX
NCBI GI	g2760837
BLAST score	302
E value	1.0e-27
Match length	125
% identity	43

NCBI Description	(AC003105) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.	225307
Seq. ID	LIB3166-030-P1-K1-B2
Method	BLASTX
NCBI GI	g3493172
BLAST score	392
E value	3.0e-38
Match length	90
% identity	87
NCBI Description	(U89609) fiber annexin [Gossypium hirsutum]
Seq. No.	225308
Seq. ID	LIB3166-030-P1-K1-B3
Method	BLASTX
NCBI GI	g3386618
BLAST score	226
E value	1.0e-18
Match length	83
% identity	57
NCBI Description	(AC004665) hypothetical protein [Arabidopsis thaliana]
Seq. No.	225309
Seq. ID	LIB3166-030-P1-K1-B7
Method	BLASTX
NCBI GI	g584794
BLAST score	339
E value	3.0e-32
Match length	80
% identity	82
NCBI Description	PLASMA MEMBRANE ATPASE 1 (PROTON PUMP) >gi_282953_pir__A41779 H+-transporting ATPase (EC 3.6.1.35) - curled-leaved tobacco >gi_170289 (M80489) plasma membrane H+ ATPase [Nicotiana plumbaginifolia]
Seq. No.	225310
Seq. ID	LIB3166-030-P1-K1-B8
Method	BLASTX
NCBI GI	g3024017
BLAST score	405
E value	8.0e-40
Match length	79
% identity	96
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C) >gi_2565421 (AF026804) eukaryotic translation initiation factor eIF-1A [Onobrychis viciifolia]
Seq. No.	225311
Seq. ID	LIB3166-030-P1-K1-B9
Method	BLASTX
NCBI GI	g4469023
BLAST score	345
E value	1.0e-32
Match length	109
% identity	72
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	225312
Seq. ID	LIB3166-030-P1-K1-C11
Method	BLASTX
NCBI GI	g3559805
BLAST score	449
E value	3.0e-49
Match length	119
% identity	78
NCBI Description	(AJ006787) putative phytochelatin synthetase [Arabidopsis thaliana]

Seq. No.	225313
Seq. ID	LIB3166-030-P1-K1-C12
Method	BLASTX
NCBI GI	g2245108
BLAST score	487
E value	3.0e-49
Match length	118
% identity	73
NCBI Description	(Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No.	225314
Seq. ID	LIB3166-030-P1-K1-C2
Method	BLASTX
NCBI GI	g417592
BLAST score	166
E value	4.0e-18
Match length	78
% identity	54
NCBI Description	RIBONUCLEIC ACID TRAFFICKING PROTEIN 1 (5'-3' EXORIBONUCLEASE) (P116) >gi_83014_pir__S20126 exoribonuclease RAT1 (EC 3.1.11.-) - yeast (Saccharomyces cerevisiae) >gi_172365 (M95626) Rat1p [Saccharomyces cerevisiae] >gi_386005_bbs_132577 (S61567) transcription activator=TAP1/RAT1 [Saccharomyces cerevisiae=yeast, Peptide, 1006 aa] [Saccharomyces cerevisiae] >gi_1420179_emb_CAA99240_ (Z74956) ORF YOR048c [Saccharomyces cerevisiae]

Seq. No.	225315
Seq. ID	LIB3166-030-P1-K1-C5
Method	BLASTX
NCBI GI	g3647355
BLAST score	213
E value	4.0e-17
Match length	72
% identity	56
NCBI Description	(Z97348) predicted using hexExon; MAL3P1.12 (PFC0150w), Human hypothetical protein KIAA0249-related protein len: 1160 aa; Similarity to 2 human and an yeast hypothetical gene. Human hypothetical protein KIAA0249 (SW:Y249_HUMA

Seq. No.	225316
Seq. ID	LIB3166-030-P1-K1-C6
Method	BLASTX
NCBI GI	g3913518
BLAST score	202

E value	7.0e-16
Match length	60
% identity	68
NCBI Description	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE) (DPNPASE) >gi_1103921 (U40433) 3'(2'),5'-bisphosphate nucleotidase [Arabidopsis thaliana]

Seq. No.	225317
Seq. ID	LIB3166-030-P1-K1-C7
Method	BLASTX
NCBI GI	g4468992
BLAST score	499
E value	1.0e-50
Match length	122
% identity	79
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	225318
Seq. ID	LIB3166-030-P1-K1-D12
Method	BLASTX
NCBI GI	g1621268
BLAST score	375
E value	4.0e-36
Match length	114
% identity	69
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	225319
Seq. ID	LIB3166-030-P1-K1-D3
Method	BLASTX
NCBI GI	g3080389
BLAST score	405
E value	1.0e-39
Match length	103
% identity	79
NCBI Description	(AL022603) putative membrane associated protein [Arabidopsis thaliana]

Seq. No.	225320
Seq. ID	LIB3166-030-P1-K1-D4
Method	BLASTX
NCBI GI	g4539301
BLAST score	284
E value	5.0e-30
Match length	127
% identity	48
NCBI Description	(AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	225321
Seq. ID	LIB3166-030-P1-K1-D6
Method	BLASTX
NCBI GI	g3218467
BLAST score	149
E value	1.0e-09
Match length	100

% identity	34
NCBI Description	(AJ006529) putative phosphatase [Gallus gallus]

Seq. No.	225322
Seq. ID	LIB3166-030-P1-K1-D9
Method	BLASTX
NCBI GI	g3421087
BLAST score	420
E value	2.0e-41
Match length	88
% identity	95
NCBI Description	(AF043524) 20S proteasome subunit PAE1 [Arabidopsis thaliana]

Seq. No.	225323
Seq. ID	LIB3166-030-P1-K1-E10
Method	BLASTX
NCBI GI	g3281851
BLAST score	110
E value	2.0e-11
Match length	55
% identity	64
NCBI Description	(AL031004) RNA lariat debranching enzyme - like protein [Arabidopsis thaliana]

Seq. No.	225324
Seq. ID	LIB3166-030-P1-K1-E5
Method	BLASTX
NCBI GI	g121953
BLAST score	170
E value	4.0e-12
Match length	39
% identity	85
NCBI Description	HISTONE H1 >gi_81905_pir__S00033 histone H1.b - garden pea >gi_20762_emb_CAA29123_ (X05636) H1 histone (AA 1-263) [Pisum sativum]

Seq. No.	225325
Seq. ID	LIB3166-030-P1-K1-E7
Method	BLASTX
NCBI GI	g1350680
BLAST score	261
E value	6.0e-23
Match length	72
% identity	71
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	225326
Seq. ID	LIB3166-030-P1-K1-F1
Method	BLASTX
NCBI GI	g3860264
BLAST score	560
E value	8.0e-58
Match length	115
% identity	88
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	225327
Seq. ID	LIB3166-030-P1-K1-F2
Method	BLASTX
NCBI GI	g1220196
BLAST score	184
E value	1.0e-13
Match length	36
% identity	100
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	225328
Seq. ID	LIB3166-030-P1-K1-F3
Method	BLASTX
NCBI GI	g2739365
BLAST score	567
E value	1.0e-58
Match length	126
% identity	81
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	225329
Seq. ID	LIB3166-030-P1-K1-F4
Method	BLASTX
NCBI GI	g3695383
BLAST score	621
E value	6.0e-65
Match length	126
% identity	89
NCBI Description	(AF096370) similar to inorganic pyrophosphatase (Pfam: PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis thaliana]

Seq. No.	225330
Seq. ID	LIB3166-030-P1-K1-G1
Method	BLASTX
NCBI GI	g3549666
BLAST score	199
E value	5.0e-16
Match length	53
% identity	74
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	225331
Seq. ID	LIB3166-030-P1-K1-G12
Method	BLASTX
NCBI GI	g3668089
BLAST score	188
E value	3.0e-14
Match length	91
% identity	42
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	225332
Seq. ID	LIB3166-030-P1-K1-G2
Method	BLASTX
NCBI GI	g4490321
BLAST score	396

E value	1.0e-38
Match length	113
% identity	71
NCBI Description	(AJ011604) nitrate transporter [Arabidopsis thaliana]

Seq. No.	225333
Seq. ID	LIB3166-030-P1-K1-G3
Method	BLASTX
NCBI GI	g4090533
BLAST score	457
E value	9.0e-46
Match length	99
% identity	83
NCBI Description	(U68215) ACC oxidase [Carica papaya]

Seq. No.	225334
Seq. ID	LIB3166-030-P1-K1-G6
Method	BLASTX
NCBI GI	g1871181
BLAST score	159
E value	8.0e-11
Match length	111
% identity	41
NCBI Description	(U90439) ring zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	225335
Seq. ID	LIB3166-030-P1-K1-G7
Method	BLASTX
NCBI GI	g4512653
BLAST score	520
E value	4.0e-53
Match length	125
% identity	82
NCBI Description	(AC007048) unknown protein [Arabidopsis thaliana]

Seq. No.	225336
Seq. ID	LIB3166-030-P1-K1-G9
Method	BLASTX
NCBI GI	g1171642
BLAST score	384
E value	3.0e-37
Match length	103
% identity	68
NCBI Description	PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK >gi_481206_pir__S38326 protein kinase - Arabidopsis thaliana >gi_166809 (L07248) protein kinase [Arabidopsis thaliana]

Seq. No.	225337
Seq. ID	LIB3166-030-P1-K1-H12
Method	BLASTX
NCBI GI	g541847
BLAST score	504
E value	3.0e-51
Match length	105
% identity	87

NCBI Description	alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana
Seq. No.	225338
Seq. ID	LIB3166-030-P1-K1-H2
Method	BLASTX
NCBI GI	g1350981
BLAST score	337
E value	7.0e-41
Match length	114
% identity	78
NCBI Description	40S RIBOSOMAL PROTEIN S3A (S PHASE SPECIFIC PROTEIN BIS289) >gi_480282_pir__S36622 hypothetical protein - turnip >gi_387909 (L23553) S-phase-specific protein [Brassica rapa] >gi_397401_emb_CAA81030_ (Z25769) putative product [Brassica rapa]
Seq. No.	225339
Seq. ID	LIB3166-031-P1-K1-A1
Method	BLASTX
NCBI GI	g1710530
BLAST score	320
E value	9.0e-30
Match length	74
% identity	84
NCBI Description	60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256 ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana]
Seq. No.	225340
Seq. ID	LIB3166-031-P1-K1-A12
Method	BLASTX
NCBI GI	g2443329
BLAST score	520
E value	4.0e-53
Match length	116
% identity	83
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]
Seq. No.	225341
Seq. ID	LIB3166-031-P1-K1-A3
Method	BLASTX
NCBI GI	g2245005
BLAST score	198
E value	1.0e-15
Match length	73
% identity	53
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]
Seq. No.	225342
Seq. ID	LIB3166-031-P1-K1-B11
Method	BLASTX
NCBI GI	g4249382
BLAST score	277
E value	4.0e-25
Match length	75
% identity	71

NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]
Seq. No.	225343
Seq. ID	LIB3166-031-P1-K1-B12
Method	BLASTX
NCBI GI	g3873408
BLAST score	148
E value	2.0e-09
Match length	113
% identity	40
NCBI Description	(L76926) putative zinc finger protein [Arabidopsis thaliana]
Seq. No.	225344
Seq. ID	LIB3166-031-P1-K1-B2
Method	BLASTX
NCBI GI	g2642448
BLAST score	381
E value	8.0e-37
Match length	112
% identity	28
NCBI Description	(AC002391) hypothetical protein [Arabidopsis thaliana] >gi_3169187 (AC004401) hypothetical protein [Arabidopsis thaliana]
Seq. No.	225345
Seq. ID	LIB3166-031-P1-K1-B3
Method	BLASTX
NCBI GI	g4544427
BLAST score	409
E value	4.0e-40
Match length	83
% identity	89
NCBI Description	(AC006955) putative ferredoxin-thioredoxin reductase [Arabidopsis thaliana]
Seq. No.	225346
Seq. ID	LIB3166-031-P1-K1-B4
Method	BLASTX
NCBI GI	g2262159
BLAST score	216
E value	1.0e-17
Match length	79
% identity	53
NCBI Description	(AC002329) predicted protein similar to S.pombe protein C5H10.03 [Arabidopsis thaliana]
Seq. No.	225347
Seq. ID	LIB3166-031-P1-K1-B8
Method	BLASTX
NCBI GI	g3096944
BLAST score	228
E value	4.0e-19
Match length	68
% identity	59

NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	225348
Seq. ID	LIB3166-031-P1-K1-C1
Method	BLASTX
NCBI GI	g3641647
BLAST score	408
E value	4.0e-40
Match length	103
% identity	72
NCBI Description	(AB006804) ACC synthase [Cucumis sativus]

Seq. No.	225349
Seq. ID	LIB3166-031-P1-K1-C2
Method	BLASTX
NCBI GI	g2462834
BLAST score	146
E value	2.0e-09
Match length	50
% identity	56
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225350
Seq. ID	LIB3166-031-P1-K1-C3
Method	BLASTX
NCBI GI	g1621268
BLAST score	483
E value	7.0e-49
Match length	111
% identity	79
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	225351
Seq. ID	LIB3166-031-P1-K1-C5
Method	BLASTX
NCBI GI	g3582328
BLAST score	204
E value	4.0e-16
Match length	85
% identity	47
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225352
Seq. ID	LIB3166-031-P1-K1-C6
Method	BLASTX
NCBI GI	g4559382
BLAST score	222
E value	3.0e-18
Match length	85
% identity	45
NCBI Description	(AC006526) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	225353
Seq. ID	LIB3166-031-P1-K1-D1
Method	BLASTX
NCBI GI	g4335755

09604704 .960904

BLAST score	188
E value	3.0e-14
Match length	99
% identity	44
NCBI Description	(AC006284) putative hydroxyproline-rich glycoprotein [Arabidopsis thaliana]

Seq. No.	225354
Seq. ID	LIB3166-031-P1-K1-D10
Method	BLASTX
NCBI GI	g477280
BLAST score	244
E value	8.0e-21
Match length	56
% identity	75
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) 55K protein precursor - potato >gi_410633_bbs_136740 cytochrome c reductase-processing peptidase subunit I, MPP subunit I, P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 534 aa]

Seq. No.	225355
Seq. ID	LIB3166-031-P1-K1-D11
Method	BLASTX
NCBI GI	g4538965
BLAST score	240
E value	2.0e-20
Match length	107
% identity	47
NCBI Description	(AL049488) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225356
Seq. ID	LIB3166-031-P1-K1-D2
Method	BLASTX
NCBI GI	g4580523
BLAST score	247
E value	1.0e-21
Match length	69
% identity	72
NCBI Description	(AF036305) scarecrow-like 8 [Arabidopsis thaliana]

Seq. No.	225357
Seq. ID	LIB3166-031-P1-K1-E1
Method	BLASTX
NCBI GI	g3859598
BLAST score	311
E value	8.0e-52
Match length	125
% identity	83
NCBI Description	(AF104919) contains similarity to Myb DNA-binding domains (Pfam: PF00249, E=3.7e-27 N=3) [Arabidopsis thaliana]

Seq. No.	225358
Seq. ID	LIB3166-031-P1-K1-E2
Method	BLASTX
NCBI GI	g3915031
BLAST score	635

E value	1.0e-66
Match length	122
% identity	98
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232_ (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase [Gossypium hirsutum]

Seq. No.	225359
Seq. ID	LIB3166-031-P1-K1-E7
Method	BLASTX
NCBI GI	g4204277
BLAST score	280
E value	3.0e-25
Match length	85
% identity	68
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	225360
Seq. ID	LIB3166-031-P1-K1-E9
Method	BLASTX
NCBI GI	g2194137
BLAST score	338
E value	8.0e-32
Match length	94
% identity	73
NCBI Description	(AC002062) ESTs gb_R29947,gb_H76702 come from this gene. [Arabidopsis thaliana]

Seq. No.	225361
Seq. ID	LIB3166-031-P1-K1-F10
Method	BLASTX
NCBI GI	g4206765
BLAST score	185
E value	6.0e-14
Match length	76
% identity	53
NCBI Description	(AF104329) putative type 1 membrane protein [Arabidopsis thaliana]

Seq. No.	225362
Seq. ID	LIB3166-031-P1-K1-F3
Method	BLASTX
NCBI GI	g2275202
BLAST score	300
E value	2.0e-27
Match length	109
% identity	52
NCBI Description	(AC002337) acyl-CoA synthetase isolog [Arabidopsis thaliana]

Seq. No.	225363
Seq. ID	LIB3166-031-P1-K1-F4
Method	BLASTX
NCBI GI	g1362008
BLAST score	179
E value	3.0e-13

Match length	59
% identity	13
NCBI Description	ubiquitin-like protein 12 - Arabidopsis thaliana

Seq. No.	225364
Seq. ID	LIB3166-031-P1-K1-F7
Method	BLASTX
NCBI GI	g4006873
BLAST score	163
E value	3.0e-11
Match length	82
% identity	39
NCBI Description	(Z99707) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225365
Seq. ID	LIB3166-031-P1-K1-G10
Method	BLASTX
NCBI GI	g1076510
BLAST score	412
E value	2.0e-40
Match length	102
% identity	76
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean >gi_829119_emb_CAA52414_ (X74403) cyclophilin [Phaseolus vulgaris]

Seq. No.	225366
Seq. ID	LIB3166-031-P1-K1-G11
Method	BLASTX
NCBI GI	g3763916
BLAST score	143
E value	4.0e-09
Match length	84
% identity	38
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana] >gi_4531439_gb_AAD22124.1_AC006224_6 (AC006224) unknown protein [Arabidopsis thaliana]

Seq. No.	225367
Seq. ID	LIB3166-031-P1-K1-G3
Method	BLASTX
NCBI GI	g3759184
BLAST score	328
E value	1.0e-30
Match length	125
% identity	54
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	225368
Seq. ID	LIB3166-031-P1-K1-G4
Method	BLASTX
NCBI GI	g2760606
BLAST score	534
E value	8.0e-55
Match length	115
% identity	86
NCBI Description	(AB001568) phospholipid hydroperoxide glutathione

	peroxidase-like protein [Arabidopsis thaliana] >gi_3004869 (AF030132) glutathione peroxidase; ATGP1 [Arabidopsis thaliana] >gi_4539451_emb_CAB39931.1_ (AL049500) phospholipid hydroperoxide glutathione peroxidase [Arabidopsis thaliana]
Seq. No.	225369
Seq. ID	LIB3166-031-P1-K1-G6
Method	BLASTX
NCBI GI	g1694976
BLAST score	453
E value	2.0e-45
Match length	103
% identity	84
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis thaliana]
Seq. No.	225370
Seq. ID	LIB3166-031-P1-K1-G7
Method	BLASTX
NCBI GI	g4539545
BLAST score	446
E value	2.0e-44
Match length	90
% identity	97
NCBI Description	(Y16644) PRCI [Nicotiana tabacum]
Seq. No.	225371
Seq. ID	LIB3166-031-P1-K1-G8
Method	BLASTX
NCBI GI	g1944216
BLAST score	469
E value	3.0e-47
Match length	98
% identity	88
NCBI Description	(D84246) alcohol dehydrogenase [Arabidopsis thaliana]
Seq. No.	225372
Seq. ID	LIB3166-031-P1-K1-G9
Method	BLASTX
NCBI GI	g4249385
BLAST score	364
E value	2.0e-37
Match length	81
% identity	91
NCBI Description	(AC005966) T2K10.11 [Arabidopsis thaliana]
Seq. No.	225373
Seq. ID	LIB3166-031-P1-K1-H10
Method	BLASTX
NCBI GI	g3132675
BLAST score	168
E value	2.0e-12
Match length	40
% identity	85
NCBI Description	(AF061740) asparagine synthetase [Elaeagnus umbellata]

Seq. No.	225374
Seq. ID	LIB3166-031-P1-K1-H12
Method	BLASTX
NCBI GI	g115492
BLAST score	458
E value	7.0e-46
Match length	90
% identity	51
NCBI Description	CALMODULIN-RELATED PROTEIN >gi_169205 (M80831) calmodulin-related protein [Petunia hybrida]

Seq. No.	225375
Seq. ID	LIB3166-031-P1-K1-H3
Method	BLASTX
NCBI GI	g3860249
BLAST score	173
E value	2.0e-12
Match length	66
% identity	58
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	225376
Seq. ID	LIB3166-031-P1-K1-H7
Method	BLASTX
NCBI GI	g3114573
BLAST score	577
E value	8.0e-60
Match length	123
% identity	86
NCBI Description	(AF019383) 1-deoxyxylulose-5-phosphate synthase [Mentha x piperita]

Seq. No.	225377
Seq. ID	LIB3166-031-P1-K1-H8
Method	BLASTX
NCBI GI	g400923
BLAST score	443
E value	4.0e-44
Match length	89
% identity	97
NCBI Description	RAS-RELATED PROTEIN RAB7 >gi_485497_pir__S33531 GTP-binding protein rab - garden pea >gi_20756_emb_CAA46600_ (X65650) RAS-related GTP-binding protein [Pisum sativum]

Seq. No.	225378
Seq. ID	LIB3166-032-P1-K1-A1
Method	BLASTX
NCBI GI	g1944216
BLAST score	432
E value	6.0e-43
Match length	92
% identity	87
NCBI Description	(D84246) alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	225379
Seq. ID	LIB3166-032-P1-K1-A2

Method	BLASTX
NCBI GI	g2130149
BLAST score	614
E value	3.0e-64
Match length	120
% identity	98
NCBI Description	translation elongation factor eEF-1 alpha chain - maize (fragment)

Seq. No.	225380
Seq. ID	LIB3166-032-P1-K1-B12
Method	BLASTX
NCBI GI	g2665890
BLAST score	182
E value	5.0e-14
Match length	48
% identity	77
NCBI Description	(AF035944) calcium-dependent protein kinase [Fragaria x ananassa]

Seq. No.	225381
Seq. ID	LIB3166-032-P1-K1-C1
Method	BLASTX
NCBI GI	g231675
BLAST score	311
E value	1.0e-28
Match length	65
% identity	85
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi_282955_pir__S23525 cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) - common tobacco >gi_19839_emb_CAA44216_ (X62343) cinnamyl-alcohol dehydrogenase [Nicotiana tabacum]

Seq. No.	225382
Seq. ID	LIB3166-032-P1-K1-C2
Method	BLASTX
NCBI GI	g3603401
BLAST score	351
E value	2.0e-33
Match length	97
% identity	68
NCBI Description	(AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No.	225383
Seq. ID	LIB3166-032-P1-K1-D1
Method	BLASTX
NCBI GI	g3094012
BLAST score	426
E value	4.0e-42
Match length	99
% identity	77
NCBI Description	(AF060569) cold-regulated LTCOR12 [Lavatera thuringiaca]

Seq. No.	225384
Seq. ID	LIB3166-032-P1-K1-D2
Method	BLASTX
NCBI GI	g82306

BLAST score	302
E value	1.0e-27
Match length	82
% identity	63
NCBI Description	myb protein 305 - garden snapdragon

Seq. No.	225385
Seq. ID	LIB3166-032-P1-K1-D6
Method	BLASTX
NCBI GI	g417103
BLAST score	453
E value	2.0e-45
Match length	94
% identity	96
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	225386
Seq. ID	LIB3166-032-P1-K1-E1
Method	BLASTX
NCBI GI	g3860263
BLAST score	233
E value	1.0e-19
Match length	96
% identity	53
NCBI Description	(AC005824) putative cytochrome p450 protein [Arabidopsis thaliana]

Seq. No.	225387
Seq. ID	LIB3166-032-P1-K1-E2
Method	BLASTX
NCBI GI	g4544403
BLAST score	350
E value	3.0e-33
Match length	103
% identity	68
NCBI Description	(AC007047) putative glucan endo-1,3-beta-D-glucosidase precursor [Arabidopsis thaliana]

Seq. No.	225388

Seq. ID	LIB3166-032-P1-K1-E4
Method	BLASTX
NCBI GI	g3493172
BLAST score	245
E value	3.0e-21
Match length	67
% identity	76
NCBI Description	(U89609) fiber annexin [Gossypium hirsutum]

Seq. No.	225389
Seq. ID	LIB3166-032-P1-K1-E8
Method	BLASTX
NCBI GI	g1246823
BLAST score	185
E value	3.0e-18
Match length	70
% identity	67
NCBI Description	(X89865) unknown [Phoenix dactylifera]

Seq. No.	225390
Seq. ID	LIB3166-032-P1-K1-F1
Method	BLASTX
NCBI GI	g1346526
BLAST score	461
E value	3.0e-46
Match length	89
% identity	97
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1076533_pir__S52218 methionine adenosyltransferase (EC 2.5.1.6) - garden pea >gi_609225_emb_CAA57581_ (X82077) methionine adenosyltransferase [Pisum sativum] >gi_609559 (L36681) S-adenosylmethionine synthase [Pisum sativum]

Seq. No.	225391
Seq. ID	LIB3166-032-P1-K1-F10
Method	BLASTX
NCBI GI	g4545262
BLAST score	215
E value	2.0e-17
Match length	48
% identity	85
NCBI Description	(AF118230) metallothionein-like protein [Gossypium hirsutum]

Seq. No.	225392
Seq. ID	LIB3166-032-P1-K1-F12
Method	BLASTX
NCBI GI	g1361979
BLAST score	267
E value	2.0e-23
Match length	77
% identity	70
NCBI Description	serine O-acetyltransferase (EC 2.3.1.30) - watermelon >gi_1350550_dbj_BAA12843_ (D85624) serine acetyltransferase [Citrullus lanatus] >gi_1841312_dbj_BAA08479_ (D49535) serine acetyltransferase. [Citrullus lanatus]

>gi_2337772_dbj_BAA21827_ (AB006530) serine acetyltransferase [Citrullus lanatus]

Seq. No.	225393
Seq. ID	LIB3166-032-P1-K1-F2
Method	BLASTX
NCBI GI	g3868857
BLAST score	408
E value	5.0e-40
Match length	93
% identity	82
NCBI Description	(AB013886) RAV1 [Arabidopsis thaliana]

Seq. No.	225394
Seq. ID	LIB3166-032-P1-K1-F7
Method	BLASTX
NCBI GI	g1168727
BLAST score	250
E value	1.0e-21
Match length	71
% identity	65
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_474300_dbj_BAA03099_ (D13991) cinnamyl alcohol dehydrogenase [Aralia cordata] >gi_745086_prf__2015401A cinnamoyl alcohol dehydrogenase [Aralia cordata]

Seq. No.	225395
Seq. ID	LIB3166-032-P1-K1-G10
Method	BLASTX
NCBI GI	g3123264
BLAST score	411
E value	2.0e-40
Match length	86
% identity	88
NCBI Description	60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279_ (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225396
Seq. ID	LIB3166-032-P1-K1-G12
Method	BLASTX
NCBI GI	g2981475
BLAST score	134
E value	2.0e-14
Match length	54
% identity	81
NCBI Description	(AF053084) putative cinnamyl alcohol dehydrogenase [Malus domestica]

Seq. No.	225397
Seq. ID	LIB3166-032-P1-K1-G2
Method	BLASTX
NCBI GI	g3461848
BLAST score	203
E value	5.0e-16
Match length	118
% identity	44
NCBI Description	(AC005315) putative ATPase [Arabidopsis thaliana]

Seq. No.	225398
Seq. ID	LIB3166-032-P1-K1-H1
Method	BLASTX
NCBI GI	g625547
BLAST score	363
E value	8.0e-35
Match length	108
% identity	69
NCBI Description	chlorophyll a/b-binding protein type I - common tobacco >gi_493723_emb_CAA45523_ (X64198) photosystem I light-harvesting chlorophyll a/b-binding protein [Nicotiana tabacum]

Seq. No.	225399
Seq. ID	LIB3166-032-P1-K1-H12
Method	BLASTX
NCBI GI	g134777
BLAST score	240
E value	2.0e-20
Match length	91
% identity	51
NCBI Description	STAGE V SPORULATION PROTEIN K >gi_98485_pir__S16301 spoVJ protein - Bacillus subtilis >gi_40197_emb_CAA42049_ (X59412) spoVJ [Bacillus subtilis]

Seq. No.	225400
Seq. ID	LIB3166-033-P1-K1-A11
Method	BLASTX
NCBI GI	g3850111
BLAST score	172
E value	2.0e-12
Match length	78
% identity	46
NCBI Description	(AL033388) hypothetical integral membrane protein, putative involvement in lipid metabolism [Schizosaccharomyces pombe]

Seq. No.	225401
Seq. ID	LIB3166-033-P1-K1-A12
Method	BLASTX
NCBI GI	g2529680
BLAST score	465
E value	1.0e-46
Match length	117
% identity	57
NCBI Description	(AC002535) putative protein disulfide-isomerase precursor [Arabidopsis thaliana]

Seq. No.	225402
Seq. ID	LIB3166-033-P1-K1-A8
Method	BLASTX
NCBI GI	g445613
BLAST score	147
E value	8.0e-10
Match length	47
% identity	62
NCBI Description	ribosomal protein L7 [Solanum tuberosum]

Seq. No.	225403
Seq. ID	LIB3166-033-P1-K1-B11
Method	BLASTX
NCBI GI	g1084321
BLAST score	241
E value	2.0e-20
Match length	68
% identity	68
NCBI Description	protochlorophyllide reductase (EC 1.3.1.33) - cucumber >gi_2244614_dbj_BAA21089_ (D50085) NADPH-protochlorophyllide oxidoreductase [Cucumis sativus]

Seq. No.	225404
Seq. ID	LIB3166-033-P1-K1-B12
Method	BLASTX
NCBI GI	g1220196
BLAST score	541
E value	1.0e-55
Match length	122
% identity	87
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	225405
Seq. ID	LIB3166-033-P1-K1-B2
Method	BLASTX
NCBI GI	g2244759
BLAST score	553
E value	5.0e-57
Match length	124
% identity	81
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	225406
Seq. ID	LIB3166-033-P1-K1-B4
Method	BLASTX
NCBI GI	g4154352
BLAST score	147
E value	4.0e-10
Match length	83
% identity	48
NCBI Description	(AF110333) PrMC3 [Pinus radiata]

Seq. No.	225407
Seq. ID	LIB3166-033-P1-K1-B6
Method	BLASTX
NCBI GI	g587564
BLAST score	254
E value	2.0e-22
Match length	75
% identity	72
NCBI Description	(X80235) mitochondrial processing peptidase [Solanum tuberosum]

Seq. No.	225408
Seq. ID	LIB3166-033-P1-K1-C10
Method	BLASTX

NCBI GI	g3617770
BLAST score	147
E value	1.0e-09
Match length	34
% identity	79
NCBI Description	(Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	225409
Seq. ID	LIB3166-033-P1-K1-C12
Method	BLASTX
NCBI GI	g4531443
BLAST score	484
E value	6.0e-49
Match length	126
% identity	75
NCBI Description	(AC006224) putative 50s ribosomal protein L3 [Arabidopsis thaliana]

Seq. No.	225410
Seq. ID	LIB3166-033-P1-K1-C2
Method	BLASTX
NCBI GI	g478673
BLAST score	291
E value	3.0e-26
Match length	125
% identity	50
NCBI Description	proline-rich protein precursor - kidney bean >gi_21046_emb_CAA42942_ (X60391) proline-rich protein [Phaseolus vulgaris]

Seq. No.	225411
Seq. ID	LIB3166-033-P1-K1-D12
Method	BLASTX
NCBI GI	g3559805
BLAST score	431
E value	6.0e-43
Match length	90
% identity	80
NCBI Description	(AJ006787) putative phytochelatin synthetase [Arabidopsis thaliana]

Seq. No.	225412
Seq. ID	LIB3166-033-P1-K1-D2
Method	BLASTX
NCBI GI	g2781355
BLAST score	209
E value	1.0e-16
Match length	62
% identity	66
NCBI Description	(AC003113) F24O1.11 [Arabidopsis thaliana]

Seq. No.	225413
Seq. ID	LIB3166-033-P1-K1-D4
Method	BLASTX
NCBI GI	g4210948
BLAST score	534
E value	9.0e-55

Match length	101
% identity	99
NCBI Description	(AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No.	225414
Seq. ID	LIB3166-033-P1-K1-E2
Method	BLASTX
NCBI GI	g3249084
BLAST score	338
E value	8.0e-32
Match length	118
% identity	21
NCBI Description	(AC004473) Similar to red-1 (related to thioredoxin) gene gb_X92750 from Mus musculus. ESTs gb_AA712687 and gb_Z37223 come from this gene [Arabidopsis thaliana]

Seq. No.	225415
Seq. ID	LIB3166-033-P1-K1-E3
Method	BLASTX
NCBI GI	g2462762
BLAST score	255
E value	5.0e-22
Match length	85
% identity	59
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	225416
Seq. ID	LIB3166-033-P1-K1-E4
Method	BLASTX
NCBI GI	g2493318
BLAST score	230
E value	4.0e-19
Match length	88
% identity	50
NCBI Description	BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_ (Z25471) blue copper protein [Pisum sativum] >gi_1098264_prf__2115352A blue Cu protein [Pisum sativum]

Seq. No.	225417
Seq. ID	LIB3166-033-P1-K1-E6
Method	BLASTX
NCBI GI	g114339
BLAST score	532
E value	2.0e-54
Match length	128
% identity	84
NCBI Description	PLASMA MEMBRANE ATPASE 3 (PROTON PUMP) >gi_67974_pir__PXMUP3 H+-transporting ATPase (EC 3.6.1.35) type 3, plasma membrane - Arabidopsis thaliana >gi_166625 (J04737) ATPase [Arabidopsis thaliana]

Seq. No.	225418
Seq. ID	LIB3166-033-P1-K1-E7
Method	BLASTX
NCBI GI	g3885515
BLAST score	264

E value	1.0e-24
Match length	68
% identity	88
NCBI Description	(AF084202) similar to ribosomal protein S26 [Medicago sativa]

Seq. No.	225419
Seq. ID	LIB3166-033-P1-K1-E8
Method	BLASTX
NCBI GI	g2499708
BLAST score	143
E value	2.0e-09
Match length	39
% identity	77
NCBI Description	PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi_1020409_dbj_BAA11135_ (D73410) phospholipase D [Zea mays]

Seq. No.	225420
Seq. ID	LIB3166-033-P1-K1-F1
Method	BLASTX
NCBI GI	g2262170
BLAST score	391
E value	5.0e-38
Match length	124
% identity	60
NCBI Description	(AC002329) predicted glycosyl hydrolase [Arabidopsis thaliana]

Seq. No.	225421
Seq. ID	LIB3166-033-P1-K1-F11
Method	BLASTX
NCBI GI	g3928862
BLAST score	147
E value	2.0e-09
Match length	113
% identity	31
NCBI Description	(AF089710) disease resistance protein RPP8 [Arabidopsis thaliana]

Seq. No.	225422
Seq. ID	LIB3166-033-P1-K1-F12
Method	BLASTX
NCBI GI	g2827714
BLAST score	248
E value	3.0e-21
Match length	114
% identity	46
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	225423
Seq. ID	LIB3166-033-P1-K1-F2
Method	BLASTX
NCBI GI	g3252813
BLAST score	322

E value	6.0e-30
Match length	73
% identity	84
NCBI Description	(AC004705) vacuolar sorting receptor-like protein [Arabidopsis thaliana] >gi_3810586 (AC005398) vacuolar sorting receptor-like protein [Arabidopsis thaliana]

Seq. No.	225424
Seq. ID	LIB3166-033-P1-K1-F3
Method	BLASTX
NCBI GI	g1730109
BLAST score	452
E value	4.0e-45
Match length	108
% identity	81
NCBI Description	LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN HYDROXYLASE) >gi_499022_emb_CAA53580_ (X75966) leucoanthocyanidin dioxygenase [Vitis vinifera]

Seq. No.	225425
Seq. ID	LIB3166-033-P1-K1-F4
Method	BLASTX
NCBI GI	g1518540
BLAST score	616
E value	2.0e-64
Match length	128
% identity	94
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	225426
Seq. ID	LIB3166-033-P1-K1-F5
Method	BLASTX
NCBI GI	g2341032
BLAST score	145
E value	1.0e-17
Match length	107
% identity	48
NCBI Description	(AC000104) EST gb_ATTS0956 comes from this gene. [Arabidopsis thaliana]

Seq. No.	225427
Seq. ID	LIB3166-033-P1-K1-F6
Method	BLASTX
NCBI GI	g4098128
BLAST score	472
E value	2.0e-47
Match length	96
% identity	97
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	225428
Seq. ID	LIB3166-033-P1-K1-G1
Method	BLASTX
NCBI GI	g3461817
BLAST score	288
E value	6.0e-26
Match length	65

% identity	82
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	225429
Seq. ID	LIB3166-033-P1-K1-G2
Method	BLASTX
NCBI GI	g3080398
BLAST score	312
E value	1.0e-28
Match length	123
% identity	26
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana]

Seq. No.	225430
Seq. ID	LIB3166-033-P1-K1-G5
Method	BLASTX
NCBI GI	g3860245
BLAST score	360
E value	2.0e-34
Match length	119
% identity	60
NCBI Description	(AC005824) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	225431
Seq. ID	LIB3166-033-P1-K1-G9
Method	BLASTX
NCBI GI	g2392771
BLAST score	350
E value	3.0e-33
Match length	100
% identity	71
NCBI Description	(AC002534) putative kinesin-like protein [Arabidopsis thaliana]

Seq. No.	225432
Seq. ID	LIB3166-033-P1-K1-H1
Method	BLASTX
NCBI GI	g1518540
BLAST score	600
E value	2.0e-62
Match length	125
% identity	94
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	225433
Seq. ID	LIB3166-033-P1-K1-H12
Method	BLASTX
NCBI GI	g4545262
BLAST score	163
E value	3.0e-11
Match length	43
% identity	67
NCBI Description	(AF118230) metallothionein-like protein [Gossypium hirsutum]

Seq. No. 225434

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Seq. ID	LIB3166-033-P1-K1-H2
Method	BLASTX
NCBI GI	g4218535
BLAST score	387
E value	2.0e-37
Match length	96
% identity	68
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]

Seq. No.	225435
Seq. ID	LIB3166-033-P1-K1-H3
Method	BLASTX
NCBI GI	g2407800
BLAST score	363
E value	1.0e-34
Match length	98
% identity	78
NCBI Description	(Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No.	225436
Seq. ID	LIB3166-033-P1-K1-H8
Method	BLASTX
NCBI GI	g4538903
BLAST score	264
E value	4.0e-23
Match length	55
% identity	87
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

Seq. No.	225437
Seq. ID	LIB3166-033-P1-K1-H9
Method	BLASTX
NCBI GI	g3763917
BLAST score	226
E value	9.0e-19
Match length	94
% identity	49
NCBI Description	(AC004450) hypothetical protein [Arabidopsis thaliana] >gi_4531438_gb_AAD22123.1_AC006224_5 (AC006224) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225438
Seq. ID	LIB3166-034-P1-K1-A10
Method	BLASTX
NCBI GI	g4559342
BLAST score	475
E value	7.0e-48
Match length	125
% identity	66
NCBI Description	(AC007087) putative copper methylamine oxidase [Arabidopsis thaliana]

Seq. No.	225439
Seq. ID	LIB3166-034-P1-K1-A12
Method	BLASTX
NCBI GI	g2842744
BLAST score	304

E value	7.0e-28
Match length	70
% identity	79
NCBI Description	ENHANCER OF RUDIMENTARY HOMOLOG >gi_1595812 (U67398) enhancer of rudimentary homolog ATER [Arabidopsis thaliana]

Seq. No.	225440
Seq. ID	LIB3166-034-P1-K1-A2
Method	BLASTX
NCBI GI	g1170373
BLAST score	537
E value	3.0e-55
Match length	118
% identity	88
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	225441
Seq. ID	LIB3166-034-P1-K1-A4
Method	BLASTX
NCBI GI	g3287693
BLAST score	384
E value	2.0e-37
Match length	87
% identity	82
NCBI Description	(AC003979) Similar to LIM17 gene product gb_1653769 from the genome of Synechocystis sp. gb_D90916. [Arabidopsis thaliana]

Seq. No.	225442
Seq. ID	LIB3166-034-P1-K1-A9
Method	BLASTX
NCBI GI	g1362093
BLAST score	157
E value	1.0e-10
Match length	37
% identity	81
NCBI Description	hypothetical protein (clone TPP15) - tomato (fragment) >gi_924632 (U20595) unknown [Solanum lycopersicum]

Seq. No.	225443
Seq. ID	LIB3166-034-P1-K1-B1
Method	BLASTX
NCBI GI	g2980795
BLAST score	420
E value	2.0e-41
Match length	89
% identity	89
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	225444
Seq. ID	LIB3166-034-P1-K1-B10
Method	BLASTX
NCBI GI	g2809255
BLAST score	279

E value	6.0e-25
Match length	73
% identity	74
NCBI Description	(AC002560) F21B7.24 [Arabidopsis thaliana]

Seq. No.	225445
Seq. ID	LIB3166-034-P1-K1-B11
Method	BLASTX
NCBI GI	g1703446
BLAST score	190
E value	1.0e-14
Match length	94
% identity	45
NCBI Description	L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE) >gi_1076292_pir__S53127 asparaginase - Arabidopsis thaliana >gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis thaliana]

Seq. No.	225446
Seq. ID	LIB3166-034-P1-K1-B12
Method	BLASTX
NCBI GI	g1351272
BLAST score	141
E value	3.0e-09
Match length	28
% identity	89
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_414550 (U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi_742408_prf__2009415A triose phosphate isomerase [Arabidopsis thaliana]

Seq. No.	225447
Seq. ID	LIB3166-034-P1-K1-B4
Method	BLASTX
NCBI GI	g1076515
BLAST score	329
E value	9.0e-31
Match length	129
% identity	56
NCBI Description	pectinesterase precursor - kidney bean >gi_732913_emb_CAA59482_ (X85216) pectinesterase [Phaseolus vulgaris]

Seq. No.	225448
Seq. ID	LIB3166-034-P1-K1-B5
Method	BLASTX
NCBI GI	g1928981
BLAST score	304
E value	6.0e-28
Match length	91
% identity	68
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	225449
Seq. ID	LIB3166-034-P1-K1-B6
Method	BLASTX

NCBI GI	g3123271
BLAST score	356
E value	1.0e-40
Match length	98
% identity	85
NCBI Description	40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No.	225450
Seq. ID	LIB3166-034-P1-K1-B7
Method	BLASTX
NCBI GI	g4539330
BLAST score	377
E value	2.0e-36
Match length	104
% identity	68
NCBI Description	(AL035679) putative receptor-like protein kinase (fragment) [Arabidopsis thaliana]

Seq. No.	225451
Seq. ID	LIB3166-034-P1-K1-B8
Method	BLASTX
NCBI GI	g2642448
BLAST score	168
E value	7.0e-12
Match length	122
% identity	37
NCBI Description	(AC002391) hypothetical protein [Arabidopsis thaliana] >gi_3169187 (AC004401) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225452
Seq. ID	LIB3166-034-P1-K1-B9
Method	BLASTX
NCBI GI	g1170938
BLAST score	507
E value	1.0e-51
Match length	118
% identity	86
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_481566_pir__S38875 methionine adenosyltransferase (EC 2.5.1.6) - tomato >gi_429106_emb_CAA80866_ (Z24742) S-adenosyl-L-methionine synthetase [Lycopersicon esculentum]

Seq. No.	225453
Seq. ID	LIB3166-034-P1-K1-C1
Method	BLASTX
NCBI GI	g4263711
BLAST score	230
E value	3.0e-19
Match length	58
% identity	81
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	225454
Seq. ID	LIB3166-034-P1-K1-C10
Method	BLASTX
NCBI GI	g4262250
BLAST score	265
E value	2.0e-23
Match length	87
% identity	69
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	225455
Seq. ID	LIB3166-034-P1-K1-C2
Method	BLASTX
NCBI GI	g1518540
BLAST score	144
E value	4.0e-09
Match length	33
% identity	82
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	225456
Seq. ID	LIB3166-034-P1-K1-C3
Method	BLASTX
NCBI GI	g4514716
BLAST score	178
E value	5.0e-13
Match length	84
% identity	37
NCBI Description	(AB017533) EPc [Nicotiana tabacum]

Seq. No.	225457
Seq. ID	LIB3166-034-P1-K1-C5
Method	BLASTX
NCBI GI	g4426565
BLAST score	211
E value	7.0e-17
Match length	112
% identity	40
NCBI Description	(AF031483) unknown [Rattus norvegicus]

Seq. No.	225458
Seq. ID	LIB3166-034-P1-K1-C6
Method	BLASTX
NCBI GI	g4490297
BLAST score	147
E value	2.0e-09
Match length	76
% identity	37
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	225459
Seq. ID	LIB3166-034-P1-K1-C7
Method	BLASTX
NCBI GI	g1495804
BLAST score	406
E value	6.0e-40
Match length	104

% identity	73
NCBI Description	(X96406) 13-lipoxygenase [Solanum tuberosum]

Seq. No.	225460
Seq. ID	LIB3166-034-P1-K1-C8
Method	BLASTX
NCBI GI	g3676818
BLAST score	215
E value	2.0e-17
Match length	55
% identity	71
NCBI Description	(AF091514) metallothionein homolog [Elaeagnus umbellata]

Seq. No.	225461
Seq. ID	LIB3166-034-P1-K1-D10
Method	BLASTX
NCBI GI	g3080437
BLAST score	142
E value	1.0e-08
Match length	50
% identity	66
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	225462
Seq. ID	LIB3166-034-P1-K1-D11
Method	BLASTX
NCBI GI	g1778376
BLAST score	566
E value	2.0e-58
Match length	130
% identity	81
NCBI Description	(U81288) PsRT17-1 [Pisum sativum]

Seq. No.	225463
Seq. ID	LIB3166-034-P1-K1-D12
Method	BLASTX
NCBI GI	g1707008
BLAST score	319
E value	1.0e-29
Match length	91
% identity	73
NCBI Description	(U78721) 30S ribosomal protein S5 isolog [Arabidopsis thaliana]

Seq. No.	225464
Seq. ID	LIB3166-034-P1-K1-D5
Method	BLASTX
NCBI GI	g3759184
BLAST score	398
E value	7.0e-39
Match length	116
% identity	66
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	225465
Seq. ID	LIB3166-034-P1-K1-D7
Method	BLASTX

NCBI GI	g533084
BLAST score	376
E value	2.0e-36
Match length	92
% identity	75
NCBI Description	(U07597) delta-9 stearoyl-acyl carrier protein desaturase precursor [Thunbergia alata]

Seq. No.	225466
Seq. ID	LIB3166-034-P1-K1-D9
Method	BLASTX
NCBI GI	g1944216
BLAST score	410
E value	2.0e-40
Match length	91
% identity	86
NCBI Description	(D84246) alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	225467
Seq. ID	LIB3166-034-P1-K1-E1
Method	BLASTX
NCBI GI	g2055374
BLAST score	501
E value	7.0e-51
Match length	127
% identity	78
NCBI Description	(U29095) serine-threonine protein kinase [Triticum aestivum]

Seq. No.	225468
Seq. ID	LIB3166-034-P1-K1-E11
Method	BLASTX
NCBI GI	g1709846
BLAST score	264
E value	4.0e-23
Match length	127
% identity	43
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_706853 (U04336) 22 kDa component of photosystem II [Lycopersicon esculentum]

Seq. No.	225469
Seq. ID	LIB3166-034-P1-K1-E12
Method	BLASTX
NCBI GI	g3493172
BLAST score	551
E value	8.0e-57
Match length	110
% identity	98
NCBI Description	(U89609) fiber annexin [Gossypium hirsutum]

Seq. No.	225470
Seq. ID	LIB3166-034-P1-K1-E4
Method	BLASTX
NCBI GI	g1351202
BLAST score	643
E value	2.0e-67

Match length	129
% identity	94
NCBI Description	TUBULIN BETA CHAIN >gi_312989_emb_CAA42777_ (X60216) beta-tubulin [Glycine max]

Seq. No.	225471
Seq. ID	LIB3166-034-P1-K1-E8
Method	BLASTX
NCBI GI	g3885334
BLAST score	371
E value	1.0e-35
Match length	125
% identity	62
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	225472
Seq. ID	LIB3166-034-P1-K1-E9
Method	BLASTX
NCBI GI	g464849
BLAST score	524
E value	1.0e-53
Match length	99
% identity	98
NCBI Description	TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha chain - almond >gi_20413_emb_CAA47635_ (X67162) alpha-tubulin [Prunus dulcis]

Seq. No.	225473
Seq. ID	LIB3166-034-P1-K1-F1
Method	BLASTX
NCBI GI	g2160166
BLAST score	170
E value	5.0e-12
Match length	70
% identity	50
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	225474
Seq. ID	LIB3166-034-P1-K1-F2
Method	BLASTX
NCBI GI	g3868853
BLAST score	240
E value	2.0e-20
Match length	71
% identity	65
NCBI Description	(AB013853) GPI-anchored protein [Vigna radiata]

Seq. No.	225475
Seq. ID	LIB3166-034-P1-K1-F7
Method	BLASTX
NCBI GI	g3286721
BLAST score	187
E value	2.0e-14
Match length	53
% identity	72
NCBI Description	(AJ007449) trans-cinnamic 4-monooxygenase [Cicer arietinum]

Seq. No. 225476
Seq. ID LIB3166-034-P1-K1-G1
Method BLASTX
NCBI GI g3901012
BLAST score 231
E value 1.0e-27
Match length 97
% identity 70
NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]

Seq. No. 225477
Seq. ID LIB3166-034-P1-K1-G10
Method BLASTX
NCBI GI g2507281
BLAST score 273
E value 2.0e-24
Match length 56
% identity 93
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_ (X97380) atran2 [Arabidopsis thaliana]

Seq. No. 225478
Seq. ID LIB3166-034-P1-K1-G2
Method BLASTX
NCBI GI g2194128
BLAST score 296
E value 7.0e-27
Match length 113
% identity 54
NCBI Description (AC002062) Strong similarity to Arabidopsis receptor-like kinase (gb_ATLECGENE) and F20P5.15. [Arabidopsis thaliana]

Seq. No. 225479
Seq. ID LIB3166-034-P1-K1-G3
Method BLASTX
NCBI GI g4557062
BLAST score 256
E value 2.0e-22
Match length 99
% identity 58
NCBI Description (AC007045) hypothetical protein [Arabidopsis thaliana]

Seq. No. 225480
Seq. ID LIB3166-034-P1-K1-G4
Method BLASTX
NCBI GI g228210
BLAST score 504
E value 3.0e-51
Match length 117
% identity 77
NCBI Description granule-bound starch synthase [Solanum tuberosum].

Seq. No. 225481
Seq. ID LIB3166-034-P1-K1-G9
Method BLASTX

09604016.1000

NCBI GI	g3367534
BLAST score	481
E value	1.0e-48
Match length	107
% identity	86
NCBI Description	(AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	225482
Seq. ID	LIB3166-034-P1-K1-H1
Method	BLASTX
NCBI GI	g3286691
BLAST score	367
E value	3.0e-35
Match length	94
% identity	74
NCBI Description	(AJ007450) auxilin-like protein [Arabidopsis thaliana]

Seq. No.	225483
Seq. ID	LIB3166-034-P1-K1-H10
Method	BLASTX
NCBI GI	g1351271
BLAST score	314
E value	2.0e-29
Match length	70
% identity	83
NCBI Description	TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) >gi_1084309_pir__S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi_806312 (L36387) triosephosphate isomerase, chloroplast isozyme [Spinacia oleracea]

Seq. No.	225484
Seq. ID	LIB3166-034-P1-K1-H2
Method	BLASTX
NCBI GI	g113461
BLAST score	259
E value	3.0e-26
Match length	72
% identity	86
NCBI Description	ADP,ATP CARRIER PROTEIN PRECURSOR (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT) >gi_100423_pir__S14874 ADP,ATP carrier protein, ACC - potato >gi_21405_emb_CAA40782_ (X57557) adenine nucleotide translocator [Solanum tuberosum]

Seq. No.	225485
Seq. ID	LIB3166-034-P1-K1-H5
Method	BLASTX
NCBI GI	g3080437
BLAST score	202
E value	8.0e-16
Match length	50
% identity	84
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No. 225486
Seq. ID LIB3166-034-P1-K1-H7
Method BLASTX
NCBI GI g2864614
BLAST score 366
E value 4.0e-35
Match length 119
% identity 56
NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 225487
Seq. ID LIB3166-034-P1-K1-H8
Method BLASTX
NCBI GI g3063396
BLAST score 349
E value 2.0e-33
Match length 77
% identity 86
NCBI Description (AB012947) vcCyP [Vicia faba]

Seq. No. 225488
Seq. ID LIB3166-035-P1-K1-A12
Method BLASTX
NCBI GI g542125
BLAST score 201
E value 1.0e-16
Match length 52
% identity 94
NCBI Description translation elongation factor eEF-1 alpha chain - barley >gi_396134_emb_CAA80666_ (Z23130) protein synthesis elongation factor-1 alpha [Hordeum vulgare]

Seq. No. 225489
Seq. ID LIB3166-035-P1-K1-A2
Method BLASTX
NCBI GI g3309243
BLAST score 461
E value 3.0e-46
Match length 93
% identity 92
NCBI Description (AF073507) aconitase-iron regulated protein 1 [Citrus limon]

Seq. No. 225490
Seq. ID LIB3166-035-P1-K1-A3
Method BLASTX
NCBI GI g4567245
BLAST score 231
E value 2.0e-19
Match length 77
% identity 62
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]

Seq. No. 225491
Seq. ID LIB3166-035-P1-K1-A4
Method BLASTX
NCBI GI g4220474

BLAST score	208
E value	1.0e-16
Match length	104
% identity	54
NCBI Description	(AC006069) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No.	225492
Seq. ID	LIB3166-035-P1-K1-A5
Method	BLASTX
NCBI GI	g1220196
BLAST score	293
E value	4.0e-29
Match length	80
% identity	85
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	225493
Seq. ID	LIB3166-035-P1-K1-A6
Method	BLASTX
NCBI GI	g4262250
BLAST score	524
E value	1.0e-53
Match length	105
% identity	92
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	225494
Seq. ID	LIB3166-035-P1-K1-B1
Method	BLASTX
NCBI GI	g2431769
BLAST score	227
E value	7.0e-19
Match length	56
% identity	77
NCBI Description	(U62752) acidic ribosomal protein P1a [Zea mays]

Seq. No.	225495
Seq. ID	LIB3166-035-P1-K1-B11
Method	BLASTX
NCBI GI	g421989
BLAST score	292
E value	2.0e-26
Match length	89
% identity	60
NCBI Description	serpin - barley >gi_19071_emb_CAA78822_ (Z15116) protein zx [Hordeum vulgare] >gi_444778_prf__1908213A protein Zx [Hordeum vulgare]

Seq. No.	225496
Seq. ID	LIB3166-035-P1-K1-B2
Method	BLASTX
NCBI GI	g3935184
BLAST score	264
E value	4.0e-23
Match length	120
% identity	53

NCBI Description	(AC004557) F17L21.27 [Arabidopsis thaliana]

Seq. No.	225497
Seq. ID	LIB3166-035-P1-K1-B3
Method	BLASTX
NCBI GI	g2213610
BLAST score	167
E value	1.0e-11
Match length	102
% identity	20
NCBI Description	(AC000103) F21J9.4 [Arabidopsis thaliana]

Seq. No.	225498
Seq. ID	LIB3166-035-P1-K1-B8
Method	BLASTX
NCBI GI	g547683
BLAST score	604
E value	6.0e-63
Match length	126
% identity	94
NCBI Description	HEAT SHOCK COGNATE PROTEIN 80 >gi_170456 (M96549) heat shock cognate protein 80 [Solanum lycopersicum] >gi_445601_prf__1909348A heat shock protein hsp80 [Lycopersicon esculentum]

Seq. No.	225499
Seq. ID	LIB3166-035-P1-K1-C12
Method	BLASTX
NCBI GI	g3242723
BLAST score	401
E value	4.0e-39
Match length	125
% identity	62
NCBI Description	(AC003040) putative acetone-cyanohydrin lyase [Arabidopsis thaliana]

Seq. No.	225500
Seq. ID	LIB3166-035-P1-K1-C3
Method	BLASTX
NCBI GI	g4335764
BLAST score	477
E value	4.0e-48
Match length	117
% identity	46
NCBI Description	(AC006284) putative WRKY DNA-binding protein [Arabidopsis thaliana]

Seq. No.	225501
Seq. ID	LIB3166-035-P1-K1-C8
Method	BLASTX
NCBI GI	g729442
BLAST score	385
E value	2.0e-37
Match length	105
% identity	73
NCBI Description	PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR >gi_166380 (M80235) glucose-regulated endoplasmic reticular

protein precursor [Medicago sativa]

Seq. No.	225502
Seq. ID	LIB3166-035-P1-K1-D2
Method	BLASTX
NCBI GI	g2088651
BLAST score	143
E value	5.0e-09
Match length	50
% identity	64
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	225503
Seq. ID	LIB3166-035-P1-K1-D5
Method	BLASTX
NCBI GI	g3176965
BLAST score	500
E value	9.0e-51
Match length	122
% identity	84
NCBI Description	(AF067967) pyrroline-5-carboxylate synthetase [Mesembryanthemum crystallinum]

Seq. No.	225504
Seq. ID	LIB3166-035-P1-K1-D7
Method	BLASTX
NCBI GI	g2832629
BLAST score	143
E value	3.0e-10
Match length	118
% identity	33
NCBI Description	(AL021711) 4-coumarate-CoA ligase - like [Arabidopsis thaliana]

Seq. No.	225505
Seq. ID	LIB3166-035-P1-K1-E1
Method	BLASTX
NCBI GI	g3036840
BLAST score	298
E value	4.0e-27
Match length	118
% identity	49
NCBI Description	(AJ222967) cystinosin [Homo sapiens] >gi_3036851_emb_CAA75882_ (Y15924) cystinosin [Homo sapiens]

Seq. No.	225506
Seq. ID	LIB3166-035-P1-K1-E12
Method	BLASTX
NCBI GI	g586318
BLAST score	153
E value	4.0e-10
Match length	70
% identity	47
NCBI Description	HYPOTHETICAL 30.3 KD PROTEIN IN MBA1-RPS13 INTERGENIC REGION >gi_626233_pir__S46059 probable membrane protein

09504705.1000

	YBR187w - yeast (Saccharomyces cerevisiae) >gi_536548_emb_CAA85148_ (Z36056) ORF YBR187w [Saccharomyces cerevisiae] >gi_575915 (U02073) unknown [Saccharomyces cerevisiae]
Seq. No.	225507
Seq. ID	LIB3166-035-P1-K1-E5
Method	BLASTX
NCBI GI	g4508073
BLAST score	288
E value	5.0e-26
Match length	86
% identity	63
NCBI Description	(AC005882) 43220 [Arabidopsis thaliana]
Seq. No.	225508
Seq. ID	LIB3166-035-P1-K1-E7
Method	BLASTX
NCBI GI	g4220481
BLAST score	193
E value	5.0e-15
Match length	89
% identity	44
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]
Seq. No.	225509
Seq. ID	LIB3166-035-P1-K1-F11
Method	BLASTX
NCBI GI	g2896801
BLAST score	151
E value	2.0e-10
Match length	61
% identity	52
NCBI Description	(AC004155) ERCC4_MOUSE [Mus musculus]
Seq. No.	225510
Seq. ID	LIB3166-035-P1-K1-F12
Method	BLASTX
NCBI GI	g2558664
BLAST score	200
E value	1.0e-15
Match length	112
% identity	38
NCBI Description	(AC002354) hypothetical protein [Arabidopsis thaliana]
Seq. No.	225511
Seq. ID	LIB3166-035-P1-K1-F5
Method	BLASTX
NCBI GI	g1208776
BLAST score	155
E value	8.0e-11
Match length	38
% identity	68
NCBI Description	(U48367) alcohol dehydrogenase [Pinus banksiana] >gi_1208788 (U48373) alcohol dehydrogenase [Pinus banksiana]

Seq. No.	225512
Seq. ID	LIB3166-035-P1-K1-G10
Method	BLASTX
NCBI GI	g1174162
BLAST score	501
E value	6.0e-51
Match length	95
% identity	91
NCBI Description	(U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi_3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No.	225513
Seq. ID	LIB3166-035-P1-K1-G12
Method	BLASTX
NCBI GI	g131772
BLAST score	536
E value	5.0e-55
Match length	116
% identity	92
NCBI Description	40S RIBOSOMAL PROTEIN S14 (CLONE MCH1) >gi_82723_pir__A30097 ribosomal protein S14 (clone MCH1) - maize

Seq. No.	225514
Seq. ID	LIB3166-035-P1-K1-G3
Method	BLASTX
NCBI GI	g2275201
BLAST score	228
E value	5.0e-19
Match length	92
% identity	47
NCBI Description	(AC002337) unknown protein [Arabidopsis thaliana]

Seq. No.	225515
Seq. ID	LIB3166-035-P1-K1-G5
Method	BLASTX
NCBI GI	g4572674
BLAST score	235
E value	5.0e-20
Match length	78
% identity	59
NCBI Description	(AC006954) unknown protein [Arabidopsis thaliana]

Seq. No.	225516
Seq. ID	LIB3166-035-P1-K1-G7
Method	BLASTX
NCBI GI	g2275204
BLAST score	296
E value	6.0e-27
Match length	73
% identity	70
NCBI Description	(AC002337) DNA binding protein isolog [Arabidopsis thaliana]

Seq. No.	225517
Seq. ID	LIB3166-035-P1-K1-G9

Method	BLASTX
NCBI GI	g99893
BLAST score	456
E value	1.0e-45
Match length	95
% identity	93
NCBI Description	chlorophyll a/b-binding protein 4 - soybean

Seq. No.	225518
Seq. ID	LIB3166-035-P1-K1-H1
Method	BLASTX
NCBI GI	g4218535
BLAST score	220
E value	4.0e-18
Match length	58
% identity	66
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]

Seq. No.	225519
Seq. ID	LIB3166-035-P1-K1-H10
Method	BLASTX
NCBI GI	g3552003
BLAST score	496
E value	2.0e-50
Match length	120
% identity	81
NCBI Description	(AF085083) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3552005 (AF085084) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3552007 (AF085085) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140632 (AF090165) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140634 (AF090166) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140636 (AF090167) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140638 (AF090168) alcohol dehydrogenase A [Gossypium hirsutum]

Seq. No.	225520
Seq. ID	LIB3166-035-P1-K1-H2
Method	BLASTX
NCBI GI	g4469026
BLAST score	182
E value	2.0e-17
Match length	59
% identity	81
NCBI Description	(AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225521
Seq. ID	LIB3166-035-P1-K1-H9
Method	BLASTX
NCBI GI	g3023190
BLAST score	268
E value	7.0e-24
Match length	64
% identity	84
NCBI Description	14-3-3-LIKE PROTEIN 16R >gi_1888459_emb_CAA72381_ (Y11685) 14-3-3 protein [Solanum tuberosum]

Seq. No.	225522
Seq. ID	LIB3166-036-P1-K1-A1
Method	BLASTX
NCBI GI	g4220512
BLAST score	279
E value	7.0e-25
Match length	107
% identity	51
NCBI Description	(AL035356) putative pectate lyase [Arabidopsis thaliana]

Seq. No.	225523
Seq. ID	LIB3166-036-P1-K1-A10
Method	BLASTX
NCBI GI	g4538911
BLAST score	432
E value	7.0e-43
Match length	107
% identity	81
NCBI Description	(AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225524
Seq. ID	LIB3166-036-P1-K1-A12
Method	BLASTX
NCBI GI	g586069
BLAST score	155
E value	2.0e-10
Match length	58
% identity	45
NCBI Description	VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS) >gi_541424_pir__S41420 valine--tRNA ligase (EC 6.1.1.9) - Bacillus subtilis >gi_452309_emb_CAA54458_ (X77239) valyl-tRNA synthetase [Bacillus subtilis] >gi_2635274_emb_CAB14769_ (Z99118) valyl-tRNA synthetase [Bacillus subtilis]

Seq. No.	225525
Seq. ID	LIB3166-036-P1-K1-A2
Method	BLASTX
NCBI GI	g120673
BLAST score	389
E value	6.0e-38
Match length	95
% identity	79
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66013_pir__DEPJG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - garden petunia >gi_20551_emb_CAA42904_ (X60346) glyceraldehyde 3-phosphate dehydrogenase [Petunia x hybrida]

Seq. No.	225526
Seq. ID	LIB3166-036-P1-K1-A4
Method	BLASTX
NCBI GI	g4105772
BLAST score	442
E value	5.0e-44
Match length	116
% identity	43

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NCBI Description	(AF049917) PGP9B [Petunia x hybrida]

Seq. No.	225527
Seq. ID	LIB3166-036-P1-K1-A8
Method	BLASTX
NCBI GI	g2760345
BLAST score	539
E value	2.0e-55
Match length	115
% identity	26
NCBI Description	(U84967) ubiquitin [Arabidopsis thaliana]

Seq. No.	225528
Seq. ID	LIB3166-036-P1-K1-B1
Method	BLASTX
NCBI GI	g3451078
BLAST score	207
E value	2.0e-16
Match length	112
% identity	38
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	225529
Seq. ID	LIB3166-036-P1-K1-B11
Method	BLASTX
NCBI GI	g3522938
BLAST score	166
E value	1.0e-11
Match length	73
% identity	41
NCBI Description	(AC004411) unknown protein [Arabidopsis thaliana]

Seq. No.	225530
Seq. ID	LIB3166-036-P1-K1-B3
Method	BLASTX
NCBI GI	g2507421
BLAST score	283
E value	2.0e-25
Match length	61
% identity	89
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi_1800277 (U81042) translation initiation factor [Arabidopsis thaliana] >gi_4490709_emb_CAB38843.1_ (AL035680) translation initiation factor [Arabidopsis thaliana]

Seq. No.	225531
Seq. ID	LIB3166-036-P1-K1-B8
Method	BLASTX
NCBI GI	g401322
BLAST score	295
E value	8.0e-27
Match length	64
% identity	92
NCBI Description	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi_167313 (L03186) vacuolar H+-ATPase catalytic subunit [Gossypium hirsutum]

Seq. No.	225532
Seq. ID	LIB3166-036-P1-K1-C4
Method	BLASTX
NCBI GI	g3033400
BLAST score	344
E value	2.0e-32
Match length	119
% identity	60
NCBI Description	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	225533
Seq. ID	LIB3166-036-P1-K1-D2
Method	BLASTX
NCBI GI	g4210948
BLAST score	307
E value	2.0e-28
Match length	67
% identity	91
NCBI Description	(AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No.	225534
Seq. ID	LIB3166-036-P1-K1-D3
Method	BLASTX
NCBI GI	g1263291
BLAST score	448
E value	4.0e-47
Match length	105
% identity	89
NCBI Description	(U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No.	225535
Seq. ID	LIB3166-036-P1-K1-D4
Method	BLASTX
NCBI GI	g4115936
BLAST score	158
E value	9.0e-11
Match length	55
% identity	51
NCBI Description	(AF118223) No definition line found [Arabidopsis thaliana]

Seq. No.	225536
Seq. ID	LIB3166-036-P1-K1-D5
Method	BLASTX
NCBI GI	g266946
BLAST score	226
E value	8.0e-19
Match length	57
% identity	81
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN) >gi_71143_pir__R5UBP0 acidic ribosomal protein P0 - red goosefoot >gi_18141_emb_CAA33276_ (X15206) 34kD light-induced protein [Chenopodium rubrum]

Seq. No.	225537
Seq. ID	LIB3166-036-P1-K1-D8
Method	BLASTX

NCBI GI	g3249088
BLAST score	196
E value	3.0e-15
Match length	67
% identity	48
NCBI Description	(AC004473) Contains similarity to goliath protein gb_M97204 from D. melanogster. [Arabidopsis thaliana]

Seq. No.	225538
Seq. ID	LIB3166-036-P1-K1-D9
Method	BLASTX
NCBI GI	g4336426
BLAST score	164
E value	3.0e-12
Match length	81
% identity	49
NCBI Description	(AF090835) Ca2+-dependent protein kinase [Mesembryanthemum crystallinum]

Seq. No.	225539
Seq. ID	LIB3166-036-P1-K1-E11
Method	BLASTX
NCBI GI	g416922
BLAST score	222
E value	3.0e-18
Match length	94
% identity	52
NCBI Description	DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (DUTPASE) (DUTP PYROPHOSPHATASE) (P18) >gi_282947_pir__JQ1599 dUTP pyrophosphatase (EC 3.6.1.23) - tomato >gi_251897_bbs_109276 (S40549) deoxyuridine triphosphatase, dUTPase, P18 {EC 3.6.1.23} [tomatoes, Tint Tim cultivar LA154, Peptide, 169 aa] [Lycopersicon esculentum]

Seq. No.	225540
Seq. ID	LIB3166-036-P1-K1-E12
Method	BLASTX
NCBI GI	g2853087
BLAST score	234
E value	5.0e-20
Match length	64
% identity	75
NCBI Description	(AL021768) putative protein [Arabidopsis thaliana]

Seq. No.	225541
Seq. ID	LIB3166-036-P1-K1-E2
Method	BLASTX
NCBI GI	g2688824
BLAST score	276
E value	1.0e-24
Match length	70
% identity	79
NCBI Description	(U93273) putative auxin-repressed protein [Prunus armeniaca]

Seq. No.	225542
Seq. ID	LIB3166-036-P1-K1-E3

Method	BLASTX
NCBI GI	g3860274
BLAST score	144
E value	3.0e-09
Match length	32
% identity	81
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana] >gi_4314397_gb_AAD15607_ (AC006232) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	225543
Seq. ID	LIB3166-036-P1-K1-E6
Method	BLASTX
NCBI GI	g3169182
BLAST score	178
E value	2.0e-13
Match length	69
% identity	42
NCBI Description	(AC004401) unknown protein [Arabidopsis thaliana]

Seq. No.	225544
Seq. ID	LIB3166-036-P1-K1-F1
Method	BLASTX
NCBI GI	g3142300
BLAST score	162
E value	1.0e-17
Match length	112
% identity	59
NCBI Description	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this gene. [Arabidopsis thaliana]

Seq. No.	225545
Seq. ID	LIB3166-036-P1-K1-F12
Method	BLASTX
NCBI GI	g1729860
BLAST score	255
E value	4.0e-22
Match length	80
% identity	66
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) (MG(2+)-DEPENDENT ATPASE 1) (LEMA-1) >gi_1362099_pir__S56672 probable 26S proteinase chain MA-1 - tomato >gi_732815_emb_CAA52445_ (X74426) Mg-dependent ATPase 1 [Lycopersicon esculentum]

Seq. No.	225546
Seq. ID	LIB3166-036-P1-K1-F2
Method	BLASTX
NCBI GI	g462195
BLAST score	351
E value	2.0e-33
Match length	77
% identity	88
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir__S21636 GOS2 protein - rice

	>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]
Seq. No.	225547
Seq. ID	LIB3166-036-P1-K1-F3
Method	BLASTX
NCBI GI	g3901012
BLAST score	248
E value	8.0e-27
Match length	102
% identity	68
NCBI Description	(AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]
Seq. No.	225548
Seq. ID	LIB3166-036-P1-K1-F8
Method	BLASTX
NCBI GI	g485518
BLAST score	247
E value	1.0e-26
Match length	80
% identity	78
NCBI Description	ubiquitin / ribosomal protein CEP52 - rice >gi_303857_dbj_BAA02154_ (D12629) ubiquitin/ribosomal polyprotein [Oryza sativa]
Seq. No.	225549
Seq. ID	LIB3166-036-P1-K1-F9
Method	BLASTX
NCBI GI	g3915021
BLAST score	379
E value	8.0e-37
Match length	92
% identity	78
NCBI Description	SUCROSE-PHOSPHATE SYNTHASE 1 (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1) >gi_2190348_emb_CAA72506_ (Y11821) sucrose-phosphate synthase [Craterostigma plantagineum]
Seq. No.	225550
Seq. ID	LIB3166-036-P1-K1-G1
Method	BLASTX
NCBI GI	g20729
BLAST score	169
E value	6.0e-12
Match length	55
% identity	64
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]
Seq. No.	225551
Seq. ID	LIB3166-036-P1-K1-G10
Method	BLASTX
NCBI GI	g4544431
BLAST score	141
E value	1.0e-08
Match length	41

% identity	68
NCBI Description	(AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225552
Seq. ID	LIB3166-036-P1-K1-G12
Method	BLASTX
NCBI GI	g119350
BLAST score	533
E value	1.0e-54
Match length	113
% identity	90
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana]

Seq. No.	225553
Seq. ID	LIB3166-036-P1-K1-G3
Method	BLASTX
NCBI GI	g2190548
BLAST score	307
E value	2.0e-28
Match length	72
% identity	78
NCBI Description	(AC001229) EST gb_ATTS1121 comes from this gene. [Arabidopsis thaliana]

Seq. No.	225554
Seq. ID	LIB3166-036-P1-K1-G6
Method	BLASTX
NCBI GI	g464981
BLAST score	292
E value	1.0e-26
Match length	70
% identity	80
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No.	225555
Seq. ID	LIB3166-036-P1-K1-H10
Method	BLASTX
NCBI GI	g2194142
BLAST score	414
E value	1.0e-40
Match length	122
% identity	74
NCBI Description	(AC002062) ESTs gb_N38288,gb_T43486,gb_AA395242 come from this gene. [Arabidopsis thaliana]

Seq. No.	225556
Seq. ID	LIB3166-036-P1-K1-H11
Method	BLASTX
NCBI GI	g2894599
BLAST score	455
E value	2.0e-45

Match length	95
% identity	81
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	225557
Seq. ID	LIB3166-036-P1-K1-H12
Method	BLASTX
NCBI GI	g4539460
BLAST score	227
E value	9.0e-19
Match length	122
% identity	5
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	225558
Seq. ID	LIB3166-036-P1-K1-H5
Method	BLASTX
NCBI GI	g543905
BLAST score	407
E value	7.0e-40
Match length	102
% identity	79
NCBI Description	BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162) brassinosteroid-regulated protein [Glycine max]

Seq. No.	225559
Seq. ID	LIB3166-036-P1-K1-H8
Method	BLASTX
NCBI GI	g3914666
BLAST score	175
E value	1.0e-12
Match length	61
% identity	57
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L4 PRECURSOR >gi_2791998_emb_CAA74895_ (Y14566) ribosomal protein L4 [Arabidopsis thaliana] >gi_2792000_emb_CAA74894_ (Y14565) ribosomal protein L4 [Arabidopsis thaliana]

Seq. No.	225560
Seq. ID	LIB3166-037-P1-K1-A11
Method	BLASTX
NCBI GI	g1170747
BLAST score	194
E value	5.0e-15
Match length	56
% identity	73
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345 (M88324) late embryogenesis-abundant protein [Gossypium hirsutum] >gi_167347 (M37697) Lea5-A late embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No.	225561
Seq. ID	LIB3166-037-P1-K1-A3
Method	BLASTX
NCBI GI	g4490732
BLAST score	341
E value	2.0e-32

Match length	73
% identity	88
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	225562
Seq. ID	LIB3166-037-P1-K1-A4
Method	BLASTX
NCBI GI	g464986
BLAST score	286
E value	6.0e-26
Match length	69
% identity	81
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No.	225563
Seq. ID	LIB3166-037-P1-K1-A5
Method	BLASTX
NCBI GI	g2072356
BLAST score	245
E value	7.0e-21
Match length	62
% identity	74
NCBI Description	(U96713) aminoalcoholphosphotransferase [Brassica rapa]

Seq. No.	225564
Seq. ID	LIB3166-037-P1-K1-A8
Method	BLASTX
NCBI GI	g3128168
BLAST score	361
E value	1.0e-34
Match length	87
% identity	71
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No.	225565
Seq. ID	LIB3166-037-P1-K1-B1
Method	BLASTX
NCBI GI	g1174749
BLAST score	547
E value	3.0e-56
Match length	127
% identity	85
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_1362177_pir__S53760 triose-phosphate isomerase (EC 5.3.1.1), cytosolic - rye >gi_407525_emb_CAA81487_ (Z26875)

	triosephosphate isomerase [Secale cereale] >gi_1095493_prf__2109226A triosephosphate isomerase [Secale cereale]
Seq. No.	225566
Seq. ID	LIB3166-037-P1-K1-B11
Method	BLASTX
NCBI GI	g3355465
BLAST score	432
E value	7.0e-43
Match length	120
% identity	68
NCBI Description	(AC004218) putative Ser/Thr protein kinase [Arabidopsis thaliana]
Seq. No.	225567
Seq. ID	LIB3166-037-P1-K1-B2
Method	BLASTX
NCBI GI	g3763930
BLAST score	341
E value	4.0e-32
Match length	98
% identity	63
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana]
Seq. No.	225568
Seq. ID	LIB3166-037-P1-K1-B7
Method	BLASTX
NCBI GI	g3482977
BLAST score	277
E value	1.0e-24
Match length	86
% identity	62
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]
Seq. No.	225569
Seq. ID	LIB3166-037-P1-K1-B8
Method	BLASTX
NCBI GI	g2497543
BLAST score	512
E value	3.0e-52
Match length	115
% identity	85
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_542061_pir__S41379 pyruvate kinase - common tobacco >gi_444023_emb_CAA82628_ (Z29492) pyruvate kinase [Nicotiana tabacum]
Seq. No.	225570
Seq. ID	LIB3166-037-P1-K1-C10
Method	BLASTX
NCBI GI	g4538963
BLAST score	462
E value	1.0e-50
Match length	110
% identity	71
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana]

Seq. No.	225571
Seq. ID	LIB3166-037-P1-K1-C11
Method	BLASTX
NCBI GI	g19184
BLAST score	137
E value	1.0e-08
Match length	64
% identity	50
NCBI Description	(X61287) Type I (26 kD) CP29 polypeptide [Lycopersicon esculentum]

Seq. No.	225572
Seq. ID	LIB3166-037-P1-K1-C12
Method	BLASTX
NCBI GI	g1174867
BLAST score	331
E value	6.0e-31
Match length	72
% identity	86
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2 KD PROTEIN) >gi_633687_emb_CAA55862_ (X79275) ubiquinol--cytochrome c reductase [Solanum tuberosum] >gi_1094912_prf__2107179A cytochrome c oxidase:SUBUNIT=8.2kD [Solanum tuberosum]

Seq. No.	225573
Seq. ID	LIB3166-037-P1-K1-C2
Method	BLASTX
NCBI GI	g2833375
BLAST score	350
E value	3.0e-33
Match length	71
% identity	90
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 8.2 KD POLYPEPTIDE (RPB10) (RP10) (ABC10) >gi_533690 (U12133) RNA polymerase II subunit RPB10 homolog; similar to yeast RNA polymerase II subunit RPB10, Swiss-Prot Accession Number P22139 [Brassica napus]

Seq. No.	225574
Seq. ID	LIB3166-037-P1-K1-C4
Method	BLASTX
NCBI GI	g441457
BLAST score	551
E value	1.0e-56
Match length	104
% identity	98
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]

Seq. No.	225575
Seq. ID	LIB3166-037-P1-K1-C5
Method	BLASTX
NCBI GI	g2088651
BLAST score	305

E value	7.0e-28
Match length	110
% identity	50
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	225576
Seq. ID	LIB3166-037-P1-K1-C6
Method	BLASTX
NCBI GI	g3123745
BLAST score	525
E value	1.0e-53
Match length	123
% identity	80
NCBI Description	(AB013447) aluminum-induced [Brassica napus]

Seq. No.	225577
Seq. ID	LIB3166-037-P1-K1-C7
Method	BLASTX
NCBI GI	g1076515
BLAST score	212
E value	5.0e-17
Match length	112
% identity	42
NCBI Description	pectinesterase precursor - kidney bean >gi_732913_emb_CAA59482_ (X85216) pectinesterase [Phaseolus vulgaris]

Seq. No.	225578
Seq. ID	LIB3166-037-P1-K1-C8
Method	BLASTX
NCBI GI	g421826
BLAST score	138
E value	1.0e-08
Match length	29
% identity	90
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	225579
Seq. ID	LIB3166-037-P1-K1-C9
Method	BLASTX
NCBI GI	g122007
BLAST score	282
E value	3.0e-25
Match length	81
% identity	70
NCBI Description	HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley >gi_20448_emb_CAA37828_ (X53831) H2A histone protein (AA 1 - 149) [Petroselinum crispum]

Seq. No.	225580
Seq. ID	LIB3166-037-P1-K1-D1
Method	BLASTX
NCBI GI	g2511693
BLAST score	334

E value	3.0e-31
Match length	88
% identity	72
NCBI Description	(Z99954) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No.	225581
Seq. ID	LIB3166-037-P1-K1-D10
Method	BLASTX
NCBI GI	g3164222
BLAST score	180
E value	3.0e-13
Match length	44
% identity	64
NCBI Description	(AB008518) RMA1 [Arabidopsis thaliana] >gi_4206205 (AF071527) RMA1 RING zinc finger protein [Arabidopsis thaliana]

Seq. No.	225582
Seq. ID	LIB3166-037-P1-K1-D11
Method	BLASTX
NCBI GI	g2194142
BLAST score	219
E value	8.0e-18
Match length	67
% identity	58
NCBI Description	(AC002062) ESTs gb_N38288,gb_T43486,gb_AA395242 come from this gene. [Arabidopsis thaliana]

Seq. No.	225583
Seq. ID	LIB3166-037-P1-K1-D12
Method	BLASTX
NCBI GI	g4097915
BLAST score	164
E value	2.0e-11
Match length	116
% identity	34
NCBI Description	(U72147) unknown [Anabaena sp. CA]

Seq. No.	225584
Seq. ID	LIB3166-037-P1-K1-D2
Method	BLASTX
NCBI GI	g2262170
BLAST score	194
E value	7.0e-15
Match length	125
% identity	40
NCBI Description	(AC002329) predicted glycosyl hydrolase [Arabidopsis thaliana]

Seq. No.	225585
Seq. ID	LIB3166-037-P1-K1-D3
Method	BLASTX
NCBI GI	g1402877
BLAST score	165
E value	1.0e-11
Match length	75
% identity	57

NCBI Description	(X98130) unknown [Arabidopsis thaliana] >gi_1495257_emb_CAA66117_ (X97485) orf03 [Arabidopsis thaliana]
Seq. No.	225586
Seq. ID	LIB3166-037-P1-K1-D6
Method	BLASTX
NCBI GI	g4193382
BLAST score	382
E value	5.0e-37
Match length	86
% identity	81
NCBI Description	(AF083336) ribosomal protein S27 [Arabidopsis thaliana] >gi_4193384 (AF083337) ribosomal protein S27 [Arabidopsis thaliana]
Seq. No.	225587
Seq. ID	LIB3166-037-P1-K1-D7
Method	BLASTX
NCBI GI	g289920
BLAST score	348
E value	3.0e-33
Match length	95
% identity	78
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]
Seq. No.	225588
Seq. ID	LIB3166-037-P1-K1-D8
Method	BLASTX
NCBI GI	g4415908
BLAST score	164
E value	2.0e-11
Match length	71
% identity	49
NCBI Description	(AC006282) unknown protein [Arabidopsis thaliana]
Seq. No.	225589
Seq. ID	LIB3166-037-P1-K1-D9
Method	BLASTX
NCBI GI	g3924609
BLAST score	310
E value	2.0e-28
Match length	118
% identity	56
NCBI Description	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
Seq. No.	225590
Seq. ID	LIB3166-037-P1-K1-E1
Method	BLASTX
NCBI GI	g2506139
BLAST score	395
E value	2.0e-38
Match length	99
% identity	77
NCBI Description	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)

(ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962)
archain/delta-COP [Oryza sativa]

Seq. No.	225591
Seq. ID	LIB3166-037-P1-K1-E12
Method	BLASTX
NCBI GI	g3158376
BLAST score	442
E value	6.0e-44
Match length	120
% identity	75
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	225592
Seq. ID	LIB3166-037-P1-K1-E5
Method	BLASTX
NCBI GI	g2961385
BLAST score	215
E value	2.0e-17
Match length	72
% identity	62
NCBI Description	(AL022141) putative protein [Arabidopsis thaliana]

Seq. No.	225593
Seq. ID	LIB3166-037-P1-K1-E6
Method	BLASTX
NCBI GI	g4490736
BLAST score	584
E value	1.0e-60
Match length	125
% identity	50
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	225594
Seq. ID	LIB3166-037-P1-K1-E7
Method	BLASTX
NCBI GI	g167367
BLAST score	237
E value	3.0e-20
Match length	49
% identity	90
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	225595
Seq. ID	LIB3166-037-P1-K1-E9
Method	BLASTX
NCBI GI	g726334
BLAST score	602
E value	1.0e-62
Match length	127
% identity	90
NCBI Description	(U22533) NADP-malate dehydrogenase [Flaveria trinervia]

Seq. No.	225596
Seq. ID	LIB3166-037-P1-K1-F1
Method	BLASTX
NCBI GI	g1172571

BLAST score	616
E value	2.0e-64
Match length	126
% identity	91
NCBI Description	PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP) >gi_1076277_pir__S52637 phosphoenolpyruvate carboxykinase (ATP) (EC 4.1.1.49) - cucumber >gi_567102 (L31899) phosphoenolpyruvate carboxykinase [Cucumis sativus]

Seq. No.	225597
Seq. ID	LIB3166-037-P1-K1-F10
Method	BLASTX
NCBI GI	g3688191
BLAST score	204
E value	5.0e-16
Match length	91
% identity	51
NCBI Description	(AJ010090) MAP3K alpha protein kinase [Arabidopsis thaliana]

Seq. No.	225598
Seq. ID	LIB3166-037-P1-K1-G1
Method	BLASTX
NCBI GI	g170131
BLAST score	253
E value	8.0e-22
Match length	68
% identity	74
NCBI Description	(M55322) ribosomal protein 30S subunit [Spinacia oleracea]

Seq. No.	225599
Seq. ID	LIB3166-037-P1-K1-G3
Method	BLASTX
NCBI GI	g4218535
BLAST score	449
E value	9.0e-45
Match length	117
% identity	67
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]

Seq. No.	225600
Seq. ID	LIB3166-037-P1-K1-G7
Method	BLASTX
NCBI GI	g2739387
BLAST score	152
E value	6.0e-10
Match length	57
% identity	47
NCBI Description	(AC002505) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225601
Seq. ID	LIB3166-038-P1-K1-A1
Method	BLASTX
NCBI GI	g1906830
BLAST score	263
E value	5.0e-23
Match length	110

% identity	47
NCBI Description	(Y11829) heat shock protein [Arabidopsis thaliana]
Seq. No.	225602
Seq. ID	LIB3166-038-P1-K1-A11
Method	BLASTX
NCBI GI	g2494111
BLAST score	403
E value	2.0e-39
Match length	97
% identity	77
NCBI Description	(AC002376) Contains similarity to Glycine protein kinase 6 (gb_M67449). [Arabidopsis thaliana]
Seq. No.	225603
Seq. ID	LIB3166-038-P1-K1-A2
Method	BLASTX
NCBI GI	g730463
BLAST score	294
E value	1.0e-26
Match length	100
% identity	57
NCBI Description	60S RIBOSOMAL PROTEIN L37B (YL37) (RP47) >gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast (Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal protein L37 [Saccharomyces cerevisiae] >gi_1420537_emb_CAA99454_ (Z75142) ORF YOR234c [Saccharomyces cerevisiae]
Seq. No.	225604
Seq. ID	LIB3166-038-P1-K1-A5
Method	BLASTX
NCBI GI	g4557078
BLAST score	244
E value	9.0e-21
Match length	123
% identity	41
NCBI Description	(AC007045) putative Ta11-1 pol polyprotein, 5' partial [Arabidopsis thaliana]
Seq. No.	225605
Seq. ID	LIB3166-038-P1-K1-A8
Method	BLASTX
NCBI GI	g537313
BLAST score	363
E value	1.0e-34
Match length	96
% identity	75
NCBI Description	(L36159) unknown protein [Medicago sativa]
Seq. No.	225606
Seq. ID	LIB3166-038-P1-K1-B10
Method	BLASTX
NCBI GI	g3881976
BLAST score	368
E value	3.0e-35
Match length	109

% identity	63
NCBI Description	(AJ012409) hypothetical protein [Homo sapiens]
Seq. No.	225607
Seq. ID	LIB3166-038-P1-K1-B2
Method	BLASTX
NCBI GI	g4406816
BLAST score	562
E value	5.0e-58
Match length	113
% identity	93
NCBI Description	(AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]
Seq. No.	225608
Seq. ID	LIB3166-038-P1-K1-B3
Method	BLASTX
NCBI GI	g2982320
BLAST score	229
E value	5.0e-19
Match length	98
% identity	47
NCBI Description	(AF051245) hypothetical protein [Picea mariana]
Seq. No.	225609
Seq. ID	LIB3166-038-P1-K1-B4
Method	BLASTX
NCBI GI	g100490
BLAST score	589
E value	3.0e-61
Match length	120
% identity	28
NCBI Description	polyubiquitin - garden snapdragon (fragment) >gi_16071_emb_CAA48140_ (X67957) ubiquitin [Antirrhinum majus]
Seq. No.	225610
Seq. ID	LIB3166-038-P1-K1-B8
Method	BLASTX
NCBI GI	g464986
BLAST score	423
E value	9.0e-42
Match length	79
% identity	97
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]
Seq. No.	225611
Seq. ID	LIB3166-038-P1-K1-B9

Method	BLASTX
NCBI GI	g2347199
BLAST score	514
E value	2.0e-52
Match length	120
% identity	75
NCBI Description	(AC002338) protein kinase isolog [Arabidopsis thaliana]

Seq. No.	225612
Seq. ID	LIB3166-038-P1-K1-C2
Method	BLASTX
NCBI GI	g2980768
BLAST score	298
E value	4.0e-27
Match length	93
% identity	72
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	225613
Seq. ID	LIB3166-038-P1-K1-C5
Method	BLASTX
NCBI GI	g2459424
BLAST score	395
E value	2.0e-38
Match length	108
% identity	71
NCBI Description	(AC002332) unknown protein [Arabidopsis thaliana]

Seq. No.	225614
Seq. ID	LIB3166-038-P1-K1-C6
Method	BLASTX
NCBI GI	g3885515
BLAST score	199
E value	2.0e-15
Match length	54
% identity	69
NCBI Description	(AF084202) similar to ribosomal protein S26 [Medicago sativa]

Seq. No.	225615
Seq. ID	LIB3166-038-P1-K1-C9
Method	BLASTX
NCBI GI	g3024020
BLAST score	418
E value	3.0e-41
Match length	89
% identity	89
NCBI Description	INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D) >gi_2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation factor 5A3 [Solanum tuberosum]

Seq. No.	225616
Seq. ID	LIB3166-038-P1-K1-D1
Method	BLASTX
NCBI GI	g3264767
BLAST score	372
E value	9.0e-36

Match length	74
% identity	92
NCBI Description	(AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No.	225617
Seq. ID	LIB3166-038-P1-K1-D2
Method	BLASTX
NCBI GI	g3892054
BLAST score	514
E value	2.0e-52
Match length	123
% identity	71
NCBI Description	(AC002330) putative glycosyltransferase [Arabidopsis thaliana]

Seq. No.	225618
Seq. ID	LIB3166-038-P1-K1-D4
Method	BLASTX
NCBI GI	g1173256
BLAST score	540
E value	2.0e-55
Match length	104
% identity	99
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal protein S4 - upland cotton >gi_488739_emb_CAA55882_ (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]

Seq. No.	225619
Seq. ID	LIB3166-038-P1-K1-D5
Method	BLASTX
NCBI GI	g927025
BLAST score	271
E value	6.0e-24
Match length	127
% identity	44
NCBI Description	(L44134) SPF1-like DNA-binding protein [Cucumis sativus]

Seq. No.	225620
Seq. ID	LIB3166-038-P1-K1-D6
Method	BLASTX
NCBI GI	g115765
BLAST score	387
E value	2.0e-37
Match length	103
% identity	71
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	225621
Seq. ID	LIB3166-038-P1-K1-D7

Method	BLASTX
NCBI GI	g3123295
BLAST score	194
E value	7.0e-15
Match length	114
% identity	38
NCBI Description	CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi_2583169 (AF026473) calmodulin-related protein [Arabidopsis thaliana]

Seq. No.	225622
Seq. ID	LIB3166-038-P1-K1-D9
Method	BLASTX
NCBI GI	g2791834
BLAST score	488
E value	2.0e-49
Match length	111
% identity	86
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No.	225623
Seq. ID	LIB3166-038-P1-K1-E1
Method	BLASTX
NCBI GI	g2245108
BLAST score	156
E value	2.0e-10
Match length	46
% identity	63
NCBI Description	(Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No.	225624
Seq. ID	LIB3166-038-P1-K1-E10
Method	BLASTX
NCBI GI	g3608485
BLAST score	504
E value	3.0e-51
Match length	103
% identity	92
NCBI Description	(AF088915) proteasome beta subunit [Petunia x hybrida]

Seq. No.	225625
Seq. ID	LIB3166-038-P1-K1-E11
Method	BLASTX
NCBI GI	g3928086
BLAST score	198
E value	2.0e-15
Match length	60
% identity	65
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	225626
Seq. ID	LIB3166-038-P1-K1-E12
Method	BLASTX
NCBI GI	g2388963
BLAST score	146
E value	3.0e-09
Match length	45

% identity	49
NCBI Description	(Z98979) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	225627
Seq. ID	LIB3166-038-P1-K1-E2
Method	BLASTX
NCBI GI	g3869088
BLAST score	566
E value	2.0e-58
Match length	108
% identity	100
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No.	225628
Seq. ID	LIB3166-038-P1-K1-E3
Method	BLASTX
NCBI GI	g3860249
BLAST score	359
E value	3.0e-34
Match length	124
% identity	64
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	225629
Seq. ID	LIB3166-038-P1-K1-E5
Method	BLASTX
NCBI GI	g4056568
BLAST score	184
E value	7.0e-20
Match length	80
% identity	61
NCBI Description	(U90944) PDI-like protein [Zea mays]

Seq. No.	225630
Seq. ID	LIB3166-038-P1-K1-F11
Method	BLASTX
NCBI GI	g4263519
BLAST score	107
E value	3.0e-10
Match length	73
% identity	64
NCBI Description	(AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis thaliana]

Seq. No.	225631
Seq. ID	LIB3166-038-P1-K1-F12
Method	BLASTX
NCBI GI	g3024126
BLAST score	487
E value	3.0e-49
Match length	96
% identity	96
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine synthetase 1 [Catharanthus roseus]

Seq. No.	225632
Seq. ID	LIB3166-038-P1-K1-F6
Method	BLASTX
NCBI GI	g1345698
BLAST score	640
E value	3.0e-67
Match length	126
% identity	96
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR (CAB-151) (LHCP) >gi_99601_pir__S20917 chlorophyll a/b-binding protein - upland cotton >gi_452314_emb_CAA38025_ (X54090) chlorophyll ab binding protein [Gossypium hirsutum]

Seq. No.	225633
Seq. ID	LIB3166-038-P1-K1-F7
Method	BLASTX
NCBI GI	g465921
BLAST score	268
E value	1.0e-23
Match length	82
% identity	65
NCBI Description	PROBABLE VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT) >gi_482192_pir__S40985 hypothetical protein F55H2.2 - Caenorhabditis elegans >gi_3877608_emb_CAA81600_ (Z27080) similar to membrane-associated atpase gamma chain; cDNA EST CEMSA49R comes from this gene; cDNA EST yk466a12.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	225634
Seq. ID	LIB3166-038-P1-K1-F9
Method	BLASTX
NCBI GI	g4006873
BLAST score	366
E value	4.0e-35
Match length	116
% identity	60
NCBI Description	(Z99707) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225635
Seq. ID	LIB3166-038-P1-K1-G12
Method	BLASTX
NCBI GI	g3236259
BLAST score	248
E value	3.0e-30
Match length	94
% identity	76
NCBI Description	(AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	225636
Seq. ID	LIB3166-038-P1-K1-G3
Method	BLASTX
NCBI GI	g3287695
BLAST score	424
E value	8.0e-42
Match length	127

% identity	66
NCBI Description	(AC003979) Similar to hypothetical protein C34B7.2 gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis thaliana]

Seq. No.	225637
Seq. ID	LIB3166-038-P1-K1-G5
Method	BLASTX
NCBI GI	g4455246
BLAST score	204
E value	4.0e-16
Match length	50
% identity	74
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	225638
Seq. ID	LIB3166-038-P1-K1-G6
Method	BLASTX
NCBI GI	g4102861
BLAST score	475
E value	7.0e-48
Match length	95
% identity	91
NCBI Description	(AF016893) copper/zinc-superoxide dismutase [Populus tremuloides]

Seq. No.	225639
Seq. ID	LIB3166-038-P1-K1-H11
Method	BLASTX
NCBI GI	g1332579
BLAST score	574
E value	2.0e-59
Match length	124
% identity	9
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	225640
Seq. ID	LIB3166-038-P1-K1-H12
Method	BLASTX
NCBI GI	g3860263
BLAST score	220
E value	6.0e-24
Match length	114
% identity	58
NCBI Description	(AC005824) putative cytochrome p450 protein [Arabidopsis thaliana]

Seq. No.	225641
Seq. ID	LIB3166-038-P1-K1-H2
Method	BLASTX
NCBI GI	g1370589
BLAST score	223
E value	3.0e-18
Match length	98
% identity	53
NCBI Description	(X98304) protein induced upon tuberization [Solanum demissum]

Seq. No.	225642
Seq. ID	LIB3166-038-P1-K1-H3
Method	BLASTX
NCBI GI	g2582381
BLAST score	628
E value	1.0e-65
Match length	120
% identity	91
NCBI Description	(AF021220) cation-chloride co-transporter [Nicotiana tabacum]

Seq. No.	225643
Seq. ID	LIB3166-038-P1-K1-H4
Method	BLASTX
NCBI GI	g3641868
BLAST score	127
E value	1.0e-13
Match length	74
% identity	61
NCBI Description	(AJ011012) hypothetical protein [Cicer arietinum]

Seq. No.	225644
Seq. ID	LIB3166-038-P1-K1-H6
Method	BLASTX
NCBI GI	g2275196
BLAST score	554
E value	3.0e-57
Match length	110
% identity	88
NCBI Description	(AC002337) water stress-induced protein, WSI76 isolog [Arabidopsis thaliana]

Seq. No.	225645
Seq. ID	LIB3166-038-P1-K1-H8
Method	BLASTX
NCBI GI	g119194
BLAST score	160
E value	5.0e-15
Match length	61
% identity	72
NCBI Description	ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >gi_81607_pir__S09152 translation elongation factor Tu precursor, chloroplast - Arabidopsis thaliana >gi_22565_emb_CAA36498_ (X52256) elongation factor Tu precursor [Arabidopsis thaliana] >gi_226817_prf__1607332A elongation factor Tu [Arabidopsis thaliana]

Seq. No.	225646
Seq. ID	LIB3166-039-P1-K1-A1
Method	BLASTX
NCBI GI	g3033389
BLAST score	248
E value	3.0e-21
Match length	116
% identity	4
NCBI Description	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]

Seq. No.	225647
Seq. ID	LIB3166-039-P1-K1-A10
Method	BLASTX
NCBI GI	g2618698
BLAST score	140
E value	1.0e-08
Match length	34
% identity	79
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	225648
Seq. ID	LIB3166-039-P1-K1-A11
Method	BLASTX
NCBI GI	g3122071
BLAST score	479
E value	2.0e-48
Match length	97
% identity	95
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_2130148_pir__S66339 translation elongation factor eEF-1 alpha chain - maize >gi_1321656_dbj_BAA08249_ (D45408) alpha subunit of tlanslation elongation factor 1 [Zea mays]

Seq. No.	225649
Seq. ID	LIB3166-039-P1-K1-A12
Method	BLASTX
NCBI GI	g1888557
BLAST score	596
E value	5.0e-62
Match length	126
% identity	83
NCBI Description	(U89841) diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase [Lupinus angustifolius]

Seq. No.	225650
Seq. ID	LIB3166-039-P1-K1-A6
Method	BLASTX
NCBI GI	g1771381
BLAST score	324
E value	4.0e-30
Match length	102
% identity	58
NCBI Description	(X95877) phosphoinositide-specific phospholipase C [Nicotiana rustica]

Seq. No.	225651
Seq. ID	LIB3166-039-P1-K1-A7
Method	BLASTX
NCBI GI	g133872
BLAST score	420
E value	2.0e-41
Match length	114
% identity	77
NCBI Description	30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1) >gi_282838_pir__S26494 ribosomal protein S1, chloroplast - spinach >gi_322404_pir__A44121 small subunit ribosomal

protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_ (X66135) ribosomal protein S1 [Spinacia oleracea] >gi_170143 (M82923) chloroplast ribosomal protein S1 [Spinacia oleracea]

Seq. No.	225652
Seq. ID	LIB3166-039-P1-K1-A9
Method	BLASTX
NCBI GI	g2895510
BLAST score	203
E value	3.0e-16
Match length	81
% identity	48
NCBI Description	(AF033204) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	225653
Seq. ID	LIB3166-039-P1-K1-B1
Method	BLASTX
NCBI GI	g3309620
BLAST score	169
E value	6.0e-12
Match length	125
% identity	40
NCBI Description	(AF074916) resistance to Pseudomonas syringae protein 5 [Arabidopsis thaliana]

Seq. No.	225654
Seq. ID	LIB3166-039-P1-K1-B11
Method	BLASTX
NCBI GI	g4127688
BLAST score	298
E value	4.0e-27
Match length	84
% identity	68
NCBI Description	(AJ006065) isochorismate synthase [Catharanthus roseus]

Seq. No.	225655
Seq. ID	LIB3166-039-P1-K1-B2
Method	BLASTX
NCBI GI	g1621268
BLAST score	370
E value	2.0e-35
Match length	112
% identity	69
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	225656
Seq. ID	LIB3166-039-P1-K1-B3
Method	BLASTX
NCBI GI	g2244847
BLAST score	301
E value	1.0e-27
Match length	97
% identity	65
NCBI Description	(Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No.	225657
Seq. ID	LIB3166-039-P1-K1-B6
Method	BLASTX
NCBI GI	g2833386
BLAST score	452
E value	4.0e-45
Match length	111
% identity	84
NCBI Description	RIBULOSE-PHOSPHATE 3-EPIMERASE PRECURSOR (PENTOSE-5-PHOSPHATE 3-EPIMERASE) (PPE) (RPE) (R5P3E) >gi_2129493_pir__S62724 ribulose-phosphate 3-epimerase (EC 5.1.3.1) precursor - spinach >gi_1162980 (L42328) ribulose-5-phosphate 3-epimerase [Spinacia oleracea] >gi_3264788 (AF070941) ribulose-phosphate 3-epimerase [Spinacia oleracea] >gi_1587969_prf__2207382A D-ribulose-5-phosphate 3-epimerase [Sorghum bicolor]

Seq. No.	225658
Seq. ID	LIB3166-039-P1-K1-B7
Method	BLASTX
NCBI GI	g464987
BLAST score	554
E value	4.0e-57
Match length	107
% identity	95
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10) >gi_421858_pir__S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana >gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	225659
Seq. ID	LIB3166-039-P1-K1-B9
Method	BLASTX
NCBI GI	g417103
BLAST score	464
E value	1.0e-46
Match length	93
% identity	100
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa]

>gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	225660
Seq. ID	LIB3166-039-P1-K1-C11
Method	BLASTX
NCBI GI	g1237250
BLAST score	461
E value	3.0e-46
Match length	109
% identity	80
NCBI Description	(X96784) cytochrome P450 [Nicotiana tabacum]

Seq. No.	225661
Seq. ID	LIB3166-039-P1-K1-C12
Method	BLASTX
NCBI GI	g3687246
BLAST score	176
E value	8.0e-13
Match length	88
% identity	38
NCBI Description	(AC005169) putative suppressor protein [Arabidopsis thaliana]

Seq. No.	225662
Seq. ID	LIB3166-039-P1-K1-C3
Method	BLASTX
NCBI GI	g2827139
BLAST score	612
E value	6.0e-64
Match length	127
% identity	88
NCBI Description	(AF027172) cellulose synthase catalytic subunit [Arabidopsis thaliana] >gi_4049343_emb_CAA22568_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis thaliana]

Seq. No.	225663
Seq. ID	LIB3166-039-P1-K1-C6
Method	BLASTX
NCBI GI	g4056487
BLAST score	397
E value	1.0e-38
Match length	105
% identity	72
NCBI Description	(AC005896) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225664
Seq. ID	LIB3166-039-P1-K1-C8
Method	BLASTX
NCBI GI	g2088647
BLAST score	150
E value	9.0e-10
Match length	71
% identity	66

NCBI Description	(AF002109) hypothetical protein [Arabidopsis thaliana] >gi_3158394 (AF036340) LRR-containing F-box protein [Arabidopsis thaliana]
Seq. No.	225665
Seq. ID	LIB3166-039-P1-K1-C9
Method	BLASTX
NCBI GI	g1495804
BLAST score	420
E value	2.0e-41
Match length	112
% identity	73
NCBI Description	(X96406) 13-lipoxygenase [Solanum tuberosum]
Seq. No.	225666
Seq. ID	LIB3166-039-P1-K1-D10
Method	BLASTX
NCBI GI	g422418
BLAST score	206
E value	3.0e-16
Match length	98
% identity	42
NCBI Description	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) >gi_394705_emb_CAA80824_ (Z24451) pol protein [Drosophila ananassae]
Seq. No.	225667
Seq. ID	LIB3166-039-P1-K1-D11
Method	BLASTX
NCBI GI	g4490715
BLAST score	187
E value	4.0e-14
Match length	122
% identity	35
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]
Seq. No.	225668
Seq. ID	LIB3166-039-P1-K1-D4
Method	BLASTX
NCBI GI	g421843
BLAST score	458
E value	8.0e-46
Match length	126
% identity	70
NCBI Description	protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana >gi_217861_dbj_BAA01715_ (D10909) serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.	225669
Seq. ID	LIB3166-039-P1-K1-D5
Method	BLASTX
NCBI GI	g1161575
BLAST score	390
E value	7.0e-38
Match length	113
% identity	69
NCBI Description	(X94947) homeobox [Lycopersicon esculentum]

Seq. No.	225670
Seq. ID	LIB3166-039-P1-K1-D8
Method	BLASTX
NCBI GI	g1781348
BLAST score	473
E value	1.0e-47
Match length	101
% identity	90
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No.	225671
Seq. ID	LIB3166-039-P1-K1-D9
Method	BLASTX
NCBI GI	g2983447
BLAST score	245
E value	7.0e-21
Match length	123
% identity	41
NCBI Description	(AE000714) large subunit of isopropylmalate isomerase [Aquifex aeolicus]

Seq. No.	225672
Seq. ID	LIB3166-039-P1-K1-E10
Method	BLASTX
NCBI GI	g2815246
BLAST score	225
E value	2.0e-18
Match length	55
% identity	73
NCBI Description	(X95709) class I type 2 metallothionein [Cicer arietinum]

Seq. No.	225673
Seq. ID	LIB3166-039-P1-K1-E11
Method	BLASTX
NCBI GI	g3913047
BLAST score	494
E value	4.0e-50
Match length	105
% identity	91
NCBI Description	FLORAL HOMEOTIC PROTEIN APETALA1 (MADS C) >gi_1076477_pir__S52236 Saap1 protein - white mustard >gi_609253_emb_CAA57233_ (X81480) Saap1 [Sinapis alba]

Seq. No.	225674
Seq. ID	LIB3166-039-P1-K1-E12
Method	BLASTX
NCBI GI	g1781299
BLAST score	251
E value	1.0e-21
Match length	114
% identity	46
NCBI Description	(Y09506) transformer-SR ribonucleoprotein [Nicotiana tabacum]

Seq. No.	225675

Seq. ID LIB3166-039-P1-K1-E2
Method BLASTX
NCBI GI g1944216
BLAST score 526
E value 8.0e-54
Match length 117
% identity 84
NCBI Description (D84246) alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No. 225676
Seq. ID LIB3166-039-P1-K1-E3
Method BLASTX
NCBI GI g1771160
BLAST score 475
E value 7.0e-48
Match length 121
% identity 75
NCBI Description (X98929) SBT1 [Lycopersicon esculentum] >gi_3687305_emb_CAA06999_ (AJ006378) subtilisin-like protease [Lycopersicon esculentum]

Seq. No. 225677
Seq. ID LIB3166-039-P1-K1-E4
Method BLASTX
NCBI GI g2213592
BLAST score 226
E value 1.0e-18
Match length 123
% identity 51
NCBI Description (AC000348) T7N9.12 [Arabidopsis thaliana]

Seq. No. 225678
Seq. ID LIB3166-039-P1-K1-E6
Method BLASTX
NCBI GI g2213600
BLAST score 465
E value 1.0e-46
Match length 127
% identity 70
NCBI Description (AC000348) T7N9.20 [Arabidopsis thaliana]

Seq. No. 225679
Seq. ID LIB3166-039-P1-K1-E9
Method BLASTX
NCBI GI g4309698
BLAST score 466
E value 1.0e-48
Match length 113
% identity 87
NCBI Description (AC006266) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No. 225680
Seq. ID LIB3166-039-P1-K1-F10
Method BLASTX
NCBI GI g1483150
BLAST score 564

E value	3.0e-58
Match length	120
% identity	85
NCBI Description	(D84417) monodehydroascorbate reductase [Arabidopsis thaliana]

Seq. No.	225681
Seq. ID	LIB3166-039-P1-K1-F12
Method	BLASTX
NCBI GI	g289920
BLAST score	641
E value	3.0e-67
Match length	122
% identity	98
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No.	225682
Seq. ID	LIB3166-039-P1-K1-F2
Method	BLASTX
NCBI GI	g4455210
BLAST score	214
E value	3.0e-17
Match length	97
% identity	58
NCBI Description	(AL035440) putative aspartate-tRNA ligase [Arabidopsis thaliana]

Seq. No.	225683
Seq. ID	LIB3166-039-P1-K1-F3
Method	BLASTX
NCBI GI	g2833388
BLAST score	528
E value	4.0e-54
Match length	126
% identity	79
NCBI Description	GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi_629660_pir__S43341 ADPglucose--starch glucosyltransferase (EC 2.4.1.21) precursor - cassava >gi_437042_emb_CAA52273_ (X74160) starch (bacterial glycogen) synthase [Manihot esculenta]

Seq. No.	225684
Seq. ID	LIB3166-039-P1-K1-F4
Method	BLASTX
NCBI GI	g2388689
BLAST score	458
E value	7.0e-46
Match length	128
% identity	70
NCBI Description	(AF016633) GH1 protein [Glycine max]

Seq. No.	225685
Seq. ID	LIB3166-039-P1-K1-F7
Method	BLASTX
NCBI GI	g3702321
BLAST score	530

E value	3.0e-54
Match length	125
% identity	45
NCBI Description	(AC005397) putative TGF-beta receptor interacting protein [Arabidopsis thaliana]

Seq. No.	225686
Seq. ID	LIB3166-039-P1-K1-G1
Method	BLASTX
NCBI GI	g4455201
BLAST score	456
E value	1.0e-45
Match length	113
% identity	78
NCBI Description	(AL035440) grpE like protein [Arabidopsis thaliana]

Seq. No.	225687
Seq. ID	LIB3166-039-P1-K1-G10
Method	BLASTX
NCBI GI	g1373125
BLAST score	297
E value	6.0e-27
Match length	106
% identity	60
NCBI Description	(U43709) similar to the metB gene product of Escherichia coli; cloned by functional complementation of a metB mutant strain of Escherichia coli LE392 [Arabidopsis thaliana]

Seq. No.	225688
Seq. ID	LIB3166-039-P1-K1-G11
Method	BLASTX
NCBI GI	g2500047
BLAST score	639
E value	4.0e-67
Match length	127
% identity	91
NCBI Description	SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi_534916_emb_CAA85362_ (Z36894) soluble inorganic pyrophosphatase [Solanum tuberosum]

Seq. No.	225689
Seq. ID	LIB3166-039-P1-K1-G2
Method	BLASTX
NCBI GI	g4572679
BLAST score	335
E value	2.0e-31
Match length	74
% identity	84
NCBI Description	(AC006954) RSZp22 splicing factor; contains RNA recognition motif [Arabidopsis thaliana]

Seq. No.	225690
Seq. ID	LIB3166-039-P1-K1-G4
Method	BLASTX
NCBI GI	g3123295
BLAST score	223

E value	3.0e-18
Match length	118
% identity	41
NCBI Description	CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi_2583169 (AF026473) calmodulin-related protein [Arabidopsis thaliana]

Seq. No.	225691
Seq. ID	LIB3166-039-P1-K1-G5
Method	BLASTX
NCBI GI	g2088651
BLAST score	395
E value	2.0e-38
Match length	128
% identity	58
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	225692
Seq. ID	LIB3166-039-P1-K1-G6
Method	BLASTX
NCBI GI	g3183088
BLAST score	209
E value	1.0e-16
Match length	71
% identity	56
NCBI Description	PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer like protein [Vigna unguiculata]

Seq. No.	225693
Seq. ID	LIB3166-039-P1-K1-G8
Method	BLASTX
NCBI GI	g4099914
BLAST score	271
E value	5.0e-24
Match length	79
% identity	70
NCBI Description	(U91857) ethylene-responsive element binding protein homolog [Stylosanthes hamata]

Seq. No.	225694
Seq. ID	LIB3166-039-P1-K1-H11
Method	BLASTX
NCBI GI	g3341687
BLAST score	179
E value	4.0e-13
Match length	86
% identity	47
NCBI Description	(AC003672) putative ras protein [Arabidopsis thaliana]

Seq. No.	225695
Seq. ID	LIB3166-039-P1-K1-H12
Method	BLASTX
NCBI GI	g1743354
BLAST score	504

E value	3.0e-51
Match length	130
% identity	74
NCBI Description	(Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No.	225696
Seq. ID	LIB3166-039-P1-K1-H7
Method	BLASTX
NCBI GI	g1084482
BLAST score	166
E value	5.0e-16
Match length	90
% identity	60
NCBI Description	heat shock protein 70 - Maize

Seq. No.	225697
Seq. ID	LIB3166-039-P1-K1-H8
Method	BLASTX
NCBI GI	g1169013
BLAST score	473
E value	1.0e-47
Match length	116
% identity	72
NCBI Description	COP9 PROTEIN (FUSCA PROTEIN FUS7) >gi_625971_pir__A54842 COP9 protein - Arabidopsis thaliana >gi_530870 (L32874) COP9 [Arabidopsis thaliana] >gi_2244767_emb_CAB10190_ (Z97335) COP9 protein [Arabidopsis thaliana]

Seq. No.	225698
Seq. ID	LIB3166-040-P1-K1-A2
Method	BLASTX
NCBI GI	g2541876
BLAST score	189
E value	3.0e-14
Match length	105
% identity	43
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	225699
Seq. ID	LIB3166-040-P1-K1-A4
Method	BLASTX
NCBI GI	g2541876
BLAST score	164
E value	2.0e-11
Match length	94
% identity	35
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	225700
Seq. ID	LIB3166-040-P1-K1-A5
Method	BLASTX
NCBI GI	g135449
BLAST score	295
E value	5.0e-30
Match length	88

% identity	80
NCBI Description	TUBULIN BETA-1 CHAIN >gi_100932_pir__S14701 tubulin beta-1 chain - maize >gi_295851_emb_CAA37060_ (X52878) beta 1 tubulin [Zea mays]
Seq. No.	225701
Seq. ID	LIB3166-040-P1-K1-A8
Method	BLASTX
NCBI GI	g1362093
BLAST score	266
E value	1.0e-23
Match length	66
% identity	74
NCBI Description	hypothetical protein (clone TPP15) - tomato (fragment) >gi_924632 (U20595) unknown [Solanum lycopersicum]
Seq. No.	225702
Seq. ID	LIB3166-040-P1-K1-B10
Method	BLASTX
NCBI GI	g3915031
BLAST score	643
E value	1.0e-67
Match length	122
% identity	98
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232_ (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase [Gossypium hirsutum]
Seq. No.	225703
Seq. ID	LIB3166-040-P1-K1-B11
Method	BLASTX
NCBI GI	g2464855
BLAST score	179
E value	4.0e-13
Match length	43
% identity	74
NCBI Description	(Z99707) myb-related protein [Arabidopsis thaliana]
Seq. No.	225704
Seq. ID	LIB3166-040-P1-K1-B12
Method	BLASTX
NCBI GI	g3643085
BLAST score	392
E value	4.0e-38
Match length	112
% identity	65
NCBI Description	(AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]
Seq. No.	225705
Seq. ID	LIB3166-040-P1-K1-B3
Method	BLASTX
NCBI GI	g2245125
BLAST score	197
E value	3.0e-15
Match length	61

% identity	66
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225706
Seq. ID	LIB3166-040-P1-K1-B7
Method	BLASTX
NCBI GI	g3242785
BLAST score	528
E value	4.0e-54
Match length	119
% identity	79
NCBI Description	(AF055355) respiratory burst oxidase protein C [Arabidopsis thaliana]

Seq. No.	225707
Seq. ID	LIB3166-040-P1-K1-B8
Method	BLASTX
NCBI GI	g2970641
BLAST score	343
E value	1.0e-32
Match length	84
% identity	74
NCBI Description	(AF052194) xyloglucan endotransglycosylase precursor [Actinidia deliciosa]

Seq. No.	225708
Seq. ID	LIB3166-040-P1-K1-B9
Method	BLASTX
NCBI GI	g4220535
BLAST score	515
E value	1.0e-52
Match length	121
% identity	81
NCBI Description	(AL035356) clathrin coat assembly like protein [Arabidopsis thaliana]

Seq. No.	225709
Seq. ID	LIB3166-040-P1-K1-C1
Method	BLASTX
NCBI GI	g3550454
BLAST score	573
E value	2.0e-59
Match length	106
% identity	98
NCBI Description	(AF085820) alcohol dehydrogenase A [Gossypium barbadense] >gi_3550458 (AF085821) alcohol dehydrogenase A [Gossypium barbadense] >gi_3551965 (AF085064) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551967 (AF085065) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551971 (AF085067) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551975 (AF085069) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551977 (AF085070) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140594 (AF090146) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140604 (AF090151) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140606 (AF090152) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140608 (AF090153) alcohol dehydrogenase A [Gossypium hirsutum]

	>gi_4140610 (AF090154) alcohol dehydrogenase A [Gossypium hirsutum]
Seq. No.	225710
Seq. ID	LIB3166-040-P1-K1-C11
Method	BLASTX
NCBI GI	g3327275
BLAST score	359
E value	3.0e-34
Match length	114
% identity	63
NCBI Description	(AB016002) PKn3 [Ipomoea nil]
Seq. No.	225711
Seq. ID	LIB3166-040-P1-K1-C12
Method	BLASTX
NCBI GI	g1737218
BLAST score	206
E value	8.0e-17
Match length	47
% identity	77
NCBI Description	(U79959) vacuolar sorting receptor homolog [Arabidopsis thaliana]
Seq. No.	225712
Seq. ID	LIB3166-040-P1-K1-C2
Method	BLASTX
NCBI GI	g436307
BLAST score	174
E value	1.0e-12
Match length	71
% identity	61
NCBI Description	(S66686) synaptic vesicle protein=n-syb [Drosophila, head, Peptide, 181 aa] [Drosophila sp.] >gi_738733_prf__2001392A synaptic vesicle protein [Drosophila melanogaster]
Seq. No.	225713
Seq. ID	LIB3166-040-P1-K1-C7
Method	BLASTX
NCBI GI	g2129630
BLAST score	294
E value	1.0e-26
Match length	76
% identity	66
NCBI Description	lamin - Arabidopsis thaliana >gi_1262754_emb_CAA65750_ (X97023) lamin [Arabidopsis thaliana] >gi_3395760 (U77721) unknown [Arabidopsis thaliana]
Seq. No.	225714
Seq. ID	LIB3166-040-P1-K1-C8
Method	BLASTX
NCBI GI	g2583117
BLAST score	240
E value	3.0e-20
Match length	74
% identity	65
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225715
Seq. ID	LIB3166-040-P1-K1-C9
Method	BLASTX
NCBI GI	g3451068
BLAST score	320
E value	1.0e-29
Match length	85
% identity	74
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	225716
Seq. ID	LIB3166-040-P1-K1-D10
Method	BLASTX
NCBI GI	g1171579
BLAST score	526
E value	8.0e-54
Match length	124
% identity	81
NCBI Description	(X95342) cytochrome P450 [Nicotiana tabacum]

Seq. No.	225717
Seq. ID	LIB3166-040-P1-K1-D11
Method	BLASTX
NCBI GI	g4263787
BLAST score	432
E value	6.0e-43
Match length	107
% identity	76
NCBI Description	(AC006068) unknown protein [Arabidopsis thaliana]

Seq. No.	225718
Seq. ID	LIB3166-040-P1-K1-D12
Method	BLASTX
NCBI GI	g3269284
BLAST score	269
E value	9.0e-24
Match length	92
% identity	62
NCBI Description	(AL030978) histone H2A- like protein [Arabidopsis thaliana]

Seq. No.	225719
Seq. ID	LIB3166-040-P1-K1-D5
Method	BLASTX
NCBI GI	g4468813
BLAST score	224
E value	3.0e-23
Match length	104
% identity	47
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	225720
Seq. ID	LIB3166-040-P1-K1-D7
Method	BLASTX
NCBI GI	g2465923
BLAST score	146
E value	3.0e-09

Match length	105
% identity	27
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	225721
Seq. ID	LIB3166-040-P1-K1-E1
Method	BLASTX
NCBI GI	g3540181
BLAST score	233
E value	2.0e-19
Match length	87
% identity	52
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	225722
Seq. ID	LIB3166-040-P1-K1-E3
Method	BLASTX
NCBI GI	g1777443
BLAST score	156
E value	2.0e-10
Match length	123
% identity	39
NCBI Description	(U28422) CCA1 [Arabidopsis thaliana] >gi_3510263 (AC005310) DNA-binding protein CCA1 [Arabidopsis thaliana] >gi_4090569 (U79156) CCA1 [Arabidopsis thaliana]

Seq. No.	225723
Seq. ID	LIB3166-040-P1-K1-E4
Method	BLASTX
NCBI GI	g3868758
BLAST score	223
E value	3.0e-18
Match length	42
% identity	90
NCBI Description	(D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No.	225724
Seq. ID	LIB3166-040-P1-K1-E5
Method	BLASTX
NCBI GI	g4204575
BLAST score	342
E value	3.0e-32
Match length	101
% identity	64
NCBI Description	(AF098510) cytochrome b5 DIF-F [Petunia x hybrida]

Seq. No.	225725
Seq. ID	LIB3166-040-P1-K1-E6
Method	BLASTX
NCBI GI	g4220482
BLAST score	226
E value	1.0e-18
Match length	88
% identity	52
NCBI Description	(AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225726
Seq. ID	LIB3166-040-P1-K1-E7
Method	BLASTX
NCBI GI	g3776005
BLAST score	218
E value	1.0e-17
Match length	81
% identity	56
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	225727
Seq. ID	LIB3166-040-P1-K1-E9
Method	BLASTX
NCBI GI	g4193388
BLAST score	367
E value	3.0e-35
Match length	91
% identity	79
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	225728
Seq. ID	LIB3166-040-P1-K1-F10
Method	BLASTX
NCBI GI	g1762945
BLAST score	308
E value	3.0e-28
Match length	117
% identity	52
NCBI Description	(U66269) ORF; able to induce HR-like lesions [Nicotiana tabacum]

Seq. No.	225729
Seq. ID	LIB3166-040-P1-K1-F12
Method	BLASTX
NCBI GI	g3861068
BLAST score	141
E value	1.0e-08
Match length	65
% identity	43
NCBI Description	(AJ235272) unknown [Rickettsia prowazekii]

Seq. No.	225730
Seq. ID	LIB3166-040-P1-K1-F2
Method	BLASTX
NCBI GI	g2462754
BLAST score	282
E value	3.0e-25
Match length	103
% identity	57
NCBI Description	(AC002292) Unknown protein [Arabidopsis thaliana]

Seq. No.	225731
Seq. ID	LIB3166-040-P1-K1-F5
Method	BLASTX
NCBI GI	g3334661
BLAST score	283

E value 2.0e-25
Match length 101
% identity 54
NCBI Description (Y10490) putative cytochrome P450 [Glycine max]

Seq. No. 225732
Seq. ID LIB3166-040-P1-K1-F8
Method BLASTX
NCBI GI g289920
BLAST score 557
E value 2.0e-57
Match length 103
% identity 97
NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No. 225733
Seq. ID LIB3166-040-P1-K1-F9
Method BLASTX
NCBI GI g3132476
BLAST score 257
E value 3.0e-22
Match length 80
% identity 68
NCBI Description (AC003096) unknown protein [Arabidopsis thaliana]

Seq. No. 225734
Seq. ID LIB3166-040-P1-K1-G1
Method BLASTX
NCBI GI g4559372
BLAST score 294
E value 1.0e-26
Match length 75
% identity 73
NCBI Description (AC006585) putative CONSTANS protein [Arabidopsis thaliana]

Seq. No. 225735
Seq. ID LIB3166-040-P1-K1-G10
Method BLASTX
NCBI GI g2464855
BLAST score 436
E value 3.0e-43
Match length 100
% identity 76
NCBI Description (Z99707) myb-related protein [Arabidopsis thaliana]

Seq. No. 225736
Seq. ID LIB3166-040-P1-K1-G11
Method BLASTX
NCBI GI g1531674
BLAST score 638
E value 5.0e-67
Match length 119
% identity 99
NCBI Description (U68462) actin [Striga asiatica]

Seq. No. 225737

Seq. ID	LIB3166-040-P1-K1-G4
Method	BLASTX
NCBI GI	g2369714
BLAST score	157
E value	1.0e-10
Match length	57
% identity	58
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	225738
Seq. ID	LIB3166-040-P1-K1-G6
Method	BLASTX
NCBI GI	g4432857
BLAST score	365
E value	6.0e-35
Match length	124
% identity	54
NCBI Description	(AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225739
Seq. ID	LIB3166-040-P1-K1-G7
Method	BLASTX
NCBI GI	g2494144
BLAST score	216
E value	2.0e-17
Match length	120
% identity	25
NCBI Description	(AC002329) predicted leucine-rich protein [Arabidopsis thaliana]

Seq. No.	225740
Seq. ID	LIB3166-040-P1-K1-G9
Method	BLASTX
NCBI GI	g1220196
BLAST score	539
E value	2.0e-55
Match length	111
% identity	89
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	225741
Seq. ID	LIB3166-040-P1-K1-H11
Method	BLASTX
NCBI GI	g3915083
BLAST score	605
E value	4.0e-63
Match length	123
% identity	93
NCBI Description	TUBULIN BETA CHAIN >gi_1403143_emb_CAA67056_ (X98406) beta-tubulin [Cicer arietinum]

Seq. No.	225742
Seq. ID	LIB3166-040-P1-K1-H12
Method	BLASTX
NCBI GI	g131015
BLAST score	334
E value	2.0e-31

Match length	77
% identity	73
NCBI Description	PATHOGENESIS-RELATED PROTEIN R MAJOR FORM PRECURSOR (THAUMATIN-LIKE PROTEIN E22) >gi_100385_pir__JH0230 pathogenesis-related protein R precursor - common tobacco >gi_19855_emb_CAA33293_ (X15224) thaumatin-like protein [Nicotiana tabacum] >gi_19980_emb_CAA31235_ (X12739) pathogenesis-related protein R (AA 1 - 226) [Nicotiana tabacum]

Seq. No.	225743
Seq. ID	LIB3166-040-P1-K1-H2
Method	BLASTX
NCBI GI	g2244965
BLAST score	315
E value	3.0e-29
Match length	84
% identity	71
NCBI Description	(Z97340) unnamed protein product [Arabidopsis thaliana]

Seq. No.	225744
Seq. ID	LIB3166-040-P1-K1-H6
Method	BLASTX
NCBI GI	g1200205
BLAST score	314
E value	6.0e-29
Match length	60
% identity	97
NCBI Description	(X95753) DAG [Antirrhinum majus]

Seq. No.	225745
Seq. ID	LIB3166-040-P1-K1-H7
Method	BLASTX
NCBI GI	g2738248
BLAST score	325
E value	2.0e-30
Match length	93
% identity	75
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	225746
Seq. ID	LIB3166-040-P1-K1-H8
Method	BLASTX
NCBI GI	g2244965
BLAST score	300
E value	2.0e-27
Match length	121
% identity	52
NCBI Description	(Z97340) unnamed protein product [Arabidopsis thaliana]

Seq. No.	225747
Seq. ID	LIB3166-042-P1-K1-A1
Method	BLASTX
NCBI GI	g2062174
BLAST score	194
E value	7.0e-15

Match length	118
% identity	35
NCBI Description	(AC001645) transcription factor (TINY) isolog [Arabidopsis thaliana]

Seq. No.	225748
Seq. ID	LIB3166-042-P1-K1-A10
Method	BLASTX
NCBI GI	g2738915
BLAST score	299
E value	4.0e-27
Match length	118
% identity	50
NCBI Description	(AF020760) serine protease [Homo sapiens]

Seq. No.	225749
Seq. ID	LIB3166-042-P1-K1-A2
Method	BLASTX
NCBI GI	g3252807
BLAST score	215
E value	2.0e-17
Match length	71
% identity	54
NCBI Description	(AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225750
Seq. ID	LIB3166-042-P1-K1-A3
Method	BLASTX
NCBI GI	g4008006
BLAST score	169
E value	5.0e-12
Match length	61
% identity	61
NCBI Description	(AF084034) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	225751
Seq. ID	LIB3166-042-P1-K1-A4
Method	BLASTX
NCBI GI	g4206124
BLAST score	597
E value	4.0e-62
Match length	129
% identity	89
NCBI Description	(AF097668) T-complex protein 1 epsilon subunit [Mesembryanthemum crystallinum]

Seq. No.	225752
Seq. ID	LIB3166-042-P1-K1-A5
Method	BLASTX
NCBI GI	g2384669
BLAST score	400
E value	5.0e-39
Match length	104
% identity	73
NCBI Description	(AF012656) putative potassium transporter AtKT1p [Arabidopsis thaliana]

Seq. No.	225753
Seq. ID	LIB3166-042-P1-K1-B10
Method	BLASTX
NCBI GI	g2208903
BLAST score	295
E value	7.0e-27
Match length	107
% identity	54
NCBI Description	(AB004798) ascorbate oxidase [Arabidopsis thaliana]

Seq. No.	225754
Seq. ID	LIB3166-042-P1-K1-B11
Method	BLASTX
NCBI GI	g1220196
BLAST score	661
E value	1.0e-69
Match length	129
% identity	98
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	225755
Seq. ID	LIB3166-042-P1-K1-B12
Method	BLASTX
NCBI GI	g3779218
BLAST score	300
E value	3.0e-27
Match length	94
% identity	62
NCBI Description	(AF030879) protein kinase CPK1 [Solanum tuberosum]

Seq. No.	225756
Seq. ID	LIB3166-042-P1-K1-B3
Method	BLASTX
NCBI GI	g2342685
BLAST score	418
E value	4.0e-41
Match length	123
% identity	63
NCBI Description	(AC000106) Contains similarity to Rhodococcus amidase (gb_D16207). ESTs gb_T20504,gb_H36650,gb_N97423,gb_H36595 come from this gene. [Arabidopsis thaliana]

Seq. No.	225757
Seq. ID	LIB3166-042-P1-K1-B5
Method	BLASTX
NCBI GI	g2160694
BLAST score	422
E value	1.0e-41
Match length	123
% identity	64
NCBI Description	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq. No.	225758
Seq. ID	LIB3166-042-P1-K1-B7
Method	BLASTX

NCBI GI	g1458245
BLAST score	143
E value	7.0e-09
Match length	111
% identity	33
NCBI Description	(U64834) coded for by C. elegans cDNA cm17a1; coded for by C. elegans cDNA cm7g1; coded for by C. elegans cDNA CEMSE26F; similar to methyltransferases [Caenorhabditis elegans]

Seq. No.	225759
Seq. ID	LIB3166-042-P1-K1-C11
Method	BLASTX
NCBI GI	g3242789
BLAST score	271
E value	6.0e-24
Match length	118
% identity	59
NCBI Description	(AF055357) respiratory burst oxidase protein D [Arabidopsis thaliana]

Seq. No.	225760
Seq. ID	LIB3166-042-P1-K1-C3
Method	BLASTX
NCBI GI	g4406770
BLAST score	177
E value	7.0e-13
Match length	42
% identity	79
NCBI Description	(AC006836) unknown protein [Arabidopsis thaliana]

Seq. No.	225761
Seq. ID	LIB3166-042-P1-K1-C4
Method	BLASTX
NCBI GI	g4262378
BLAST score	164
E value	2.0e-11
Match length	86
% identity	37
NCBI Description	(AF092910) stage specific peptide 24 [Trypanosoma cruzi]

Seq. No.	225762
Seq. ID	LIB3166-042-P1-K1-C8
Method	BLASTX
NCBI GI	g2194138
BLAST score	151
E value	7.0e-10
Match length	66
% identity	48
NCBI Description	(AC002062) Similar to Arabidopsis receptor-like protein kinase precursor (gb_M84659). [Arabidopsis thaliana]

Seq. No.	225763
Seq. ID	LIB3166-042-P1-K1-D4
Method	BLASTX
NCBI GI	g1871194
BLAST score	227

09604705.060501

E value	9.0e-19
Match length	95
% identity	49
NCBI Description	(U90439) DNA binding protein isolog [Arabidopsis thaliana] >gi_2335092 (AC002339) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	225764
Seq. ID	LIB3166-042-P1-K1-D6
Method	BLASTX
NCBI GI	g4557078
BLAST score	272
E value	5.0e-24
Match length	103
% identity	49
NCBI Description	(AC007045) putative Tal1-1 pol polyprotein, 5' partial [Arabidopsis thaliana]

Seq. No.	225765
Seq. ID	LIB3166-042-P1-K1-D7
Method	BLASTX
NCBI GI	g2827715
BLAST score	311
E value	1.0e-28
Match length	84
% identity	7
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	225766
Seq. ID	LIB3166-042-P1-K1-D8
Method	BLASTX
NCBI GI	g4388818
BLAST score	241
E value	1.0e-20
Match length	87
% identity	55
NCBI Description	(AC006528) putative pol polyprotein with a Zn-finger CCHC type domain (prosite:QDOC50158) and a DDE integrase signature motif [Arabidopsis thaliana]

Seq. No.	225767
Seq. ID	LIB3166-042-P1-K1-D9
Method	BLASTX
NCBI GI	g4455246
BLAST score	521
E value	3.0e-53
Match length	130
% identity	74
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	225768
Seq. ID	LIB3166-042-P1-K1-E1
Method	BLASTX
NCBI GI	g1518540
BLAST score	602
E value	9.0e-63

Match length	126
% identity	93
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	225769
Seq. ID	LIB3166-042-P1-K1-E10
Method	BLASTX
NCBI GI	g2829910
BLAST score	376
E value	3.0e-36
Match length	102
% identity	64
NCBI Description	(AC002291) Unknown protein, contains regulator of chromosome condensation motifs [Arabidopsis thaliana]

Seq. No.	225770
Seq. ID	LIB3166-042-P1-K1-E11
Method	BLASTX
NCBI GI	g1197461
BLAST score	656
E value	5.0e-69
Match length	130
% identity	95
NCBI Description	(X78819) casein kinase I [Arabidopsis thaliana]

Seq. No.	225771
Seq. ID	LIB3166-042-P1-K1-E2
Method	BLASTX
NCBI GI	g3834302
BLAST score	473
E value	1.0e-47
Match length	127
% identity	79
NCBI Description	(AC005679) Similar to gb_D45384 vacuolar H+-pyrophosphatase from Oryza sativa. ESTs gb_F14272 and gb_F14273 come from this gene. [Arabidopsis thaliana]

Seq. No.	225772
Seq. ID	LIB3166-042-P1-K1-E3
Method	BLASTX
NCBI GI	g115492
BLAST score	559
E value	1.0e-57
Match length	109
% identity	52
NCBI Description	CALMODULIN-RELATED PROTEIN >gi_169205 (M80831) calmodulin-related protein [Petunia hybrida]

Seq. No.	225773
Seq. ID	LIB3166-042-P1-K1-E4
Method	BLASTX
NCBI GI	g2499710
BLAST score	577
E value	8.0e-60
Match length	124
% identity	87
NCBI Description	PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)

(PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
>gi_1438075 (L33686) phospholipase D [Ricinus communis]

Seq. No.	225774
Seq. ID	LIB3166-042-P1-K1-F1
Method	BLASTX
NCBI GI	g547683
BLAST score	343
E value	2.0e-32
Match length	122
% identity	58
NCBI Description	HEAT SHOCK COGNATE PROTEIN 80 >gi_170456 (M96549) heat shock cognate protein 80 [Solanum lycopersicum] >gi_445601_prf__1909348A heat shock protein hsp80 [Lycopersicon esculentum]

Seq. No.	225775
Seq. ID	LIB3166-042-P1-K1-F10
Method	BLASTX
NCBI GI	g2829751
BLAST score	187
E value	5.0e-14
Match length	110
% identity	36
NCBI Description	MACROPHAGE MIGRATION INHIBITORY FACTOR HOMOLOG (BMMIF) >gi_1850559 (U88035) macrophage migration inhibitory factor [Brugia malayi] >gi_2190976 (AF002699) macrophage migration inhibitory factor [Brugia malayi]

Seq. No.	225776
Seq. ID	LIB3166-042-P1-K1-F11
Method	BLASTX
NCBI GI	g2828280
BLAST score	149
E value	1.0e-09
Match length	33
% identity	85
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana] >gi_2832633_emb_CAA16762_ (AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	225777
Seq. ID	LIB3166-042-P1-K1-F12
Method	BLASTX
NCBI GI	g4539453
BLAST score	297
E value	6.0e-27
Match length	88
% identity	61
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	225778
Seq. ID	LIB3166-042-P1-K1-F2
Method	BLASTX
NCBI GI	g509810
BLAST score	523
E value	2.0e-53

Match length	126
% identity	79
NCBI Description	(L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	225779
Seq. ID	LIB3166-042-P1-K1-F3
Method	BLASTX
NCBI GI	g1931655
BLAST score	313
E value	7.0e-29
Match length	109
% identity	61
NCBI Description	(U95973) receptor-kinase isolog [Arabidopsis thaliana]

Seq. No.	225780
Seq. ID	LIB3166-042-P1-K1-F4
Method	BLASTX
NCBI GI	g485514
BLAST score	145
E value	4.0e-09
Match length	33
% identity	79
NCBI Description	ADR11-2 protein - soybean (fragment) >gi_296443_emb_CAA49341_ (X69640) auxin down regulated [Glycine max]

Seq. No.	225781
Seq. ID	LIB3166-042-P1-K1-F6
Method	BLASTX
NCBI GI	g1150406
BLAST score	194
E value	7.0e-15
Match length	100
% identity	39
NCBI Description	(Z46868) exo-1,3-beta-glucanase/1,3-beta-D-glucan glucanohydrolase [Pichia angusta]

Seq. No.	225782
Seq. ID	LIB3166-042-P1-K1-F9
Method	BLASTX
NCBI GI	g3258647
BLAST score	228
E value	7.0e-19
Match length	125
% identity	8
NCBI Description	(AF044677) retinitis pigmentosa GTPase regulator [Mus musculus]

Seq. No.	225783
Seq. ID	LIB3166-042-P1-K1-G1
Method	BLASTX
NCBI GI	g3548802
BLAST score	207
E value	2.0e-16
Match length	66
% identity	62
NCBI Description	(AC005313) axi 1-like protein [Arabidopsis thaliana]

>gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein [Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No.	225784
Seq. ID	LIB3166-042-P1-K1-G12
Method	BLASTX
NCBI GI	g3236253
BLAST score	301
E value	2.0e-27
Match length	120
% identity	52
NCBI Description	(AC004684) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	225785
Seq. ID	LIB3166-042-P1-K1-G2
Method	BLASTX
NCBI GI	g167367
BLAST score	494
E value	4.0e-50
Match length	125
% identity	77
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	225786
Seq. ID	LIB3166-042-P1-K1-G3
Method	BLASTX
NCBI GI	g2760320
BLAST score	345
E value	1.0e-32
Match length	104
% identity	68
NCBI Description	(AC002130) F1N21.4 [Arabidopsis thaliana]

Seq. No.	225787
Seq. ID	LIB3166-042-P1-K1-G4
Method	BLASTX
NCBI GI	g4193382
BLAST score	386
E value	2.0e-37
Match length	86
% identity	83
NCBI Description	(AF083336) ribosomal protein S27 [Arabidopsis thaliana] >gi_4193384 (AF083337) ribosomal protein S27 [Arabidopsis thaliana]

Seq. No.	225788
Seq. ID	LIB3166-042-P1-K1-G5
Method	BLASTX
NCBI GI	g4006924
BLAST score	589
E value	3.0e-61
Match length	126
% identity	83
NCBI Description	(Z99708) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No.	225789
Seq. ID	LIB3166-042-P1-K1-G6
Method	BLASTX
NCBI GI	g1084321
BLAST score	521
E value	3.0e-53
Match length	123
% identity	80
NCBI Description	protochlorophyllide reductase (EC 1.3.1.33) - cucumber >gi_2244614_dbj_BAA21089_ (D50085) NADPH-protochlorophyllide oxidoreductase [Cucumis sativus]

Seq. No.	225790
Seq. ID	LIB3166-042-P1-K1-G9
Method	BLASTX
NCBI GI	g2764941
BLAST score	348
E value	6.0e-33
Match length	90
% identity	68
NCBI Description	(X98255) transcriptionally stimulated by gibberellins; expressed in meristematic region, and style [Arabidopsis thaliana]

Seq. No.	225791
Seq. ID	LIB3166-042-P1-K1-H10
Method	BLASTX
NCBI GI	g2804278
BLAST score	553
E value	6.0e-57
Match length	129
% identity	81
NCBI Description	(AB003516) squalene epoxidase [Panax ginseng]

Seq. No.	225792
Seq. ID	LIB3166-042-P1-K1-H11
Method	BLASTX
NCBI GI	g2088653
BLAST score	214
E value	3.0e-17
Match length	109
% identity	41
NCBI Description	(AF002109) Hs1pro-1 related protein isolog [Arabidopsis thaliana]

Seq. No.	225793
Seq. ID	LIB3166-042-P1-K1-H12
Method	BLASTX
NCBI GI	g3868758
BLAST score	418
E value	4.0e-41
Match length	101
% identity	75
NCBI Description	(D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No.	225794
Seq. ID	LIB3166-042-P1-K1-H2

Method	BLASTX
NCBI GI	g3319345
BLAST score	117
E value	2.0e-09
Match length	82
% identity	49
NCBI Description	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]

Seq. No.	225795
Seq. ID	LIB3166-042-P1-K1-H5
Method	BLASTX
NCBI GI	g2088653
BLAST score	214
E value	3.0e-17
Match length	109
% identity	41
NCBI Description	(AF002109) Hslpro-1 related protein isolog [Arabidopsis thaliana]

Seq. No.	225796
Seq. ID	LIB3166-042-P1-K1-H7
Method	BLASTX
NCBI GI	g113621
BLAST score	470
E value	3.0e-47
Match length	105
% identity	89
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A cytoplasmic aldolase [Zea mays]

Seq. No.	225797
Seq. ID	LIB3166-042-P1-K1-H8
Method	BLASTX
NCBI GI	g3122139
BLAST score	375
E value	4.0e-36
Match length	122
% identity	55
NCBI Description	GLYCEROL KINASE (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE) (GLYCEROKINASE) (GK) (ATP-STIMULATED GLUCOCORTICOID-RECEPTOR TRANSLOCATON PROMOTER) (ASTP) >gi_484372_pir__JN0606 ATP-stimulated glucocorticoid-receptor translocation promoter protein - rat >gi_433211_dbj_BAA03677_ (D16102) ATP-stimulated glucocorticoid-receptor translocaton promoter [Rattus rattus]

Seq. No.	225798
Seq. ID	LIB3166-043-P1-K1-A11
Method	BLASTX
NCBI GI	g3913413
BLAST score	390

E value	7.0e-38
Match length	85
% identity	89
NCBI Description	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME 1 (ADOMETDC 1) (SAMDC 1) (SAMDC9) >gi_1155240 (U38526) S-adenosylmethionine decarboxylase 1 [Dianthus caryophyllus] >gi_2406585 (U94786) S-adenosylmethionine decarboxylase [Dianthus caryophyllus]

Seq. No.	225799
Seq. ID	LIB3166-043-P1-K1-A2
Method	BLASTX
NCBI GI	g1730502
BLAST score	215
E value	2.0e-17
Match length	87
% identity	45
NCBI Description	TRANSMEMBRANE PROTEIN PFT27 >gi_110903_pir__A31351 probable transmembrane protein FT27 - mouse >gi_535682 (M23568) transmembrane protein [Mus musculus]

Seq. No.	225800
Seq. ID	LIB3166-043-P1-K1-A3
Method	BLASTX
NCBI GI	g4062934
BLAST score	491
E value	8.0e-50
Match length	110
% identity	82
NCBI Description	(D88272) formate dehydrogenase [Hordeum vulgare]

Seq. No.	225801
Seq. ID	LIB3166-043-P1-K1-A4
Method	BLASTX
NCBI GI	g3746069
BLAST score	160
E value	6.0e-11
Match length	108
% identity	31
NCBI Description	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	225802
Seq. ID	LIB3166-043-P1-K1-A9
Method	BLASTX
NCBI GI	g4218120
BLAST score	347
E value	7.0e-33
Match length	101
% identity	65
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	225803
Seq. ID	LIB3166-043-P1-K1-B2
Method	BLASTX
NCBI GI	g3201680

BLAST score 322
E value 7.0e-30
Match length 127
% identity 55
NCBI Description (AF060941) extra-large G-protein [Arabidopsis thaliana]

Seq. No. 225804
Seq. ID LIB3166-043-P1-K1-B4
Method BLASTX
NCBI GI g4220533
BLAST score 333
E value 4.0e-31
Match length 108
% identity 34
NCBI Description (AL035356) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No. 225805
Seq. ID LIB3166-043-P1-K1-B8
Method BLASTX
NCBI GI g1928981
BLAST score 532
E value 1.0e-54
Match length 120
% identity 89
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No. 225806
Seq. ID LIB3166-043-P1-K1-B9
Method BLASTX
NCBI GI g1710124
BLAST score 181
E value 2.0e-13
Match length 117
% identity 37
NCBI Description (U62279) leucine-rich repeat-containing extracellular glycoprotein; contains six N-glycosylation sites [NX(S/T)] [Sorghum bicolor]

Seq. No. 225807
Seq. ID LIB3166-043-P1-K1-C1
Method BLASTX
NCBI GI g4006924
BLAST score 197
E value 2.0e-15
Match length 46
% identity 76
NCBI Description (Z99708) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No. 225808
Seq. ID LIB3166-043-P1-K1-C10
Method BLASTX
NCBI GI g4455208
BLAST score 464
E value 1.0e-46

Match length	115
% identity	79
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	225809
Seq. ID	LIB3166-043-P1-K1-C11
Method	BLASTX
NCBI GI	g4325324
BLAST score	627
E value	1.0e-65
Match length	125
% identity	93
NCBI Description	(AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis thaliana]

Seq. No.	225810
Seq. ID	LIB3166-043-P1-K1-C12
Method	BLASTX
NCBI GI	g4325324
BLAST score	258
E value	2.0e-22
Match length	103
% identity	58
NCBI Description	(AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis thaliana]

Seq. No.	225811
Seq. ID	LIB3166-043-P1-K1-C3
Method	BLASTX
NCBI GI	g2979552
BLAST score	435
E value	4.0e-43
Match length	123
% identity	71
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana]

Seq. No.	225812
Seq. ID	LIB3166-043-P1-K1-C6
Method	BLASTX
NCBI GI	g2499611
BLAST score	468
E value	6.0e-47
Match length	117
% identity	79
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 7 (MAP KINASE 7) (ATMPK7) >gi_629548_pir__S40473 mitogen-activated protein kinase 7 (EC 2.7.1.-) - Arabidopsis thaliana >gi_457406_dbj_BAA04870_ (D21843) MAP kinase [Arabidopsis thaliana]

Seq. No.	225813
Seq. ID	LIB3166-043-P1-K1-C7
Method	BLASTX
NCBI GI	g130600
BLAST score	407
E value	7.0e-40
Match length	122

% identity	64
NCBI Description	ENZYMATIC POLYPROTEIN [CONTAINS: ASPARTIC PROTEASE ; ENDONUCLEASE; REVERSE TRANSCRIPTASE] >gi_76782_pir__S01283 hypothetical protein 5 - figwort mosaic virus >gi_58813_emb_CAA29527_ (X06166) ORF V (AA 1-666) [Figwort mosaic virus]

Seq. No.	225814
Seq. ID	LIB3166-043-P1-K1-C8
Method	BLASTX
NCBI GI	g393707
BLAST score	509
E value	8.0e-52
Match length	117
% identity	84
NCBI Description	(X67696) acetyl-CoA acyltransferase [Cucumis sativus]

Seq. No.	225815
Seq. ID	LIB3166-043-P1-K1-D1
Method	BLASTX
NCBI GI	g3063396
BLAST score	349
E value	2.0e-33
Match length	87
% identity	77
NCBI Description	(AB012947) vcCyP [Vicia faba]

Seq. No.	225816
Seq. ID	LIB3166-043-P1-K1-D10
Method	BLASTX
NCBI GI	g1531758
BLAST score	605
E value	4.0e-63
Match length	124
% identity	94
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	225817
Seq. ID	LIB3166-043-P1-K1-D11
Method	BLASTX
NCBI GI	g3858935
BLAST score	522
E value	2.0e-53
Match length	119
% identity	82
NCBI Description	(AL021636) synaptobrevin-like protein [Arabidopsis thaliana] >gi_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana]

Seq. No.	225818
Seq. ID	LIB3166-043-P1-K1-D12
Method	BLASTX
NCBI GI	g3858935
BLAST score	225
E value	5.0e-19

Match length	71
% identity	62
NCBI Description	(AL021636) synaptobrevin-like protein [Arabidopsis thaliana] >gi_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana]

Seq. No.	225819
Seq. ID	LIB3166-043-P1-K1-D3
Method	BLASTX
NCBI GI	g4455276
BLAST score	167
E value	1.0e-11
Match length	71
% identity	54
NCBI Description	(AL035527) peptide transporter-like protein [Arabidopsis thaliana]

Seq. No.	225820
Seq. ID	LIB3166-043-P1-K1-D5
Method	BLASTX
NCBI GI	g1220196
BLAST score	543
E value	8.0e-56
Match length	111
% identity	90
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	225821
Seq. ID	LIB3166-043-P1-K1-D6
Method	BLASTX
NCBI GI	g1332411
BLAST score	505
E value	2.0e-51
Match length	109
% identity	88
NCBI Description	(D85102) dihydroflavonol 4-reductase [Rosa hybrida]

Seq. No.	225822
Seq. ID	LIB3166-043-P1-K1-D8
Method	BLASTX
NCBI GI	g2244780
BLAST score	266
E value	2.0e-23
Match length	57
% identity	93
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225823
Seq. ID	LIB3166-043-P1-K1-E1
Method	BLASTX
NCBI GI	g1170621
BLAST score	355
E value	7.0e-34
Match length	103
% identity	67
NCBI Description	KINESIN-LIKE PROTEIN C >gi_1084342_pir__S48020

kinesin-related protein katC - Arabidopsis thaliana >gi_1438844_dbj_BAA04674_ (D21138) heavy chain polypeptide of kinesin-like protein [Arabidopsis thaliana]

Seq. No.	225824
Seq. ID	LIB3166-043-P1-K1-E10
Method	BLASTX
NCBI GI	g2995384
BLAST score	177
E value	3.0e-13
Match length	65
% identity	63
NCBI Description	(AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No.	225825
Seq. ID	LIB3166-043-P1-K1-E12
Method	BLASTX
NCBI GI	g1408471
BLAST score	153
E value	4.0e-12
Match length	59
% identity	66
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	225826
Seq. ID	LIB3166-043-P1-K1-E2
Method	BLASTX
NCBI GI	g4558661
BLAST score	368
E value	3.0e-35
Match length	114
% identity	66
NCBI Description	(AC007063) putative malate oxidoreductase (NAD) [Arabidopsis thaliana]

Seq. No.	225827
Seq. ID	LIB3166-043-P1-K1-E4
Method	BLASTX
NCBI GI	g832876
BLAST score	535
E value	7.0e-55
Match length	119
% identity	87
NCBI Description	(L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi_1097368_prf__2113407A ascorbate free radical reductase [Lycopersicon esculentum]

Seq. No.	225828
Seq. ID	LIB3166-043-P1-K1-E5
Method	BLASTX
NCBI GI	g3914002
BLAST score	367
E value	3.0e-35
Match length	115
% identity	64

NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_2935279 (AF033862) Lon protease [Arabidopsis thaliana]
Seq. No.	225829
Seq. ID	LIB3166-043-P1-K1-E7
Method	BLASTX
NCBI GI	g1173256
BLAST score	526
E value	8.0e-54
Match length	125
% identity	83
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal protein S4 - upland cotton >gi_488739_emb_CAA55882_ (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]
Seq. No.	225830
Seq. ID	LIB3166-043-P1-K1-E8
Method	BLASTX
NCBI GI	g2654868
BLAST score	154
E value	7.0e-13
Match length	52
% identity	77
NCBI Description	(AF015301) RbohAp108 [Arabidopsis thaliana]
Seq. No.	225831
Seq. ID	LIB3166-043-P1-K1-F1
Method	BLASTX
NCBI GI	g2098705
BLAST score	294
E value	1.0e-26
Match length	118
% identity	55
NCBI Description	(U82973) pectinesterase [Citrus sinensis]
Seq. No.	225832
Seq. ID	LIB3166-043-P1-K1-F10
Method	BLASTX
NCBI GI	g3643607
BLAST score	470
E value	3.0e-47
Match length	113
% identity	43
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.	225833
Seq. ID	LIB3166-043-P1-K1-F11
Method	BLASTX
NCBI GI	g2253442
BLAST score	188
E value	3.0e-14
Match length	46
% identity	67
NCBI Description	(AF007784) LTCOR11 [Lavatera thuringiaca]
Seq. No.	225834

Seq. ID	LIB3166-043-P1-K1-F12
Method	BLASTX
NCBI GI	g2829868
BLAST score	187
E value	4.0e-14
Match length	50
% identity	68
NCBI Description	(AC002396) Unknown protein [Arabidopsis thaliana]

Seq. No.	225835
Seq. ID	LIB3166-043-P1-K1-F3
Method	BLASTX
NCBI GI	g2288981
BLAST score	310
E value	2.0e-28
Match length	97
% identity	40
NCBI Description	(AC002335) calcium binding protein isolog [Arabidopsis thaliana] >gi_3763938 (AC004450) putative calcium binding protein [Arabidopsis thaliana]

Seq. No.	225836
Seq. ID	LIB3166-043-P1-K1-F4
Method	BLASTX
NCBI GI	g3929545
BLAST score	281
E value	4.0e-25
Match length	126
% identity	49
NCBI Description	(AF067194) S-adenosylmethionine decarboxylase [Oryza sativa]

Seq. No.	225837
Seq. ID	LIB3166-043-P1-K1-F5
Method	BLASTX
NCBI GI	g2583123
BLAST score	318
E value	2.0e-29
Match length	98
% identity	63
NCBI Description	(AC002387) putative nucleotide sugar epimerase [Arabidopsis thaliana]

Seq. No.	225838
Seq. ID	LIB3166-043-P1-K1-F6
Method	BLASTX
NCBI GI	g3643085
BLAST score	246
E value	4.0e-21
Match length	109
% identity	50
NCBI Description	(AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]

Seq. No.	225839
Seq. ID	LIB3166-043-P1-K1-F8
Method	BLASTX

NCBI GI	g4220533
BLAST score	317
E value	2.0e-29
Match length	126
% identity	56
NCBI Description	(AL035356) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	225840
Seq. ID	LIB3166-043-P1-K1-G1
Method	BLASTX
NCBI GI	g3355468
BLAST score	507
E value	1.0e-51
Match length	122
% identity	86
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No.	225841
Seq. ID	LIB3166-043-P1-K1-G10
Method	BLASTX
NCBI GI	g3646340
BLAST score	536
E value	5.0e-55
Match length	119
% identity	87
NCBI Description	(AJ000763) MADS-box protein [Malus domestica]

Seq. No.	225842
Seq. ID	LIB3166-043-P1-K1-G11
Method	BLASTX
NCBI GI	g4090535
BLAST score	366
E value	3.0e-35
Match length	82
% identity	79
NCBI Description	(U68216) ACC synthase [Carica papaya]

Seq. No.	225843
Seq. ID	LIB3166-043-P1-K1-G12
Method	BLASTX
NCBI GI	g1702983
BLAST score	231
E value	2.0e-19
Match length	96
% identity	48
NCBI Description	AUXIN-REPRESSED 12.5 KD PROTEIN >gi_99855_pir__S11850 hypothetical protein - garden strawberry >gi_22573_emb_CAA36676_ (X52429) 12.5 kDa protein [Fragaria x ananassa] >gi_927034 (L44142) auxin-repressed protein [Fragaria ananassa]

Seq. No.	225844
Seq. ID	LIB3166-043-P1-K1-G2
Method	BLASTX
NCBI GI	g1169544

BLAST score	228
E value	1.0e-32
Match length	121
% identity	69
NCBI Description	ERD1 PROTEIN PRECURSOR >gi_541859_pir__JN0901 ERD1 protein - Arabidopsis thaliana >gi_497629_dbj_BAA04506_ (D17582) ERD1 protein [Arabidopsis thaliana]

Seq. No.	225845
Seq. ID	LIB3166-043-P1-K1-G3
Method	BLASTX
NCBI GI	g3087805
BLAST score	203
E value	9.0e-25
Match length	81
% identity	78
NCBI Description	(AJ223038) latex allergen [Hevea brasiliensis]

Seq. No.	225846
Seq. ID	LIB3166-043-P1-K1-G4
Method	BLASTX
NCBI GI	g3236240
BLAST score	325
E value	3.0e-30
Match length	103
% identity	65
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	225847
Seq. ID	LIB3166-043-P1-K1-G6
Method	BLASTX
NCBI GI	g1263291
BLAST score	457
E value	9.0e-46
Match length	97
% identity	88
NCBI Description	(U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No.	225848
Seq. ID	LIB3166-043-P1-K1-G7
Method	BLASTX
NCBI GI	g729335
BLAST score	153
E value	4.0e-10
Match length	65
% identity	48
NCBI Description	SUCCINATE DEHYDROGENASE (UBIQUINONE) IRON-SULFUR PROTEIN PRECURSOR (IP) >gi_508849 (L27705) succinate dehydrogenase iron-protein subunit [Drosophila melanogaster]

Seq. No.	225849
Seq. ID	LIB3166-043-P1-K1-G8
Method	BLASTX
NCBI GI	g3023190
BLAST score	426
E value	4.0e-42
Match length	104

% identity	81
NCBI Description	14-3-3-LIKE PROTEIN 16R >gi_1888459_emb_CAA72381_ (Y11685) 14-3-3 protein [Solanum tuberosum]
Seq. No.	225850
Seq. ID	LIB3166-043-P1-K1-H1
Method	BLASTX
NCBI GI	g4415942
BLAST score	219
E value	6.0e-22
Match length	122
% identity	52
NCBI Description	(AC006418) hypothetical protein [Arabidopsis thaliana]
Seq. No.	225851
Seq. ID	LIB3166-043-P1-K1-H2
Method	BLASTX
NCBI GI	g3548810
BLAST score	160
E value	6.0e-11
Match length	98
% identity	43
NCBI Description	(AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]
Seq. No.	225852
Seq. ID	LIB3166-043-P1-K1-H3
Method	BLASTX
NCBI GI	g4455340
BLAST score	211
E value	7.0e-17
Match length	105
% identity	43
NCBI Description	(AL035522) putative protein [Arabidopsis thaliana]
Seq. No.	225853
Seq. ID	LIB3166-043-P1-K1-H8
Method	BLASTX
NCBI GI	g1871182
BLAST score	494
E value	4.0e-50
Match length	119
% identity	75
NCBI Description	(U90439) phospholipase D isolog [Arabidopsis thaliana]
Seq. No.	225854
Seq. ID	LIB3166-043-P1-K1-H9
Method	BLASTX
NCBI GI	g2980760
BLAST score	242
E value	2.0e-20
Match length	85
% identity	58
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]
Seq. No.	225855
Seq. ID	LIB3166-044-P1-K1-A1

Method	BLASTX
NCBI GI	g3668089
BLAST score	138
E value	7.0e-09
Match length	67
% identity	36
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	225856
Seq. ID	LIB3166-044-P1-K1-A12
Method	BLASTX
NCBI GI	g2558938
BLAST score	241
E value	2.0e-20
Match length	76
% identity	61
NCBI Description	(AF024625) arm repeat containing protein [Brassica napus]

Seq. No.	225857
Seq. ID	LIB3166-044-P1-K1-A2
Method	BLASTX
NCBI GI	g3668089
BLAST score	344
E value	2.0e-32
Match length	126
% identity	50
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	225858
Seq. ID	LIB3166-044-P1-K1-A3
Method	BLASTX
NCBI GI	g4455192
BLAST score	498
E value	2.0e-50
Match length	129
% identity	70
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	225859
Seq. ID	LIB3166-044-P1-K1-A4
Method	BLASTX
NCBI GI	g2146731
BLAST score	572
E value	3.0e-59
Match length	125
% identity	29
NCBI Description	FK506-binding protein - Arabidopsis thaliana >gi_1354207 (U49453) rof1 [Arabidopsis thaliana]

Seq. No.	225860
Seq. ID	LIB3166-044-P1-K1-A6
Method	BLASTX
NCBI GI	g3367578
BLAST score	214
E value	3.0e-17
Match length	75
% identity	53

NCBI Description	(AL031135) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	225861
Seq. ID	LIB3166-044-P1-K1-A7
Method	BLASTX
NCBI GI	g3668089
BLAST score	271
E value	5.0e-24
Match length	83
% identity	60
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	225862
Seq. ID	LIB3166-044-P1-K1-B10
Method	BLASTX
NCBI GI	g1362008
BLAST score	340
E value	5.0e-32
Match length	104
% identity	15
NCBI Description	ubiquitin-like protein 12 - Arabidopsis thaliana

Seq. No.	225863
Seq. ID	LIB3166-044-P1-K1-B2
Method	BLASTX
NCBI GI	g3063448
BLAST score	368
E value	3.0e-35
Match length	130
% identity	85
NCBI Description	(AC003981) F22O13.10 [Arabidopsis thaliana]

Seq. No.	225864
Seq. ID	LIB3166-044-P1-K1-B3
Method	BLASTX
NCBI GI	g3766368
BLAST score	220
E value	6.0e-18
Match length	106
% identity	47
NCBI Description	(AL031907) putative trascription factor, ccr4-associated factor homolog [Schizosaccharomyces pombe]

Seq. No.	225865
Seq. ID	LIB3166-044-P1-K1-B6
Method	BLASTX
NCBI GI	g2129578
BLAST score	569
E value	7.0e-59
Match length	117
% identity	91
NCBI Description	dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi_1585435_prf__2124427B diamide resistance gene [Arabidopsis thaliana]

Seq. No.	225866
Seq. ID	LIB3166-044-P1-K1-B8
Method	BLASTX
NCBI GI	g1565225
BLAST score	284
E value	2.0e-25
Match length	62
% identity	84
NCBI Description	(X95572) salt-tolerance protein [Arabidopsis thaliana]

Seq. No.	225867
Seq. ID	LIB3166-044-P1-K1-C1
Method	BLASTX
NCBI GI	g3023858
BLAST score	637
E value	8.0e-67
Match length	127
% identity	47
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_1256608 (U44850) G protein beta subunit [Glycine max]

Seq. No.	225868
Seq. ID	LIB3166-044-P1-K1-C10
Method	BLASTX
NCBI GI	g3201554
BLAST score	535
E value	1.0e-56
Match length	126
% identity	80
NCBI Description	(AJ006501) beta-D-glucosidase [Tropaeolum majus]

Seq. No.	225869
Seq. ID	LIB3166-044-P1-K1-C11
Method	BLASTX
NCBI GI	g1545805
BLAST score	251
E value	3.0e-23
Match length	95
% identity	62
NCBI Description	(D64052) cytochrome P450 like_TBP [Nicotiana tabacum]

Seq. No.	225870
Seq. ID	LIB3166-044-P1-K1-C12
Method	BLASTX
NCBI GI	g1362103
BLAST score	150
E value	3.0e-10
Match length	42
% identity	67
NCBI Description	ubiquitin conjugating enzyme - tomato >gi_886679_emb_CAA58111_ (X82938) ubiquitin conjugating enzyme [Lycopersicon esculentum]

Seq. No.	225871
Seq. ID	LIB3166-044-P1-K1-C2

Method	BLASTX
NCBI GI	g3033400
BLAST score	242
E value	2.0e-20
Match length	81
% identity	56
NCBI Description	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	225872
Seq. ID	LIB3166-044-P1-K1-C3
Method	BLASTX
NCBI GI	g3043656
BLAST score	239
E value	4.0e-20
Match length	86
% identity	52
NCBI Description	(AB011138) KIAA0566 protein [Homo sapiens]

Seq. No.	225873
Seq. ID	LIB3166-044-P1-K1-C4
Method	BLASTX
NCBI GI	g1657948
BLAST score	501
E value	7.0e-51
Match length	119
% identity	83
NCBI Description	(U73466) MipC [Mesembryanthemum crystallinum]

Seq. No.	225874
Seq. ID	LIB3166-044-P1-K1-D10
Method	BLASTX
NCBI GI	g3901012
BLAST score	322
E value	6.0e-30
Match length	88
% identity	68
NCBI Description	(AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]

Seq. No.	225875
Seq. ID	LIB3166-044-P1-K1-D12
Method	BLASTX
NCBI GI	g2833388
BLAST score	455
E value	2.0e-45
Match length	126
% identity	71
NCBI Description	GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi_629660_pir__S43341 ADPglucose--starch glucosyltransferase (EC 2.4.1.21) precursor - cassava >gi_437042_emb_CAA52273_ (X74160) starch (bacterial glycogen) synthase [Manihot esculenta]

Seq. No.	225876
Seq. ID	LIB3166-044-P1-K1-D4
Method	BLASTX

NCBI GI g1619321
BLAST score 378
E value 2.0e-36
Match length 123
% identity 57
NCBI Description (Y07563) hin1 [Nicotiana tabacum]

Seq. No. 225877
Seq. ID LIB3166-044-P1-K1-D7
Method BLASTX
NCBI GI g4538911
BLAST score 227
E value 3.0e-19
Match length 61
% identity 79
NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No. 225878
Seq. ID LIB3166-044-P1-K1-E1
Method BLASTX
NCBI GI g3901012
BLAST score 506
E value 2.0e-51
Match length 123
% identity 71
NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]

Seq. No. 225879
Seq. ID LIB3166-044-P1-K1-E12
Method BLASTX
NCBI GI g169363
BLAST score 218
E value 6.0e-18
Match length 43
% identity 81
NCBI Description (M75856) PVPR3 [Phaseolus vulgaris]

Seq. No. 225880
Seq. ID LIB3166-044-P1-K1-E2
Method BLASTX
NCBI GI g2982459
BLAST score 187
E value 4.0e-14
Match length 60
% identity 67
NCBI Description (AL022223) putative protein [Arabidopsis thaliana]

Seq. No. 225881
Seq. ID LIB3166-044-P1-K1-E4
Method BLASTX
NCBI GI g2632252
BLAST score 433
E value 6.0e-43
Match length 119
% identity 68
NCBI Description (Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No.	225882
Seq. ID	LIB3166-044-P1-K1-E6
Method	BLASTX
NCBI GI	g1174622
BLAST score	332
E value	4.0e-31
Match length	118
% identity	49
NCBI Description	T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA) (CCT-THETA) >gi_1078408_pir__S56779 t-complex protein 1 homolog YJL008c - yeast (Saccharomyces cerevisiae) >gi_1006721_emb_CAA89300_ (Z49284) ORF YJL008c [Saccharomyces cerevisiae]

Seq. No.	225883
Seq. ID	LIB3166-044-P1-K1-E7
Method	BLASTX
NCBI GI	g4262250
BLAST score	341
E value	4.0e-32
Match length	102
% identity	74
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	225884
Seq. ID	LIB3166-044-P1-K1-E8
Method	BLASTX
NCBI GI	g2414650
BLAST score	351
E value	2.0e-33
Match length	107
% identity	63
NCBI Description	(Z99296) 60s ribosomal protein L32 [Schizosaccharomyces pombe]

Seq. No.	225885
Seq. ID	LIB3166-044-P1-K1-E9
Method	BLASTX
NCBI GI	g2924784
BLAST score	405
E value	1.0e-39
Match length	127
% identity	30
NCBI Description	(AC002334) similar to jasmonate inducible protein [Arabidopsis thaliana]

Seq. No.	225886
Seq. ID	LIB3166-044-P1-K1-F10
Method	BLASTX
NCBI GI	g3775985
BLAST score	478
E value	3.0e-48
Match length	114
% identity	82
NCBI Description	(AJ010456) RNA helicase [Arabidopsis thaliana]

Seq. No.	225887
Seq. ID	LIB3166-044-P1-K1-F12
Method	BLASTX
NCBI GI	g4204575
BLAST score	383
E value	5.0e-37
Match length	113
% identity	65
NCBI Description	(AF098510) cytochrome b5 DIF-F [Petunia x hybrida]

Seq. No.	225888
Seq. ID	LIB3166-044-P1-K1-F2
Method	BLASTX
NCBI GI	g3913047
BLAST score	206
E value	4.0e-35
Match length	116
% identity	66
NCBI Description	FLORAL HOMEOTIC PROTEIN APETALA1 (MADS C) >gi_1076477_pir__S52236 Saap1 protein - white mustard >gi_609253_emb_CAA57233_ (X81480) Saap1 [Sinapis alba]

Seq. No.	225889
Seq. ID	LIB3166-044-P1-K1-F3
Method	BLASTX
NCBI GI	g728744
BLAST score	442
E value	6.0e-44
Match length	127
% identity	72
NCBI Description	AUXIN-INDUCED PROTEIN PCNT115 >gi_100305_pir__S16390 auxin-induced protein - common tobacco >gi_19799_emb_CAA39708_ (X56267) auxin-induced protein [Nicotiana tabacum]

Seq. No.	225890
Seq. ID	LIB3166-044-P1-K1-F4
Method	BLASTX
NCBI GI	g2282586
BLAST score	339
E value	7.0e-32
Match length	105
% identity	65
NCBI Description	(U82011) methyltransferase [Prunus armeniaca]

Seq. No.	225891
Seq. ID	LIB3166-044-P1-K1-F9
Method	BLASTX
NCBI GI	g3702327
BLAST score	177
E value	6.0e-13
Match length	97
% identity	47
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	225892
Seq. ID	LIB3166-044-P1-K1-G10

Method	BLASTX
NCBI GI	g3885338
BLAST score	228
E value	7.0e-19
Match length	107
% identity	40
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	225893
Seq. ID	LIB3166-044-P1-K1-G11
Method	BLASTX
NCBI GI	g4335720
BLAST score	289
E value	5.0e-26
Match length	121
% identity	43
NCBI Description	(AC006248) putative reverse transcriptase Tal-1 [Arabidopsis thaliana]

Seq. No.	225894
Seq. ID	LIB3166-044-P1-K1-G12
Method	BLASTX
NCBI GI	g4454026
BLAST score	315
E value	4.0e-29
Match length	110
% identity	58
NCBI Description	(AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No.	225895
Seq. ID	LIB3166-044-P1-K1-G2
Method	BLASTX
NCBI GI	g4115373
BLAST score	169
E value	6.0e-12
Match length	129
% identity	6
NCBI Description	(AC005967) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	225896
Seq. ID	LIB3166-044-P1-K1-G5
Method	BLASTX
NCBI GI	g4538913
BLAST score	381
E value	8.0e-37
Match length	94
% identity	78
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

Seq. No.	225897
Seq. ID	LIB3166-044-P1-K1-G6
Method	BLASTX
NCBI GI	g166878
BLAST score	178
E value	5.0e-13
Match length	100

% identity	23
NCBI Description	(M95796) St12p protein [Arabidopsis thaliana]

Seq. No.	225898
Seq. ID	LIB3166-044-P1-K1-G8
Method	BLASTX
NCBI GI	g2505874
BLAST score	561
E value	6.0e-58
Match length	118
% identity	90
NCBI Description	(Y12776) putative kinase [Arabidopsis thaliana]

Seq. No.	225899
Seq. ID	LIB3166-044-P1-K1-G9
Method	BLASTX
NCBI GI	g2078350
BLAST score	571
E value	4.0e-59
Match length	127
% identity	90
NCBI Description	(U95923) transaldolase [Solanum tuberosum]

Seq. No.	225900
Seq. ID	LIB3166-044-P1-K1-H1
Method	BLASTX
NCBI GI	g3024654
BLAST score	543
E value	8.0e-56
Match length	129
% identity	82
NCBI Description	HOMEOBOX PROTEIN SHOOTMERISTEMLESS >gi_2129615_pir__S68456 homeotic protein shootmeristemless - Arabidopsis thaliana >gi_1167916 (U32344) class I knotted-like homeodomain containing protein; Method: conceptual translation supplied by author [Arabidopsis thaliana] >gi_1586022_prf__2202329A homeo domain protein [Arabidopsis thaliana]

Seq. No.	225901
Seq. ID	LIB3166-044-P1-K1-H10
Method	BLASTX
NCBI GI	g3355468
BLAST score	313
E value	2.0e-30
Match length	93
% identity	83
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No.	225902
Seq. ID	LIB3166-044-P1-K1-H11
Method	BLASTX
NCBI GI	g1519241
BLAST score	205
E value	3.0e-25
Match length	80

% identity	74
NCBI Description	(U65890) 10 kDa chaperonin [Brassica napus]

Seq. No.	225903
Seq. ID	LIB3166-044-P1-K1-H12
Method	BLASTX
NCBI GI	g3046696
BLAST score	421
E value	2.0e-41
Match length	106
% identity	72
NCBI Description	(AL022224) CTP synthase like protein [Arabidopsis thaliana]

Seq. No.	225904
Seq. ID	LIB3166-044-P1-K1-H3
Method	BLASTX
NCBI GI	g4510422
BLAST score	170
E value	4.0e-12
Match length	73
% identity	42
NCBI Description	(AC006929) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No.	225905
Seq. ID	LIB3166-044-P1-K1-H4
Method	BLASTX
NCBI GI	g2827559
BLAST score	196
E value	4.0e-15
Match length	59
% identity	66
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana] >gi_3292808_emb_CAA19798_ (AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	225906
Seq. ID	LIB3166-044-P1-K1-H8
Method	BLASTX
NCBI GI	g3914359
BLAST score	577
E value	8.0e-60
Match length	127
% identity	88
NCBI Description	PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi_1928979 (U92656) phospholipase D [Vigna unguiculata]

Seq. No.	225907
Seq. ID	LIB3166-044-P1-K1-H9
Method	BLASTX
NCBI GI	g4567201
BLAST score	545
E value	5.0e-56
Match length	127
% identity	83
NCBI Description	(AC007168) putative aspartate aminotransferase [Arabidopsis

thaliana]

Seq. No.	225908
Seq. ID	LIB3166-045-P1-K1-A1
Method	BLASTX
NCBI GI	g1420887
BLAST score	147
E value	2.0e-09
Match length	86
% identity	35
NCBI Description	(U34334) non-specific lipid transfer-like protein [Phaseolus vulgaris]

Seq. No.	225909
Seq. ID	LIB3166-045-P1-K1-A2
Method	BLASTX
NCBI GI	g2829880
BLAST score	454
E value	1.0e-50
Match length	120
% identity	86
NCBI Description	(AC002396) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]

Seq. No.	225910
Seq. ID	LIB3166-045-P1-K1-A8
Method	BLASTX
NCBI GI	g3510262
BLAST score	134
E value	4.0e-15
Match length	58
% identity	69
NCBI Description	(AC005310) NAM like protein [Arabidopsis thaliana]

Seq. No.	225911
Seq. ID	LIB3166-045-P1-K1-B1
Method	BLASTX
NCBI GI	g1076627
BLAST score	428
E value	2.0e-42
Match length	85
% identity	98
NCBI Description	inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco >gi_790479_emb_CAA58701_ (X83730) inorganic pyrophosphatase [Nicotiana tabacum]

Seq. No.	225912
Seq. ID	LIB3166-045-P1-K1-B12
Method	BLASTX
NCBI GI	g729470
BLAST score	443
E value	4.0e-44
Match length	111
% identity	77
NCBI Description	MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH) >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2)

	precursor, mitochondrial - potato >gi_297798_emb_CAA79702_ (Z21493) mitochondrial formate dehydrogenase precursor [Solanum tuberosum]
Seq. No.	225913
Seq. ID	LIB3166-045-P1-K1-B2
Method	BLASTX
NCBI GI	g2244841
BLAST score	174
E value	1.0e-12
Match length	119
% identity	42
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.	225914
Seq. ID	LIB3166-045-P1-K1-B3
Method	BLASTX
NCBI GI	g3434973
BLAST score	235
E value	9.0e-20
Match length	85
% identity	60
NCBI Description	(AB008106) ethylene responsive element binding factor 4 [Arabidopsis thaliana]
Seq. No.	225915
Seq. ID	LIB3166-045-P1-K1-B5
Method	BLASTX
NCBI GI	g2982303
BLAST score	216
E value	4.0e-33
Match length	122
% identity	59
NCBI Description	(AF051236) hypothetical protein [Picea mariana]
Seq. No.	225916
Seq. ID	LIB3166-045-P1-K1-B8
Method	BLASTX
NCBI GI	g3334323
BLAST score	512
E value	3.0e-52
Match length	124
% identity	83
NCBI Description	GTP-BINDING PROTEIN SAR1A >gi_1314860 (U56929) Sar1 homolog [Arabidopsis thaliana] >gi_2104532_gb_AAC78700.1_ (AF001308) SAR1/GTP-binding secretory factor [Arabidopsis thaliana] >gi_2104550 (AF001535) AGAA.4 [Arabidopsis thaliana]
Seq. No.	225917
Seq. ID	LIB3166-045-P1-K1-C1
Method	BLASTX
NCBI GI	g2511693
BLAST score	300
E value	1.0e-29
Match length	95
% identity	72

NCBI Description	(Z99954) cysteine proteinase precursor [Phaseolus vulgaris]
Seq. No.	225918
Seq. ID	LIB3166-045-P1-K1-C10
Method	BLASTX
NCBI GI	g3033400
BLAST score	206
E value	2.0e-16
Match length	93
% identity	48
NCBI Description	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]
Seq. No.	225919
Seq. ID	LIB3166-045-P1-K1-C11
Method	BLASTX
NCBI GI	g1076758
BLAST score	310
E value	2.0e-28
Match length	74
% identity	89
NCBI Description	heat-shock protein precursor - rye >gi_2130093_pir__S65776 heat-shock protein, 82K, precursor - rye >gi_556673_emb_CAA82945_ (Z30243) heat-shock protein [Secale cereale]
Seq. No.	225920
Seq. ID	LIB3166-045-P1-K1-C3
Method	BLASTX
NCBI GI	g4454015
BLAST score	455
E value	2.0e-45
Match length	121
% identity	39
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]
Seq. No.	225921
Seq. ID	LIB3166-045-P1-K1-C6
Method	BLASTX
NCBI GI	g100196
BLAST score	184
E value	3.0e-25
Match length	97
% identity	67
NCBI Description	chlorophyll a/b-binding protein (cab-11) - tomato
Seq. No.	225922
Seq. ID	LIB3166-045-P1-K1-D2
Method	BLASTX
NCBI GI	g3738257
BLAST score	303
E value	1.0e-27
Match length	65
% identity	92
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	225923
Seq. ID	LIB3166-045-P1-K1-D3
Method	BLASTX
NCBI GI	g1136298
BLAST score	145
E value	4.0e-09
Match length	32
% identity	84
NCBI Description	(D61377) WIPK [Nicotiana tabacum]

Seq. No.	225924
Seq. ID	LIB3166-045-P1-K1-D4
Method	BLASTX
NCBI GI	g2459429
BLAST score	448
E value	1.0e-44
Match length	113
% identity	73
NCBI Description	(AC002332) unknown protein [Arabidopsis thaliana]

Seq. No.	225925
Seq. ID	LIB3166-045-P1-K1-D5
Method	BLASTX
NCBI GI	g3176707
BLAST score	165
E value	2.0e-11
Match length	54
% identity	57
NCBI Description	(AC002392) putative proline-rich protein APG [Arabidopsis thaliana]

Seq. No.	225926
Seq. ID	LIB3166-045-P1-K1-D7
Method	BLASTX
NCBI GI	g3063471
BLAST score	309
E value	2.0e-28
Match length	87
% identity	64
NCBI Description	(AC003981) F22O13.33 [Arabidopsis thaliana]

Seq. No.	225927
Seq. ID	LIB3166-045-P1-K1-E10
Method	BLASTX
NCBI GI	g122006
BLAST score	246
E value	5.0e-21
Match length	73
% identity	67
NCBI Description	HISTONE H2A >gi_81906_pir__JQ1183 histone H2A - garden pea

Seq. No.	225928
Seq. ID	LIB3166-045-P1-K1-E2
Method	BLASTX
NCBI GI	g3550454
BLAST score	352
E value	1.0e-33

Match length	95
% identity	76
NCBI Description	(AF085820) alcohol dehydrogenase A [Gossypium barbadense] >gi_3550458 (AF085821) alcohol dehydrogenase A [Gossypium barbadense] >gi_3551965 (AF085064) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551967 (AF085065) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551971 (AF085067) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551975 (AF085069) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551977 (AF085070) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140594 (AF090146) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140604 (AF090151) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140606 (AF090152) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140608 (AF090153) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140610 (AF090154) alcohol dehydrogenase A [Gossypium hirsutum]

Seq. No.	225929
Seq. ID	LIB3166-045-P1-K1-E5
Method	BLASTX
NCBI GI	g3355480
BLAST score	301
E value	2.0e-27
Match length	86
% identity	65
NCBI Description	(AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No.	225930
Seq. ID	LIB3166-045-P1-K1-E6
Method	BLASTX
NCBI GI	g3128215
BLAST score	183
E value	1.0e-13
Match length	89
% identity	49
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225931
Seq. ID	LIB3166-045-P1-K1-E9
Method	BLASTX
NCBI GI	g2244749
BLAST score	160
E value	2.0e-14
Match length	98
% identity	51
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	225932
Seq. ID	LIB3166-045-P1-K1-F1
Method	BLASTX
NCBI GI	g3047065
BLAST score	214
E value	2.0e-17
Match length	72
% identity	58

NCBI Description	(AF058825) contains similarity to human OS-9 precurosor (GB:U41635) [Arabidopsis thaliana]

Seq. No.	225933
Seq. ID	LIB3166-045-P1-K1-F11
Method	BLASTX
NCBI GI	g3694872
BLAST score	409
E value	4.0e-40
Match length	87
% identity	86
NCBI Description	(AF092547) profilin [Ricinus communis]

Seq. No.	225934
Seq. ID	LIB3166-045-P1-K1-F3
Method	BLASTX
NCBI GI	g2119353
BLAST score	241
E value	2.0e-20
Match length	97
% identity	31
NCBI Description	calmodulin - moss (Physcomitrella patens)

Seq. No.	225935
Seq. ID	LIB3166-045-P1-K1-F4
Method	BLASTX
NCBI GI	g836954
BLAST score	463
E value	2.0e-46
Match length	122
% identity	66
NCBI Description	(U20948) receptor protein kinase [Ipomoea trifida]

Seq. No.	225936
Seq. ID	LIB3166-045-P1-K1-F5
Method	BLASTX
NCBI GI	g2129578
BLAST score	475
E value	7.0e-48
Match length	106
% identity	84
NCBI Description	dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi_1585435_prf__2124427B diamide resistance gene [Arabidopsis thaliana]

Seq. No.	225937
Seq. ID	LIB3166-045-P1-K1-F7
Method	BLASTX
NCBI GI	g3033400
BLAST score	200
E value	9.0e-16
Match length	66
% identity	59
NCBI Description	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	225938
Seq. ID	LIB3166-045-P1-K1-G12
Method	BLASTX
NCBI GI	g3395436
BLAST score	232
E value	2.0e-19
Match length	90
% identity	49
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	225939
Seq. ID	LIB3166-045-P1-K1-G2
Method	BLASTX
NCBI GI	g4417286
BLAST score	346
E value	9.0e-33
Match length	120
% identity	62
NCBI Description	(AC007019) putative shikimate kinase [Arabidopsis thaliana]

Seq. No.	225940
Seq. ID	LIB3166-045-P1-K1-G3
Method	BLASTX
NCBI GI	g2462077
BLAST score	172
E value	2.0e-12
Match length	121
% identity	31
NCBI Description	(Y11871) Oxa1 protein [Arabidopsis thaliana]

Seq. No.	225941
Seq. ID	LIB3166-045-P1-K1-G4
Method	BLASTX
NCBI GI	g1220196
BLAST score	555
E value	3.0e-57
Match length	117
% identity	89
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	225942
Seq. ID	LIB3166-045-P1-K1-G6
Method	BLASTX
NCBI GI	g2104446
BLAST score	137
E value	1.0e-16
Match length	62
% identity	66
NCBI Description	(Z95396) WD-repeat protein [Schizosaccharomyces pombe]

Seq. No.	225943
Seq. ID	LIB3166-045-P1-K1-G8
Method	BLASTX
NCBI GI	g4062934
BLAST score	600
E value	2.0e-62

Match length	121
% identity	90
NCBI Description	(D88272) formate dehydrogenase [Hordeum vulgare]

Seq. No.	225944
Seq. ID	LIB3166-045-P1-K1-H1
Method	BLASTX
NCBI GI	g1220196
BLAST score	527
E value	6.0e-54
Match length	114
% identity	88
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	225945
Seq. ID	LIB3166-045-P1-K1-H12
Method	BLASTX
NCBI GI	g2244847
BLAST score	351
E value	2.0e-33
Match length	122
% identity	57
NCBI Description	(Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No.	225946
Seq. ID	LIB3166-045-P1-K1-H2
Method	BLASTX
NCBI GI	g441457
BLAST score	530
E value	3.0e-54
Match length	99
% identity	98
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]

Seq. No.	225947
Seq. ID	LIB3166-045-P1-K1-H3
Method	BLASTX
NCBI GI	g4490732
BLAST score	336
E value	1.0e-31
Match length	125
% identity	62
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	225948
Seq. ID	LIB3166-045-P1-K1-H8
Method	BLASTX
NCBI GI	g4193388
BLAST score	354
E value	1.0e-33
Match length	87
% identity	80
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	225949
Seq. ID	LIB3166-045-P1-K1-H9
Method	BLASTX
NCBI GI	g3913518
BLAST score	343
E value	2.0e-32
Match length	110
% identity	66
NCBI Description	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE) (DPNPASE) >gi_1103921 (U40433) 3'(2'),5'-bisphosphate nucleotidase [Arabidopsis thaliana]

Seq. No.	225950
Seq. ID	LIB3166-046-P1-K1-A4
Method	BLASTX
NCBI GI	g1353352
BLAST score	321
E value	9.0e-30
Match length	85
% identity	75
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	225951
Seq. ID	LIB3166-046-P1-K1-A5
Method	BLASTX
NCBI GI	g1200256
BLAST score	423
E value	9.0e-42
Match length	106
% identity	74
NCBI Description	(X90990) stpk1 protein kinase [Solanum tuberosum]

Seq. No.	225952
Seq. ID	LIB3166-046-P1-K1-A8
Method	BLASTX
NCBI GI	g4204300
BLAST score	163
E value	3.0e-11
Match length	61
% identity	57
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	225953
Seq. ID	LIB3166-046-P1-K1-B10
Method	BLASTX
NCBI GI	g4049346
BLAST score	266
E value	2.0e-23
Match length	112
% identity	46
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	225954
Seq. ID	LIB3166-046-P1-K1-B2

Method	BLASTX
NCBI GI	g543711
BLAST score	157
E value	1.0e-10
Match length	77
% identity	58
NCBI Description	14-3-3-LIKE PROTEIN S94 >gi_419796_pir__S30927 14-3-3 protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140) brain specific protein [Oryza sativa]

Seq. No.	225955
Seq. ID	LIB3166-046-P1-K1-B4
Method	BLASTX
NCBI GI	g1523800
BLAST score	451
E value	5.0e-45
Match length	110
% identity	77
NCBI Description	(Y07694) MAP kinase kinase alpha protein kinase [Arabidopsis thaliana]

Seq. No.	225956
Seq. ID	LIB3166-046-P1-K1-B5
Method	BLASTX
NCBI GI	g1711512
BLAST score	605
E value	4.0e-63
Match length	128
% identity	91
NCBI Description	SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 2 (SRP54) >gi_1076577_pir__S51598 signal recognition particle 54K protein - tomato (cv. UC82-B) >gi_556902_emb_CAA84288_ (Z34527) 54-kD signal recognition particle (SRP) specific protein [Lycopersicon esculentum]

Seq. No.	225957
Seq. ID	LIB3166-046-P1-K1-C1
Method	BLASTX
NCBI GI	g3318611
BLAST score	205
E value	3.0e-16
Match length	94
% identity	50
NCBI Description	(AB016063) mitochondrial phosphate transporter [Glycine max]

Seq. No.	225958
Seq. ID	LIB3166-046-P1-K1-C12
Method	BLASTX
NCBI GI	g4468813
BLAST score	287
E value	8.0e-26
Match length	119
% identity	43
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	225959

Seq. ID LIB3166-046-P1-K1-D1
Method BLASTX
NCBI GI g4490297
BLAST score 253
E value 8.0e-22
Match length 119
% identity 43
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 225960
Seq. ID LIB3166-046-P1-K1-D10
Method BLASTX
NCBI GI g115492
BLAST score 456
E value 1.0e-45
Match length 89
% identity 51
NCBI Description CALMODULIN-RELATED PROTEIN >gi_169205 (M80831) calmodulin-related protein [Petunia hybrida]

Seq. No. 225961
Seq. ID LIB3166-046-P1-K1-D2
Method BLASTX
NCBI GI g1617272
BLAST score 462
E value 2.0e-46
Match length 127
% identity 71
NCBI Description (Z72151) AMP-binding protein [Brassica napus]

Seq. No. 225962
Seq. ID LIB3166-046-P1-K1-D3
Method BLASTX
NCBI GI g3901012
BLAST score 247
E value 9.0e-44
Match length 101
% identity 79
NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]

Seq. No. 225963
Seq. ID LIB3166-046-P1-K1-D7
Method BLASTX
NCBI GI g1931647
BLAST score 148
E value 1.0e-15
Match length 54
% identity 81
NCBI Description (U95973) endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana]

Seq. No. 225964
Seq. ID LIB3166-046-P1-K1-D9
Method BLASTX
NCBI GI g3063396
BLAST score 462

E value	2.0e-46
Match length	107
% identity	81
NCBI Description	(AB012947) vcCyP [Vicia faba]

Seq. No.	225965
Seq. ID	LIB3166-046-P1-K1-E12
Method	BLASTX
NCBI GI	g4249385
BLAST score	522
E value	2.0e-53
Match length	106
% identity	89
NCBI Description	(AC005966) T2K10.11 [Arabidopsis thaliana]

Seq. No.	225966
Seq. ID	LIB3166-046-P1-K1-E4
Method	BLASTX
NCBI GI	g2695711
BLAST score	200
E value	1.0e-15
Match length	77
% identity	56
NCBI Description	(AJ001370) cytochome b5 [Olea europaea]

Seq. No.	225967
Seq. ID	LIB3166-046-P1-K1-E5
Method	BLASTX
NCBI GI	g2440044
BLAST score	328
E value	7.0e-44
Match length	107
% identity	86
NCBI Description	(AJ001293) major intrinsic protein PIPB [Craterostigma plantagineum]

Seq. No.	225968
Seq. ID	LIB3166-046-P1-K1-E6
Method	BLASTX
NCBI GI	g1209756
BLAST score	247
E value	1.0e-23
Match length	101
% identity	57
NCBI Description	(U43629) integral membrane protein [Beta vulgaris]

Seq. No.	225969
Seq. ID	LIB3166-046-P1-K1-E8
Method	BLASTX
NCBI GI	g3757514
BLAST score	378
E value	1.0e-36
Match length	74
% identity	95
NCBI Description	(AC005167) putative plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	225970
Seq. ID	LIB3166-046-P1-K1-E9
Method	BLASTX
NCBI GI	g1706323
BLAST score	318
E value	2.0e-29
Match length	106
% identity	58
NCBI Description	ORNITHINE DECARBOXYLASE (ODC) >gi_2118242_pir__S64704 ornithine decarboxylase (EC 4.1.1.17) - jimsonweed >gi_871008_emb_CAA61121_ (X87847) ornithine decarboxylase [Datura stramonium]

Seq. No.	225971
Seq. ID	LIB3166-046-P1-K1-F1
Method	BLASTX
NCBI GI	g3522939
BLAST score	276
E value	2.0e-24
Match length	79
% identity	65
NCBI Description	(AC004411) putative squamosa-promoter binding protein [Arabidopsis thaliana]

Seq. No.	225972
Seq. ID	LIB3166-046-P1-K1-F10
Method	BLASTX
NCBI GI	g4104242
BLAST score	197
E value	2.0e-17
Match length	68
% identity	71
NCBI Description	(AF034266) palmitoyl-acyl carrier protein thioesterase [Gossypium hirsutum]

Seq. No.	225973
Seq. ID	LIB3166-046-P1-K1-F12
Method	BLASTX
NCBI GI	g1669341
BLAST score	334
E value	3.0e-31
Match length	127
% identity	52
NCBI Description	(D45066) AOBP (ascorbate oxidase promoter-binding protein) [Cucurbita maxima]

Seq. No.	225974
Seq. ID	LIB3166-046-P1-K1-F5
Method	BLASTX
NCBI GI	g4103324
BLAST score	316
E value	3.0e-29
Match length	67
% identity	96
NCBI Description	(AF022716) GDP-mannose pyrophosphorylase [Solanum tuberosum]

Seq. No.	225975
Seq. ID	LIB3166-046-P1-K1-F6
Method	BLASTX
NCBI GI	g730583
BLAST score	235
E value	1.0e-19
Match length	62
% identity	74
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P2 >gi_551267_emb_CAA55047_ (X78213) 60s acidic ribosomal protein P2 [Parthenium argentatum]

Seq. No.	225976
Seq. ID	LIB3166-046-P1-K1-G10
Method	BLASTX
NCBI GI	g3258569
BLAST score	412
E value	2.0e-40
Match length	104
% identity	82
NCBI Description	(U89959) Similar to yeast general negative regulator of transcription subunit 1 [Arabidopsis thaliana]

Seq. No.	225977
Seq. ID	LIB3166-046-P1-K1-G12
Method	BLASTX
NCBI GI	g3914435
BLAST score	164
E value	1.0e-14
Match length	63
% identity	68
NCBI Description	PROFILIN 1 >gi_3021375_emb_CAA11756_ (AJ223982) profilin [Glycine max]

Seq. No.	225978
Seq. ID	LIB3166-046-P1-K1-G3
Method	BLASTX
NCBI GI	g486784
BLAST score	305
E value	6.0e-28
Match length	126
% identity	50
NCBI Description	Golgi-associated particle 102K chain - human

Seq. No.	225979
Seq. ID	LIB3166-046-P1-K1-G5
Method	BLASTX
NCBI GI	g4220537
BLAST score	250
E value	2.0e-21
Match length	70
% identity	67
NCBI Description	(AL035356) PsRT17-1 like protein [Arabidopsis thaliana]

Seq. No.	225980
Seq. ID	LIB3166-046-P1-K1-G6
Method	BLASTX

NCBI GI	g1710530
BLAST score	571
E value	4.0e-59
Match length	115
% identity	87
NCBI Description	60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256 ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana]

Seq. No.	225981
Seq. ID	LIB3166-046-P1-K1-G7
Method	BLASTX
NCBI GI	g1235559
BLAST score	216
E value	2.0e-17
Match length	113
% identity	43
NCBI Description	(X96639) responsible for hereditary multiple exotosis [Mus musculus]

Seq. No.	225982
Seq. ID	LIB3166-046-P1-K1-H1
Method	BLASTX
NCBI GI	g3747050
BLAST score	425
E value	6.0e-42
Match length	106
% identity	78
NCBI Description	(AF093540) ribosomal protein L26 [Zea mays]

Seq. No.	225983
Seq. ID	LIB3166-046-P1-K1-H5
Method	BLASTX
NCBI GI	g3759184
BLAST score	131
E value	2.0e-10
Match length	128
% identity	34
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	225984
Seq. ID	LIB3166-046-P1-K1-H8
Method	BLASTX
NCBI GI	g3702328
BLAST score	502
E value	4.0e-51
Match length	115
% identity	78
NCBI Description	(AC005397) putative cytochrome b5 [Arabidopsis thaliana]

Seq. No.	225985
Seq. ID	LIB3166-046-P1-K1-H9
Method	BLASTX
NCBI GI	g1255951
BLAST score	436
E value	3.0e-43

Match length	105
% identity	76
NCBI Description	(X96932) PS60 [Nicotiana tabacum]

Seq. No.	225986
Seq. ID	LIB3166-047-P1-K1-A1
Method	BLASTX
NCBI GI	g2764941
BLAST score	396
E value	1.0e-38
Match length	100
% identity	68
NCBI Description	(X98255) transcriptionally stimulated by gibberellins; expressed in meristematic region, and style [Arabidopsis thaliana]

Seq. No.	225987
Seq. ID	LIB3166-047-P1-K1-A2
Method	BLASTX
NCBI GI	g3152603
BLAST score	335
E value	2.0e-31
Match length	128
% identity	47
NCBI Description	(AC004482) unknown protein [Arabidopsis thaliana]

Seq. No.	225988
Seq. ID	LIB3166-047-P1-K1-A3
Method	BLASTX
NCBI GI	g3298502
BLAST score	175
E value	1.0e-12
Match length	113
% identity	41
NCBI Description	(AB015046) xylulokinase [Homo sapiens]

Seq. No.	225989
Seq. ID	LIB3166-047-P1-K1-A5
Method	BLASTX
NCBI GI	g4510375
BLAST score	363
E value	1.0e-34
Match length	114
% identity	65
NCBI Description	(AC007017) putative homeotic protein BEL1 [Arabidopsis thaliana]

Seq. No.	225990
Seq. ID	LIB3166-047-P1-K1-A7
Method	BLASTX
NCBI GI	g3738288
BLAST score	223
E value	3.0e-18
Match length	104
% identity	47
NCBI Description	(AC005309) auxin-responsive GH3-like protein [Arabidopsis thaliana]

Seq. No.	225991
Seq. ID	LIB3166-047-P1-K1-B1
Method	BLASTX
NCBI GI	g1946368
BLAST score	173
E value	2.0e-12
Match length	128
% identity	37
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	225992
Seq. ID	LIB3166-047-P1-K1-B10
Method	BLASTX
NCBI GI	g1906830
BLAST score	151
E value	3.0e-10
Match length	77
% identity	52
NCBI Description	(Y11829) heat shock protein [Arabidopsis thaliana]

Seq. No.	225993
Seq. ID	LIB3166-047-P1-K1-B12
Method	BLASTX
NCBI GI	g1709101
BLAST score	242
E value	2.0e-20
Match length	109
% identity	48
NCBI Description	MRP PROTEIN HOMOLOG >gi_1001155_dbj_BAA10297_ (D64001) put. ATPase [Synechocystis sp.]

Seq. No.	225994
Seq. ID	LIB3166-047-P1-K1-B2
Method	BLASTX
NCBI GI	g3892057
BLAST score	471
E value	2.0e-47
Match length	120
% identity	38
NCBI Description	(AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No.	225995
Seq. ID	LIB3166-047-P1-K1-B3
Method	BLASTX
NCBI GI	g4309698
BLAST score	183
E value	1.0e-13
Match length	74
% identity	47
NCBI Description	(AC006266) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	225996
Seq. ID	LIB3166-047-P1-K1-B4
Method	BLASTX
NCBI GI	g4455184

BLAST score	390
E value	7.0e-38
Match length	124
% identity	62
NCBI Description	(AL035521) extra-large G-protein-like [Arabidopsis thaliana]

Seq. No.	225997
Seq. ID	LIB3166-047-P1-K1-B8
Method	BLASTX
NCBI GI	g131399
BLAST score	160
E value	8.0e-19
Match length	90
% identity	62
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi_82277_pir__S00411 photosystem II 10K protein precursor - potato >gi_21489_emb_CAA28450_ (X04753) ST-LS1 protein [Solanum tuberosum]

Seq. No.	225998
Seq. ID	LIB3166-047-P1-K1-C1
Method	BLASTX
NCBI GI	g731285
BLAST score	164
E value	2.0e-11
Match length	109
% identity	38
NCBI Description	HYPOTHETICAL 27.1 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION >gi_1077483_pir__S51970 hypothetical protein YAL049c - yeast (Saccharomyces cerevisiae) >gi_595535 (U12980) Yal049cp [Saccharomyces cerevisiae]

Seq. No.	225999
Seq. ID	LIB3166-047-P1-K1-C10
Method	BLASTX
NCBI GI	g3367632
BLAST score	159
E value	5.0e-11
Match length	57
% identity	42
NCBI Description	(AJ000539) phosphatidylinositol synthase [Arabidopsis thaliana]

Seq. No.	226000
Seq. ID	LIB3166-047-P1-K1-C2
Method	BLASTX
NCBI GI	g1172664
BLAST score	217
E value	1.0e-17
Match length	47
% identity	91
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_419791_pir__S31165 photosystem I chain III precursor - Flaveria trinervia >gi_298482_bbs_127083 photosystem I

reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi_168173 (M83119) photosystem I subunit III [Flaveria trinervia]

Seq. No.	226001
Seq. ID	LIB3166-047-P1-K1-C3
Method	BLASTX
NCBI GI	g1076748
BLAST score	219
E value	8.0e-18
Match length	76
% identity	28
NCBI Description	major intrinsic protein - rice >gi_440869_dbj_BAA04257_ (D17443) major intrinsic protein [Oryza sativa]

Seq. No.	226002
Seq. ID	LIB3166-047-P1-K1-C4
Method	BLASTX
NCBI GI	g3885884
BLAST score	398
E value	7.0e-54
Match length	127
% identity	77
NCBI Description	(AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No.	226003
Seq. ID	LIB3166-047-P1-K1-C7
Method	BLASTX
NCBI GI	g1171866
BLAST score	373
E value	5.0e-36
Match length	105
% identity	69
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR (COMPLEX I-20KD) (CI-20KD) >gi_629601_pir__S48826 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain PSST - wild cabbage >gi_562282_emb_CAA57725_ (X82274) PSST subunit of NADH: ubiquinone oxidoreductase [Brassica oleracea]

Seq. No.	226004
Seq. ID	LIB3166-047-P1-K1-C8
Method	BLASTX
NCBI GI	g4481934
BLAST score	163
E value	3.0e-11
Match length	105
% identity	14
NCBI Description	(AL035640) CDA peptide synthetase I [Streptomyces coelicolor]

Seq. No.	226005
Seq. ID	LIB3166-047-P1-K1-D1
Method	BLASTX
NCBI GI	g4099914
BLAST score	296
E value	7.0e-27
Match length	81

% identity	73
NCBI Description	(U91857) ethylene-responsive element binding protein homolog [Stylosanthes hamata]

Seq. No.	226006
Seq. ID	LIB3166-047-P1-K1-D11
Method	BLASTX
NCBI GI	g1531758
BLAST score	408
E value	5.0e-40
Match length	81
% identity	86
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	226007
Seq. ID	LIB3166-047-P1-K1-D12
Method	BLASTX
NCBI GI	g4558672
BLAST score	185
E value	7.0e-14
Match length	53
% identity	66
NCBI Description	(AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis thaliana]

Seq. No.	226008
Seq. ID	LIB3166-047-P1-K1-D2
Method	BLASTX
NCBI GI	g3128228
BLAST score	467
E value	6.0e-47
Match length	96
% identity	90
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	226009
Seq. ID	LIB3166-047-P1-K1-D9
Method	BLASTX
NCBI GI	g3024871
BLAST score	372
E value	8.0e-36
Match length	116
% identity	57
NCBI Description	HYPOTHETICAL 77.3 KD PROTEIN SLL0005 >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.]

Seq. No.	226010
Seq. ID	LIB3166-047-P1-K1-E1
Method	BLASTX
NCBI GI	g1632831
BLAST score	442
E value	5.0e-44
Match length	100

% identity	86
NCBI Description	(Z49698) orf [Ricinus communis]
Seq. No.	226011
Seq. ID	LIB3166-047-P1-K1-E10
Method	BLASTX
NCBI GI	g1703375
BLAST score	214
E value	5.0e-37
Match length	107
% identity	87
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]
Seq. No.	226012
Seq. ID	LIB3166-047-P1-K1-E11
Method	BLASTX
NCBI GI	g2832680
BLAST score	435
E value	4.0e-43
Match length	105
% identity	38
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]
Seq. No.	226013
Seq. ID	LIB3166-047-P1-K1-E3
Method	BLASTX
NCBI GI	g2213592
BLAST score	281
E value	4.0e-25
Match length	105
% identity	30
NCBI Description	(AC000348) T7N9.12 [Arabidopsis thaliana]
Seq. No.	226014
Seq. ID	LIB3166-047-P1-K1-E7
Method	BLASTX
NCBI GI	g1827809
BLAST score	361
E value	1.0e-34
Match length	101
% identity	75
NCBI Description	Chain A, Bovine Mitochondrial F1-Atpase Complexed With Aurovertin B >gi_1827810_pdb_1COW_B Chain B, Bovine Mitochondrial F1-Atpase Complexed With Aurovertin B >gi_1827811_pdb_1COW_C Chain C, Bovine Mitochondrial F1-Atpase Complexed With Aurovertin B >gi_1942368_pdb_1EFR_A Chain A, Bovine Mitochondrial F1-Atpase Complexed With The Peptide Antibiotic Efrapeptin >gi_1942369_pdb_1EFR_B Chain B, Bovine Mitochondrial F1-Atpase Complexed With The Peptide Antibiotic Efrapeptin >gi_1942370_pdb_1EFR_C Chain C, Bovine Mitochondrial F1-Atpase Complexed With The Peptide Antibiotic Efrapeptin
Seq. No.	226015
Seq. ID	LIB3166-047-P1-K1-E8
Method	BLASTX

NCBI GI	g3947735
BLAST score	257
E value	2.0e-22
Match length	105
% identity	49
NCBI Description	(AJ009720) NL27 [Solanum tuberosum]

Seq. No.	226016
Seq. ID	LIB3166-047-P1-K1-F12
Method	BLASTX
NCBI GI	g4335722
BLAST score	106
E value	5.0e-10
Match length	109
% identity	47
NCBI Description	(AC006248) hypothetical protein [Arabidopsis thaliana]

Seq. No.	226017
Seq. ID	LIB3166-047-P1-K1-F2
Method	BLASTX
NCBI GI	g2462832
BLAST score	265
E value	3.0e-23
Match length	75
% identity	65
NCBI Description	(AF000657) similar to Bacillus CotA [Arabidopsis thaliana]

Seq. No.	226018
Seq. ID	LIB3166-047-P1-K1-F5
Method	BLASTX
NCBI GI	g4103324
BLAST score	608
E value	2.0e-63
Match length	127
% identity	91
NCBI Description	(AF022716) GDP-mannose pyrophosphorylase [Solanum tuberosum]

Seq. No.	226019
Seq. ID	LIB3166-047-P1-K1-F6
Method	BLASTX
NCBI GI	g2245066
BLAST score	336
E value	1.0e-31
Match length	118
% identity	60
NCBI Description	(Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No.	226020
Seq. ID	LIB3166-047-P1-K1-F8
Method	BLASTX
NCBI GI	g2558654
BLAST score	167
E value	9.0e-12
Match length	87
% identity	47
NCBI Description	(AC002354) No definition line found [Arabidopsis thaliana]

Seq. No.	226021
Seq. ID	LIB3166-047-P1-K1-G1
Method	BLASTX
NCBI GI	g282881
BLAST score	214
E value	3.0e-17
Match length	86
% identity	48
NCBI Description	receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166846 (M84658) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	226022
Seq. ID	LIB3166-047-P1-K1-G10
Method	BLASTX
NCBI GI	g4580575
BLAST score	410
E value	8.0e-42
Match length	125
% identity	67
NCBI Description	(AF082176) auxin response factor 9 [Arabidopsis thaliana]

Seq. No.	226023
Seq. ID	LIB3166-047-P1-K1-G11
Method	BLASTX
NCBI GI	g4033469
BLAST score	286
E value	9.0e-26
Match length	117
% identity	53
NCBI Description	ARGININE/SERINE-RICH SPLICING FACTOR RSP41 >gi_1707370_emb_CAA67799_ (X99436) splicing factor [Arabidopsis thaliana]

Seq. No.	226024
Seq. ID	LIB3166-047-P1-K1-G12
Method	BLASTX
NCBI GI	g2351580
BLAST score	432
E value	7.0e-43
Match length	93
% identity	86
NCBI Description	(U82433) thymidine diphospho-glucose 4-6-dehydratase homolog [Prunus armeniaca]

Seq. No.	226025
Seq. ID	LIB3166-047-P1-K1-G3
Method	BLASTX
NCBI GI	g1171978
BLAST score	547
E value	3.0e-56
Match length	126
% identity	22
NCBI Description	POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) >gi_304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961)

poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	226026
Seq. ID	LIB3166-047-P1-K1-G7
Method	BLASTX
NCBI GI	g829294
BLAST score	273
E value	3.0e-24
Match length	62
% identity	84
NCBI Description	(X67756) ferritin 5 [Vigna unguiculata]

Seq. No.	226027
Seq. ID	LIB3166-047-P1-K1-G9
Method	BLASTX
NCBI GI	g3522933
BLAST score	534
E value	9.0e-55
Match length	110
% identity	92
NCBI Description	(AC004411) putative anion exchange protein 3 [Arabidopsis thaliana]

Seq. No.	226028
Seq. ID	LIB3166-047-P1-K1-H1
Method	BLASTX
NCBI GI	g267122
BLAST score	442
E value	6.0e-44
Match length	104
% identity	78
NCBI Description	THIOREDOXIN H-TYPE (TRX-H) >gi_478400_pir__JQ2242 thioredoxin h - Arabidopsis thaliana >gi_16552_emb_CAA78462_ (Z14084) Thioredoxin H [Arabidopsis thaliana] >gi_1388080 (U35827) thioredoxin h [Arabidopsis thaliana]

Seq. No.	226029
Seq. ID	LIB3166-047-P1-K1-H10
Method	BLASTX
NCBI GI	g3687652
BLAST score	590
E value	2.0e-61
Match length	126
% identity	90
NCBI Description	(AF047352) rubisco activase precursor [Datisca glomerata]

Seq. No.	226030
Seq. ID	LIB3166-047-P1-K1-H12
Method	BLASTX
NCBI GI	g3821280
BLAST score	559
E value	1.0e-57
Match length	116
% identity	88
NCBI Description	(AJ009952) asparagine synthetase type II [Phaseolus vulgaris]

Seq. No.	226031
Seq. ID	LIB3166-047-P1-K1-H4
Method	BLASTX
NCBI GI	g2494264
BLAST score	247
E value	4.0e-21
Match length	97
% identity	52
NCBI Description	HYPOTHETICAL 66.0 KD GTP-BINDING PROTEIN SLR1105 >gi_1651837_dbj_BAA16764_ (D90900) elongation factor EF-G [Synechocystis sp.]

Seq. No.	226032
Seq. ID	LIB3166-047-P1-K1-H5
Method	BLASTX
NCBI GI	g2832672
BLAST score	450
E value	6.0e-45
Match length	110
% identity	80
NCBI Description	(AL021712) nifU-like protein [Arabidopsis thaliana]

Seq. No.	226033
Seq. ID	LIB3166-047-P1-K1-H6
Method	BLASTX
NCBI GI	g2662415
BLAST score	173
E value	2.0e-12
Match length	56
% identity	54
NCBI Description	(U97494) metallothionein-like protein [Prunus armeniaca]

Seq. No.	226034
Seq. ID	LIB3166-047-P1-K1-H9
Method	BLASTX
NCBI GI	g4545262
BLAST score	259
E value	2.0e-22
Match length	61
% identity	72
NCBI Description	(AF118230) metallothionein-like protein [Gossypium hirsutum]

Seq. No.	226035
Seq. ID	LIB3166-048-P1-K1-A11
Method	BLASTX
NCBI GI	g728905
BLAST score	283
E value	2.0e-25
Match length	128
% identity	48
NCBI Description	PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC RETICULUM CA2+-ATPASE) >gi_1078206_pir__S51995 probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae) >gi_171114 (L01795) ATPase [Saccharomyces cerevisiae] >gi_595560 (U12980) Drs2p: Membrane spanning

Ca-ATPase(P-type), member of the cation transport(E1-E2) ATPase [Saccharomyces cerevisiae]

Seq. No.	226036
Seq. ID	LIB3166-048-P1-K1-A12
Method	BLASTX
NCBI GI	g1531758
BLAST score	455
E value	2.0e-45
Match length	92
% identity	87
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	226037
Seq. ID	LIB3166-048-P1-K1-A3
Method	BLASTX
NCBI GI	g2979688
BLAST score	192
E value	1.0e-14
Match length	43
% identity	93
NCBI Description	(AF035619) pyridoxine biosynthesis protein [Cercospora nicotianae]

Seq. No.	226038
Seq. ID	LIB3166-048-P1-K1-A5
Method	BLASTX
NCBI GI	g4559330
BLAST score	285
E value	1.0e-25
Match length	127
% identity	47
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	226039
Seq. ID	LIB3166-048-P1-K1-A7
Method	BLASTX
NCBI GI	g3355468
BLAST score	375
E value	3.0e-36
Match length	103
% identity	79
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No.	226040
Seq. ID	LIB3166-048-P1-K1-A9
Method	BLASTX
NCBI GI	g3785986
BLAST score	231
E value	9.0e-20
Match length	52
% identity	83
NCBI Description	(AC005560) RGA1 protein [Arabidopsis thaliana]

Seq. No. 226041

Seq. ID	LIB3166-048-P1-K1-B10
Method	BLASTX
NCBI GI	g3023858
BLAST score	612
E value	6.0e-64
Match length	120
% identity	50
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_1256608 (U44850) G protein beta subunit [Glycine max]

Seq. No.	226042
Seq. ID	LIB3166-048-P1-K1-B11
Method	BLASTX
NCBI GI	g3560170
BLAST score	523
E value	2.0e-53
Match length	129
% identity	79
NCBI Description	(AL031525) 26s protease regulatory subunit S10b [Schizosaccharomyces pombe]

Seq. No.	226043
Seq. ID	LIB3166-048-P1-K1-B4
Method	BLASTX
NCBI GI	g4204265
BLAST score	461
E value	3.0e-46
Match length	123
% identity	69
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	226044
Seq. ID	LIB3166-048-P1-K1-B8
Method	BLASTX
NCBI GI	g1477428
BLAST score	533
E value	1.0e-54
Match length	119
% identity	84
NCBI Description	(X99623) alpha-tubulin 1 [Hordeum vulgare]

Seq. No.	226045
Seq. ID	LIB3166-048-P1-K1-C1
Method	BLASTX
NCBI GI	g1498053
BLAST score	459
E value	6.0e-46
Match length	125
% identity	74
NCBI Description	(U64436) ribosomal protein S8 [Zea mays]

Seq. No.	226046
Seq. ID	LIB3166-048-P1-K1-C11
Method	BLASTX
NCBI GI	g3328122
BLAST score	436

E value	2.0e-43
Match length	94
% identity	95
NCBI Description	(AF073473) phosphoglycerate kinase precursor [Solanum tuberosum]

Seq. No.	226047
Seq. ID	LIB3166-048-P1-K1-C12
Method	BLASTX
NCBI GI	g1084372
BLAST score	561
E value	6.0e-58
Match length	120
% identity	91
NCBI Description	glyceraldehyde-3-phosphate dehydrogenase (NADP+) (EC 1.2.1.9) - garden pea

Seq. No.	226048
Seq. ID	LIB3166-048-P1-K1-C4
Method	BLASTX
NCBI GI	g3201615
BLAST score	306
E value	5.0e-28
Match length	94
% identity	65
NCBI Description	(AC004669) unknown protein [Arabidopsis thaliana]

Seq. No.	226049
Seq. ID	LIB3166-048-P1-K1-C9
Method	BLASTX
NCBI GI	g3868758
BLAST score	202
E value	4.0e-16
Match length	92
% identity	45
NCBI Description	(D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No.	226050
Seq. ID	LIB3166-048-P1-K1-D12
Method	BLASTX
NCBI GI	g543650
BLAST score	275
E value	2.0e-24
Match length	69
% identity	68
NCBI Description	P48h-10 protein precursor - Zinnia elegans (cv. Envy)

Seq. No.	226051
Seq. ID	LIB3166-048-P1-K1-D2
Method	BLASTX
NCBI GI	g4103635
BLAST score	192
E value	1.0e-14
Match length	97
% identity	45
NCBI Description	(AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. No.	226052
Seq. ID	LIB3166-048-P1-K1-D4
Method	BLASTX
NCBI GI	g4263711
BLAST score	410
E value	3.0e-40
Match length	121
% identity	64
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	226053
Seq. ID	LIB3166-048-P1-K1-E1
Method	BLASTX
NCBI GI	g2702270
BLAST score	309
E value	2.0e-28
Match length	100
% identity	63
NCBI Description	(AC003033) unknown protein [Arabidopsis thaliana]

Seq. No.	226054
Seq. ID	LIB3166-048-P1-K1-E2
Method	BLASTX
NCBI GI	g3421087
BLAST score	425
E value	6.0e-42
Match length	87
% identity	98
NCBI Description	(AF043524) 20S proteasome subunit PAE1 [Arabidopsis thaliana]

Seq. No.	226055
Seq. ID	LIB3166-048-P1-K1-E3
Method	BLASTX
NCBI GI	g4559382
BLAST score	157
E value	1.0e-10
Match length	70
% identity	47
NCBI Description	(AC006526) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	226056
Seq. ID	LIB3166-048-P1-K1-E9
Method	BLASTX
NCBI GI	g4204265
BLAST score	268
E value	1.0e-23
Match length	99
% identity	56
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	226057
Seq. ID	LIB3166-048-P1-K1-F1
Method	BLASTX
NCBI GI	g4539423

BLAST score	513
E value	3.0e-52
Match length	124
% identity	78
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	226058
Seq. ID	LIB3166-048-P1-K1-F3
Method	BLASTX
NCBI GI	g1702983
BLAST score	237
E value	6.0e-20
Match length	85
% identity	54
NCBI Description	AUXIN-REPRESSED 12.5 KD PROTEIN >gi_99855_pir__S11850 hypothetical protein - garden strawberry >gi_22573_emb_CAA36676_ (X52429) 12.5 kDa protein [Fragaria x ananassa] >gi_927034 (L44142) auxin-repressed protein [Fragaria ananassa]

Seq. No.	226059
Seq. ID	LIB3166-048-P1-K1-G10
Method	BLASTX
NCBI GI	g2213877
BLAST score	545
E value	5.0e-56
Match length	107
% identity	95
NCBI Description	(AF003197) glutamine synthetase [Hevea brasiliensis]

Seq. No.	226060
Seq. ID	LIB3166-048-P1-K1-G12
Method	BLASTX
NCBI GI	g1621268
BLAST score	489
E value	2.0e-49
Match length	121
% identity	71
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	226061
Seq. ID	LIB3166-048-P1-K1-G2
Method	BLASTX
NCBI GI	g3153207
BLAST score	174
E value	1.0e-12
Match length	124
% identity	39
NCBI Description	(AF001949) ATHB-12 [Arabidopsis thaliana]

Seq. No.	226062
Seq. ID	LIB3166-048-P1-K1-G3
Method	BLASTX
NCBI GI	g3024871
BLAST score	191
E value	2.0e-14

Match length	116
% identity	36
NCBI Description	HYPOTHETICAL 77.3 KD PROTEIN SLL0005 >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.]

Seq. No.	226063
Seq. ID	LIB3166-048-P1-K1-G4
Method	BLASTX
NCBI GI	g1946367
BLAST score	110
E value	1.0e-10
Match length	53
% identity	68
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	226064
Seq. ID	LIB3166-048-P1-K1-G5
Method	BLASTX
NCBI GI	g1838976
BLAST score	165
E value	2.0e-11
Match length	78
% identity	54
NCBI Description	(X73635) vsf-1 [Lycopersicon esculentum]

Seq. No.	226065
Seq. ID	LIB3166-048-P1-K1-G9
Method	BLASTX
NCBI GI	g2494034
BLAST score	163
E value	6.0e-21
Match length	89
% identity	58
NCBI Description	DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG KINASE 1) >gi_2129573_pir__S71467 diacylglycerol kinase - Arabidopsis thaliana >gi_1374772_dbj_BAA09856_ (D63787) diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	226066
Seq. ID	LIB3166-048-P1-K1-H10
Method	BLASTX
NCBI GI	g4545262
BLAST score	239
E value	4.0e-20
Match length	44
% identity	100
NCBI Description	(AF118230) metallothionein-like protein [Gossypium hirsutum]

Seq. No.	226067
Seq. ID	LIB3166-048-P1-K1-H11
Method	BLASTX
NCBI GI	g1362009
BLAST score	480
E value	2.0e-48
Match length	119

% identity	51
NCBI Description	ubiquitin-like protein 7 - Arabidopsis thaliana

Seq. No.	226068
Seq. ID	LIB3166-048-P1-K1-H2
Method	BLASTX
NCBI GI	g4128133
BLAST score	274
E value	3.0e-24
Match length	119
% identity	45
NCBI Description	(AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]

Seq. No.	226069
Seq. ID	LIB3166-048-P1-K1-H5
Method	BLASTX
NCBI GI	g1351408
BLAST score	207
E value	2.0e-16
Match length	61
% identity	66
NCBI Description	VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) >gi_1076563_pir__S51117 cystein proteinase - sweet orange >gi_633185_emb_CAA87720_ (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi_1588548_prf__2208463A vascular processing protease [Citrus sinensis]

Seq. No.	226070
Seq. ID	LIB3166-048-P1-K1-H7
Method	BLASTX
NCBI GI	g3024148
BLAST score	313
E value	5.0e-29
Match length	77
% identity	79
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi_1655580_emb_CAA95858_ (Z71273) S-adenosyl-L-methionine synthetase 3 [Catharanthus roseus]

Seq. No.	226071
Seq. ID	LIB3166-049-P1-K1-A10
Method	BLASTX
NCBI GI	g3953471
BLAST score	271
E value	2.0e-24
Match length	74
% identity	68
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No.	226072
Seq. ID	LIB3166-049-P1-K1-A12
Method	BLASTX
NCBI GI	g2541876
BLAST score	219
E value	2.0e-18
Match length	110

% identity	52
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	226073
Seq. ID	LIB3166-049-P1-K1-A2
Method	BLASTX
NCBI GI	g1943751
BLAST score	458
E value	6.0e-46
Match length	103
% identity	85
NCBI Description	(U93845) Arabidopsis thaliana ER-type calcium pump protein, complete sequence >gi_2078292 (U96455) ER-type Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]

Seq. No.	226074
Seq. ID	LIB3166-049-P1-K1-A4
Method	BLASTX
NCBI GI	g4056432
BLAST score	432
E value	7.0e-43
Match length	113
% identity	68
NCBI Description	(AC005990) Similar to gi_2245014 glucosyltransferase homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97341. ESTs gb_T20778 and gb_AA586281 come from this gene. [Arabidopsis thaliana]

Seq. No.	226075
Seq. ID	LIB3166-049-P1-K1-A5
Method	BLASTX
NCBI GI	g3953471
BLAST score	116
E value	6.0e-11
Match length	65
% identity	62
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No.	226076
Seq. ID	LIB3166-049-P1-K1-A7
Method	BLASTX
NCBI GI	g1263291
BLAST score	311
E value	1.0e-28
Match length	60
% identity	98
NCBI Description	(U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No.	226077
Seq. ID	LIB3166-049-P1-K1-A9
Method	BLASTX
NCBI GI	g3184289
BLAST score	189
E value	2.0e-14
Match length	44
% identity	80

NCBI Description (AC004136) hypothetical protein [Arabidopsis thaliana]

Seq. No. 226078
Seq. ID LIB3166-049-P1-K1-B1
Method BLASTX
NCBI GI g2245094
BLAST score 168
E value 5.0e-20
Match length 80
% identity 65
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 226079
Seq. ID LIB3166-049-P1-K1-B10
Method BLASTX
NCBI GI g220838
BLAST score 204
E value 4.0e-16
Match length 118
% identity 40
NCBI Description (D10655) dihydrolipoamide acetyltransferase [Rattus rattus]

Seq. No. 226080
Seq. ID LIB3166-049-P1-K1-B11
Method BLASTX
NCBI GI g4538967
BLAST score 414
E value 9.0e-41
Match length 109
% identity 77
NCBI Description (AL049488) major intrinsic protein (MIP)-like [Arabidopsis thaliana]

Seq. No. 226081
Seq. ID LIB3166-049-P1-K1-B12
Method BLASTX
NCBI GI g2497702
BLAST score 173
E value 2.0e-12
Match length 121
% identity 36
NCBI Description OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR >gi_2121019_pir__I40710 outer membrane lipoprotein - Citrobacter freundii >gi_717136 (U21727) lipocalin precursor [Citrobacter freundii]

Seq. No. 226082
Seq. ID LIB3166-049-P1-K1-B3
Method BLASTX
NCBI GI g3759184
BLAST score 300
E value 2.0e-27
Match length 97
% identity 59
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 226083

Seq. ID	LIB3166-049-P1-K1-B7
Method	BLASTX
NCBI GI	g2245125
BLAST score	163
E value	2.0e-11
Match length	45
% identity	64
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	226084
Seq. ID	LIB3166-049-P1-K1-B9
Method	BLASTX
NCBI GI	g2465012
BLAST score	410
E value	4.0e-42
Match length	107
% identity	88
NCBI Description	(AJ001447) caffeoyl-CoA 3-O-methyltransferase [Fragaria vesca]

Seq. No.	226085
Seq. ID	LIB3166-049-P1-K1-C11
Method	BLASTX
NCBI GI	g4098128
BLAST score	388
E value	2.0e-41
Match length	109
% identity	83
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	226086
Seq. ID	LIB3166-049-P1-K1-C3
Method	BLASTX
NCBI GI	g2500550
BLAST score	147
E value	2.0e-09
Match length	48
% identity	62
NCBI Description	RIBONUCLEASE III (RNASE III) >gi_2313785_gb_AAD07725.1_ (AE000579) ribonuclease III (rnc) [Helicobacter pylori 26695]

Seq. No.	226087
Seq. ID	LIB3166-049-P1-K1-C4
Method	BLASTX
NCBI GI	g710308
BLAST score	163
E value	8.0e-12
Match length	47
% identity	68
NCBI Description	(U11693) victorin binding protein [Avena sativa]

Seq. No.	226088
Seq. ID	LIB3166-049-P1-K1-C6
Method	BLASTX
NCBI GI	g4102600
BLAST score	418

E value	3.0e-41
Match length	117
% identity	74
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]

Seq. No.	226089
Seq. ID	LIB3166-049-P1-K1-C7
Method	BLASTX
NCBI GI	g2462822
BLAST score	447
E value	1.0e-44
Match length	123
% identity	51
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	226090
Seq. ID	LIB3166-049-P1-K1-D1
Method	BLASTX
NCBI GI	g1086252
BLAST score	422
E value	1.0e-41
Match length	104
% identity	73
NCBI Description	sucrose cleavage protein - Potato >gi_707001_bbs_157931 (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa] [Solanum tuberosum]

Seq. No.	226091
Seq. ID	LIB3166-049-P1-K1-D11
Method	BLASTX
NCBI GI	g1439609
BLAST score	536
E value	5.0e-55
Match length	106
% identity	100
NCBI Description	(U62778) delta-tonoplast intrinsic protein [Gossypium hirsutum]

Seq. No.	226092
Seq. ID	LIB3166-049-P1-K1-D12
Method	BLASTX
NCBI GI	g3377803
BLAST score	235
E value	1.0e-19
Match length	63
% identity	73
NCBI Description	(AF075597) Similár to (p)ppGpp synthetase; T2H3.9 [Arabidopsis thaliana]

Seq. No.	226093
Seq. ID	LIB3166-049-P1-K1-D3
Method	BLASTX
NCBI GI	g4056469
BLAST score	631
E value	4.0e-66
Match length	125

% identity	99
NCBI Description	(AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967, gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t
Seq. No.	226094
Seq. ID	LIB3166-049-P1-K1-D4
Method	BLASTX
NCBI GI	g2213594
BLAST score	337
E value	1.0e-31
Match length	90
% identity	67
NCBI Description	(AC000348) T7N9.14 [Arabidopsis thaliana]
Seq. No.	226095
Seq. ID	LIB3166-049-P1-K1-D5
Method	BLASTX
NCBI GI	g584825
BLAST score	255
E value	3.0e-42
Match length	103
% identity	81
NCBI Description	B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus carota]
Seq. No.	226096
Seq. ID	LIB3166-049-P1-K1-E1
Method	BLASTX
NCBI GI	g3482977
BLAST score	245
E value	2.0e-22
Match length	102
% identity	62
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]
Seq. No.	226097
Seq. ID	LIB3166-049-P1-K1-E11
Method	BLASTX
NCBI GI	g99735
BLAST score	203
E value	3.0e-16
Match length	74
% identity	53
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)
Seq. No.	226098
Seq. ID	LIB3166-049-P1-K1-E12
Method	BLASTX
NCBI GI	g3023847
BLAST score	304
E value	2.0e-31
Match length	98

% identity	78
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta subunit-like [Medicago sativa]

Seq. No.	226099
Seq. ID	LIB3166-049-P1-K1-E2
Method	BLASTX
NCBI GI	g4544443
BLAST score	131
E value	7.0e-12
Match length	53
% identity	73
NCBI Description	(AC006592) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	226100
Seq. ID	LIB3166-049-P1-K1-E4
Method	BLASTX
NCBI GI	g1332579
BLAST score	316
E value	4.0e-36
Match length	98
% identity	9
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	226101
Seq. ID	LIB3166-049-P1-K1-E7
Method	BLASTX
NCBI GI	g3540181
BLAST score	181
E value	2.0e-13
Match length	80
% identity	47
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	226102
Seq. ID	LIB3166-049-P1-K1-F1
Method	BLASTX
NCBI GI	g2144271
BLAST score	195
E value	1.0e-15
Match length	68
% identity	59
NCBI Description	trans-cinnamate 4-monooxygenase (EC 1.14.13.11) C - Populus kitakamiensis (fragment) >gi_1777372_dbj_BAA11578_ (D82814) cinnamic acid 4-hydroxylase [Populus kitakamiensis]

Seq. No.	226103
Seq. ID	LIB3166-049-P1-K1-F2
Method	BLASTX
NCBI GI	g421855
BLAST score	331
E value	4.0e-31
Match length	107
% identity	68
NCBI Description	alanine--tRNA ligase (EC 6.1.1.7) - Arabidopsis thaliana

(fragment)

Seq. No.	226104
Seq. ID	LIB3166-049-P1-K1-F3
Method	BLASTX
NCBI GI	g3158474
BLAST score	392
E value	4.0e-38
Match length	99
% identity	78
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]

Seq. No.	226105
Seq. ID	LIB3166-049-P1-K1-F5
Method	BLASTX
NCBI GI	g136636
BLAST score	216
E value	2.0e-17
Match length	41
% identity	100
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	226106
Seq. ID	LIB3166-049-P1-K1-F8
Method	BLASTX
NCBI GI	g399900
BLAST score	230
E value	2.0e-23
Match length	91
% identity	68
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT5 (HD-ZIP PROTEIN 5) (HD-ZIP PROTEIN ATHB-1) >gi_99659_pir__S16325 homeotic protein Athb-1 - Arabidopsis thaliana >gi_16329_emb_CAA41625_ (X58821) Athb-1 protein [Arabidopsis thaliana]

Seq. No.	226107
Seq. ID	LIB3166-049-P1-K1-G10
Method	BLASTX
NCBI GI	g4538959
BLAST score	384
E value	3.0e-37
Match length	92
% identity	76
NCBI Description	(AL049488) putative protein [Arabidopsis thaliana]

Seq. No.	226108
Seq. ID	LIB3166-049-P1-K1-G11
Method	BLASTX

NCBI GI	g2230757
BLAST score	215
E value	1.0e-17
Match length	84
% identity	55
NCBI Description	(Y11969) dnaJ-like protein [Arabidopsis thaliana]

Seq. No.	226109
Seq. ID	LIB3166-049-P1-K1-G4
Method	BLASTX
NCBI GI	g886116
BLAST score	193
E value	6.0e-15
Match length	42
% identity	79
NCBI Description	(U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473 (AF051338) xyloglucan endotransglycosylase related protein [Arabidopsis thaliana]

Seq. No.	226110
Seq. ID	LIB3166-049-P1-K1-G5
Method	BLASTX
NCBI GI	g3080442
BLAST score	408
E value	6.0e-40
Match length	104
% identity	67
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	226111
Seq. ID	LIB3166-049-P1-K1-H10
Method	BLASTX
NCBI GI	g399046
BLAST score	147
E value	6.0e-10
Match length	37
% identity	76
NCBI Description	ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_99657_pir__S20867 adenine phosphoribosyltransferase (EC 2.4.2.7) - Arabidopsis thaliana >gi_16164_emb_CAA41497_ (X58640) adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi_433050 (L19637) adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi_3935182 (AC004557) F17L21.25 [Arabidopsis thaliana]

Seq. No.	226112
Seq. ID	LIB3166-049-P1-K1-H11
Method	BLASTX
NCBI GI	g2494034
BLAST score	636
E value	1.0e-66
Match length	129
% identity	88
NCBI Description	DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG KINASE 1) >gi_2129573_pir__S71467 diacylglycerol kinase - Arabidopsis thaliana >gi_1374772_dbj_BAA09856_ (D63787) diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	226113
Seq. ID	LIB3166-049-P1-K1-H2
Method	BLASTX
NCBI GI	g3901012
BLAST score	304
E value	4.0e-35
Match length	112
% identity	71
NCBI Description	(AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]

Seq. No.	226114
Seq. ID	LIB3166-049-P1-K1-H6
Method	BLASTX
NCBI GI	g4454484
BLAST score	270
E value	8.0e-24
Match length	88
% identity	61
NCBI Description	(AC006234) putative diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	226115
Seq. ID	LIB3166-049-P1-K1-H7
Method	BLASTX
NCBI GI	g2832625
BLAST score	208
E value	1.0e-16
Match length	54
% identity	72
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	226116
Seq. ID	LIB3166-050-P1-K1-A12
Method	BLASTX
NCBI GI	g1352821
BLAST score	466
E value	8.0e-47
Match length	90
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.	226117
Seq. ID	LIB3166-050-P1-K1-A2
Method	BLASTX
NCBI GI	g1172571
BLAST score	530
E value	2.0e-54
Match length	99
% identity	97
NCBI Description	PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP) >gi_1076277_pir__S52637 phosphoenolpyruvate carboxykinase

(ATP) (EC 4.1.1.49) - cucumber >gi_567102 (L31899) phosphoenolpyruvate carboxykinase [Cucumis sativus]

Seq. No.	226118
Seq. ID	LIB3166-050-P1-K1-A3
Method	BLASTX
NCBI GI	g1086989
BLAST score	583
E value	2.0e-60
Match length	123
% identity	95
NCBI Description	(S79323) plasma membrane H(+)-ATPase [Vicia faba, Otafuku, abaxial epidermis, guard cell protoplasts, Peptide, 963 aa] [Vicia faba]

Seq. No.	226119
Seq. ID	LIB3166-050-P1-K1-A5
Method	BLASTX
NCBI GI	g1345787
BLAST score	464
E value	1.0e-46
Match length	92
% identity	93
NCBI Description	CHALCONE SYNTHASE 2 (NARINGENIN-CHALCONE SYNTHASE 2) >gi_567937_dbj_BAA05641_ (D26594) chalcone synthase [Camellia sinensis]

Seq. No.	226120
Seq. ID	LIB3166-050-P1-K1-A9
Method	BLASTX
NCBI GI	g1703375
BLAST score	270
E value	6.0e-24
Match length	80
% identity	75
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]

Seq. No.	226121
Seq. ID	LIB3166-050-P1-K1-B2
Method	BLASTX
NCBI GI	g4033467
BLAST score	389
E value	8.0e-38
Match length	121
% identity	43
NCBI Description	ARGININE/SERINE-RICH SPLICING FACTOR RSP31 >gi_1707366_emb_CAA67798_ (X99435) splicing factor [Arabidopsis thaliana]

Seq. No.	226122
Seq. ID	LIB3166-050-P1-K1-B3
Method	BLASTX
NCBI GI	g416664
BLAST score	572
E value	3.0e-59
Match length	121

% identity	89
NCBI Description	PLASMA MEMBRANE ATPASE 4 (PROTON PUMP) >gi_485504_pir__S33548 H+-transporting ATPase (EC 3.6.1.35) type 4, plasma membrane - curled-leaved tobacco >gi_19704_emb_CAA47275_ (X66737) plasma membrane H+-ATPase [Nicotiana plumbaginifolia]

Seq. No.	226123
Seq. ID	LIB3166-050-P1-K1-C10
Method	BLASTX
NCBI GI	g2244732
BLAST score	595
E value	6.0e-62
Match length	120
% identity	92
NCBI Description	(D88413) endo-xyloglucan transferase [Gossypium hirsutum]

Seq. No.	226124
Seq. ID	LIB3166-050-P1-K1-C11
Method	BLASTX
NCBI GI	g3766368
BLAST score	122
E value	1.0e-13
Match length	73
% identity	53
NCBI Description	(AL031907) putative trascription factor, ccr4-associated factor homolog [Schizosaccharomyces pombe]

Seq. No.	226125
Seq. ID	LIB3166-050-P1-K1-C2
Method	BLASTX
NCBI GI	g1200256
BLAST score	454
E value	2.0e-45
Match length	96
% identity	89
NCBI Description	(X90990) stpk1 protein kinase [Solanum tuberosum]

Seq. No.	226126
Seq. ID	LIB3166-050-P1-K1-C6
Method	BLASTX
NCBI GI	g3193284
BLAST score	533
E value	1.0e-54
Match length	122
% identity	87
NCBI Description	(AF069298) No definition line found [Arabidopsis thaliana]

Seq. No.	226127
Seq. ID	LIB3166-050-P1-K1-C7
Method	BLASTX
NCBI GI	g4432857
BLAST score	189
E value	3.0e-17
Match length	96
% identity	50
NCBI Description	(AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No.	226128
Seq. ID	LIB3166-050-P1-K1-D1
Method	BLASTX
NCBI GI	g3980393
BLAST score	371
E value	1.0e-35
Match length	104
% identity	65
NCBI Description	(AC004561) putative glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	226129
Seq. ID	LIB3166-050-P1-K1-D10
Method	BLASTX
NCBI GI	g2262100
BLAST score	465
E value	9.0e-47
Match length	97
% identity	89
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	226130
Seq. ID	LIB3166-050-P1-K1-D12
Method	BLASTX
NCBI GI	g4539351
BLAST score	407
E value	6.0e-40
Match length	113
% identity	61
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	226131
Seq. ID	LIB3166-050-P1-K1-D2
Method	BLASTX
NCBI GI	g416651
BLAST score	191
E value	9.0e-15
Match length	74
% identity	51
NCBI Description	PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN PCNT103) >gi_100301_pir__S16269 auxin-induced protein (clone pCNT103) - common tobacco >gi_19791_emb_CAA39704_ (X56263) auxin-induced protein [Nicotiana tabacum]

Seq. No.	226132
Seq. ID	LIB3166-050-P1-K1-E12
Method	BLASTX
NCBI GI	g2739381
BLAST score	375
E value	4.0e-36
Match length	120
% identity	62
NCBI Description	(AC002505) putative patatin [Arabidopsis thaliana]

Seq. No.	226133
Seq. ID	LIB3166-050-P1-K1-E5

Method	BLASTX
NCBI GI	g1616616
BLAST score	261
E value	8.0e-23
Match length	50
% identity	98
NCBI Description	(Y08424) small GTP-binding protein [Nicotiana plumbaginifolia]

Seq. No.	226134
Seq. ID	LIB3166-050-P1-K1-F11
Method	BLASTX
NCBI GI	g2335104
BLAST score	234
E value	7.0e-20
Match length	85
% identity	56
NCBI Description	(AC002339) putative villin [Arabidopsis thaliana]

Seq. No.	226135
Seq. ID	LIB3166-050-P1-K1-F12
Method	BLASTX
NCBI GI	g2792240
BLAST score	179
E value	3.0e-13
Match length	78
% identity	47
NCBI Description	(AF032698) NBS-LRR type resistance protein [Oryza sativa]

Seq. No.	226136
Seq. ID	LIB3166-050-P1-K1-F3
Method	BLASTX
NCBI GI	g114335
BLAST score	549
E value	1.0e-56
Match length	113
% identity	94
NCBI Description	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >gi_166629 (J05570) H+-ATPase [Arabidopsis thaliana]

Seq. No.	226137
Seq. ID	LIB3166-050-P1-K1-F7
Method	BLASTX
NCBI GI	g120669
BLAST score	399
E value	6.0e-39
Match length	89
% identity	85
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	226138

Seq. ID	LIB3166-050-P1-K1-G1
Method	BLASTX
NCBI GI	g2961375
BLAST score	159
E value	8.0e-11
Match length	51
% identity	55
NCBI Description	(AL022141) NAM like protein [Arabidopsis thaliana]

Seq. No.	226139
Seq. ID	LIB3166-050-P1-K1-G10
Method	BLASTX
NCBI GI	g3236254
BLAST score	224
E value	2.0e-18
Match length	118
% identity	40
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	226140
Seq. ID	LIB3166-050-P1-K1-G11
Method	BLASTX
NCBI GI	g124224
BLAST score	468
E value	4.0e-47
Match length	113
% identity	82
NCBI Description	INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) >gi_100345_pir__S21060 translation initiation factor eIF-5A - common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No.	226141
Seq. ID	LIB3166-050-P1-K1-G3
Method	BLASTX
NCBI GI	g123580
BLAST score	351
E value	2.0e-33
Match length	109
% identity	67
NCBI Description	17.9 KD CLASS II HEAT SHOCK PROTEIN >gi_81787_pir__S01859 heat shock protein 17.9-D - soybean >gi_18652_emb_CAA30153_ (X07159) hsp17.9-D protein (AA 1 - 159) [Glycine max]

Seq. No.	226142
Seq. ID	LIB3166-050-P1-K1-G7
Method	BLASTX
NCBI GI	g1703446
BLAST score	305
E value	5.0e-28
Match length	96
% identity	67
NCBI Description	L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE) >gi_1076292_pir__S53127 asparaginase - Arabidopsis thaliana >gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis thaliana]

Seq. No.	226143
Seq. ID	LIB3166-050-P1-K1-G9
Method	BLASTX
NCBI GI	g3236254
BLAST score	289
E value	4.0e-26
Match length	120
% identity	48
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	226144
Seq. ID	LIB3166-050-P1-K1-H11
Method	BLASTX
NCBI GI	g1169382
BLAST score	394
E value	2.0e-42
Match length	105
% identity	81
NCBI Description	DNAJ PROTEIN HOMOLOG 2 >gi_542196_pir__S42031 LDJ2 protein - leek >gi_454303_emb_CAA54720_ (X77632) LDJ2 [Allium porrum]

Seq. No.	226145
Seq. ID	LIB3166-050-P1-K1-H2
Method	BLASTX
NCBI GI	g2706450
BLAST score	507
E value	1.0e-51
Match length	116
% identity	84
NCBI Description	(AJ225172) magnesium dependent soluble inorganic pyrophosphatase [Solanum tuberosum]

Seq. No.	226146
Seq. ID	LIB3166-050-P1-K1-H3
Method	BLASTX
NCBI GI	g3914442
BLAST score	463
E value	2.0e-46
Match length	107
% identity	83
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No.	226147
Seq. ID	LIB3166-050-P1-K1-H6
Method	BLASTX
NCBI GI	g3702339
BLAST score	184
E value	9.0e-14
Match length	77
% identity	48
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	226148
Seq. ID	LIB3166-050-P1-K1-H7

Method	BLASTX
NCBI GI	g3702339
BLAST score	184
E value	9.0e-14
Match length	70
% identity	54
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	226149
Seq. ID	LIB3166-050-P1-K1-H9
Method	BLASTX
NCBI GI	g3549680
BLAST score	152
E value	3.0e-10
Match length	51
% identity	59
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	226150
Seq. ID	LIB3166-051-P1-K1-A1
Method	BLASTX
NCBI GI	g2832359
BLAST score	268
E value	1.0e-23
Match length	120
% identity	51
NCBI Description	(Y14072) HMG protein [Arabidopsis thaliana]

Seq. No.	226151
Seq. ID	LIB3166-051-P1-K1-A11
Method	BLASTX
NCBI GI	g1297359
BLAST score	497
E value	2.0e-50
Match length	129
% identity	72
NCBI Description	(U53701) alcohol dehydrogenase 2d [Gossypium hirsutum]

Seq. No.	226152
Seq. ID	LIB3166-051-P1-K1-A8
Method	BLASTX
NCBI GI	g2462745
BLAST score	199
E value	3.0e-20
Match length	93
% identity	53
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	226153
Seq. ID	LIB3166-051-P1-K1-A9
Method	BLASTX
NCBI GI	g1172872
BLAST score	256
E value	2.0e-22
Match length	87
% identity	63
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718

	drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]
Seq. No.	226154
Seq. ID	LIB3166-051-P1-K1-B10
Method	BLASTX
NCBI GI	g1263291
BLAST score	595
E value	7.0e-62
Match length	130
% identity	83
NCBI Description	(U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]
Seq. No.	226155
Seq. ID	LIB3166-051-P1-K1-B11
Method	BLASTX
NCBI GI	g2529229
BLAST score	308
E value	1.0e-42
Match length	101
% identity	91
NCBI Description	(AB007907) 6-phosphogluconate dehydrogenase [Glycine max]
Seq. No.	226156
Seq. ID	LIB3166-051-P1-K1-B2
Method	BLASTX
NCBI GI	g2267153
BLAST score	277
E value	6.0e-25
Match length	65
% identity	80
NCBI Description	(AF009050) alcohol dehydrogenase 1A [Paeonia lactiflora]
Seq. No.	226157
Seq. ID	LIB3166-051-P1-K1-B3
Method	BLASTX
NCBI GI	g1049255
BLAST score	146
E value	2.0e-18
Match length	71
% identity	79
NCBI Description	(U36437) H+-pyrophosphatase [Zea mays]
Seq. No.	226158
Seq. ID	LIB3166-051-P1-K1-B8
Method	BLASTX
NCBI GI	g2769642
BLAST score	230
E value	4.0e-19
Match length	55
% identity	82
NCBI Description	(Z97215) nine-cis-epoxycarotenoid dioxygenase [Lycopersicon esculentum]

Seq. No.	226159
Seq. ID	LIB3166-051-P1-K1-C1
Method	BLASTX
NCBI GI	g3335341
BLAST score	348
E value	6.0e-33
Match length	118
% identity	64
NCBI Description	(AC004512) T8F5.10 [Arabidopsis thaliana]

Seq. No.	226160
Seq. ID	LIB3166-051-P1-K1-C11
Method	BLASTX
NCBI GI	g3834304
BLAST score	330
E value	8.0e-31
Match length	85
% identity	78
NCBI Description	(AC005679) Contains similarity to gi_1786244 hypothetical 24.9 kD protein in surA-hepA intergenic region yab0 from Escherichia coli genome gb_AE000116, and to hypothetical YABO family PF_00849. [Arabidopsis thaliana]

Seq. No.	226161
Seq. ID	LIB3166-051-P1-K1-C12
Method	BLASTX
NCBI GI	g2131525
BLAST score	146
E value	3.0e-09
Match length	95
% identity	34
NCBI Description	hypothetical protein YDR489w - yeast (Saccharomyces cerevisiae) >gi_927735 (U33050) Ydr489wp; CAI: 0.16 [Saccharomyces cerevisiae]

Seq. No.	226162
Seq. ID	LIB3166-051-P1-K1-C2
Method	BLASTX
NCBI GI	g3551983
BLAST score	508
E value	8.0e-52
Match length	107
% identity	91
NCBI Description	(AF085073) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551985 (AF085074) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551987 (AF085075) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551989 (AF085076) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140602 (AF090150) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140612 (AF090155) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140614 (AF090156) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140616 (AF090157) alcohol dehydrogenase A [Gossypium hirsutum]

Seq. No.	226163
Seq. ID	LIB3166-051-P1-K1-C3
Method	BLASTX

NCBI GI g4098129
BLAST score 592
E value 1.0e-61
Match length 126
% identity 90
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]

Seq. No. 226164
Seq. ID LIB3166-051-P1-K1-C5
Method BLASTX
NCBI GI g2833381
BLAST score 619
E value 1.0e-64
Match length 125
% identity 90
NCBI Description GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi_1172159 (U44126) starch synthase [Ipomoea batatas]

Seq. No. 226165
Seq. ID LIB3166-051-P1-K1-C6
Method BLASTX
NCBI GI g1934730
BLAST score 139
E value 1.0e-08
Match length 39
% identity 62
NCBI Description (U95036) germin-like protein [Arabidopsis thaliana]

Seq. No. 226166
Seq. ID LIB3166-051-P1-K1-C7
Method BLASTX
NCBI GI g2104681
BLAST score 316
E value 3.0e-29
Match length 126
% identity 56
NCBI Description (X97907) transcription factor [Vicia faba]

Seq. No. 226167
Seq. ID LIB3166-051-P1-K1-C8
Method BLASTX
NCBI GI g505482
BLAST score 460
E value 4.0e-46
Match length 117
% identity 80
NCBI Description (X64349) 33 kDa polypeptide of water-oxidizing complex of photosystem II [Nicotiana tabacum]

Seq. No. 226168
Seq. ID LIB3166-051-P1-K1-C9
Method BLASTX
NCBI GI g1220196
BLAST score 436
E value 3.0e-43
Match length 105
% identity 76

NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	226169
Seq. ID	LIB3166-051-P1-K1-D1
Method	BLASTX
NCBI GI	g2829862
BLAST score	209
E value	1.0e-16
Match length	118
% identity	41
NCBI Description	(AC002396) Similar to glucosyltransferases [Arabidopsis thaliana]

Seq. No.	226170
Seq. ID	LIB3166-051-P1-K1-D12
Method	BLASTX
NCBI GI	g1928981
BLAST score	145
E value	9.0e-21
Match length	76
% identity	74
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	226171
Seq. ID	LIB3166-051-P1-K1-D3
Method	BLASTX
NCBI GI	g2708624
BLAST score	589
E value	3.0e-61
Match length	110
% identity	93
NCBI Description	(AF036618) acetyl-CoA synthetase [Arabidopsis thaliana]

Seq. No.	226172
Seq. ID	LIB3166-051-P1-K1-D6
Method	BLASTX
NCBI GI	g115834
BLAST score	212
E value	5.0e-24
Match length	85
% identity	71
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN CP24 10B PRECURSOR (CAB-10B) (LHCP) >gi_100202_pir__S11878 chlorophyll a/b-binding protein Cab10B - tomato >gi_170400 (M32606) chlorophyll b-binding protein [Lycopersicon esculentum]

Seq. No.	226173
Seq. ID	LIB3166-051-P1-K1-E1
Method	BLASTX
NCBI GI	g4262226
BLAST score	298
E value	4.0e-27
Match length	101
% identity	60
NCBI Description	(AC006200) putative protein kinase [Arabidopsis thaliana]

Seq. No.	226174
Seq. ID	LIB3166-051-P1-K1-E7
Method	BLASTX
NCBI GI	g3122785
BLAST score	242
E value	8.0e-21
Match length	68
% identity	74
NCBI Description	40S RIBOSOMAL PROTEIN S14 >gi_2565340 (AF026079) ribosomal protein S14 [Lupinus luteus]

Seq. No.	226175
Seq. ID	LIB3166-051-P1-K1-E8
Method	BLASTX
NCBI GI	g479413
BLAST score	386
E value	2.0e-37
Match length	128
% identity	66
NCBI Description	myosin-like protein - Arabidopsis thaliana

Seq. No.	226176
Seq. ID	LIB3166-051-P1-K1-F10
Method	BLASTX
NCBI GI	g2130051
BLAST score	157
E value	9.0e-11
Match length	61
% identity	54
NCBI Description	xylose isomerase (EC 5.3.1.5) - barley >gi_1296807_emb_CAA64544_ (X95256) xylose isomerase [Hordeum vulgare] >gi_1588664_prf__2209268A xylose isomerase [Hordeum vulgare]

Seq. No.	226177
Seq. ID	LIB3166-051-P1-K1-F9
Method	BLASTX
NCBI GI	g1771160
BLAST score	531
E value	2.0e-54
Match length	128
% identity	79
NCBI Description	(X98929) SBT1 [Lycopersicon esculentum] >gi_3687305_emb_CAA06999_ (AJ006378) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	226178
Seq. ID	LIB3166-051-P1-K1-G2
Method	BLASTX
NCBI GI	g3377941
BLAST score	160
E value	3.0e-11
Match length	86
% identity	43
NCBI Description	(AL021960) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	226179
Seq. ID	LIB3166-051-P1-K1-G4
Method	BLASTX
NCBI GI	g2244998
BLAST score	483
E value	9.0e-49
Match length	121
% identity	72
NCBI Description	(Z97341) similarity to probable transcriptional adaptor ADA2 [Arabidopsis thaliana]

Seq. No.	226180
Seq. ID	LIB3166-051-P1-K1-G5
Method	BLASTX
NCBI GI	g4544409
BLAST score	471
E value	2.0e-47
Match length	125
% identity	63
NCBI Description	(AC006955) putative transcription factor [Arabidopsis thaliana]

Seq. No.	226181
Seq. ID	LIB3166-051-P1-K1-G6
Method	BLASTX
NCBI GI	g2191187
BLAST score	190
E value	2.0e-14
Match length	76
% identity	49
NCBI Description	(AF007271) contains similarity to a DNAJ-like domain [Arabidopsis thaliana]

Seq. No.	226182
Seq. ID	LIB3166-051-P1-K1-G7
Method	BLASTX
NCBI GI	g4150963
BLAST score	225
E value	1.0e-18
Match length	97
% identity	46
NCBI Description	(Y18620) DsPTP1 protein [Arabidopsis thaliana]

Seq. No.	226183
Seq. ID	LIB3166-051-P1-K1-G9
Method	BLASTX
NCBI GI	g113362
BLAST score	228
E value	5.0e-23
Match length	69
% identity	68
NCBI Description	ALCOHOL DEHYDROGENASE 1 (SLOW-ALLELE) >gi_65901_pir__DEILSP alcohol dehydrogenase (EC 1.1.1.1) 1-S - pearl millet >gi_20409_emb_CAA34547_ (X16547) alcohol dehydrogenase (AA 1-379) [Pennisetum americanum]

Seq. No.	226184

Seq. ID	LIB3166-051-P1-K1-H1
Method	BLASTX
NCBI GI	g3062801
BLAST score	525
E value	9.0e-54
Match length	119
% identity	78
NCBI Description	(AB012873) arginine decarboxylase [Nicotiana sylvestris]

Seq. No.	226185
Seq. ID	LIB3166-051-P1-K1-H12
Method	BLASTX
NCBI GI	g3153902
BLAST score	364
E value	7.0e-35
Match length	95
% identity	79
NCBI Description	(AF066076) 14-3-3-like protein [Helianthus annuus]

Seq. No.	226186
Seq. ID	LIB3166-051-P1-K1-H2
Method	BLASTX
NCBI GI	g134101
BLAST score	507
E value	1.0e-51
Match length	125
% identity	85
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_72958_pir__HHCSBA ribulose-bisphosphate carboxylase subunit-binding protein alpha chain - castor bean (fragment)

Seq. No.	226187
Seq. ID	LIB3166-051-P1-K1-H8
Method	BLASTX
NCBI GI	g2661422
BLAST score	261
E value	9.0e-23
Match length	66
% identity	79
NCBI Description	(AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi_3096936_emb_CAA18846.1_ (AL023094) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana]

Seq. No.	226188
Seq. ID	LIB3166-052-P1-K1-A1
Method	BLASTX
NCBI GI	g1174592
BLAST score	278
E value	4.0e-25
Match length	72
% identity	79
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	226189
Seq. ID	LIB3166-052-P1-K1-A12
Method	BLASTX
NCBI GI	g3158474
BLAST score	295
E value	9.0e-27
Match length	75
% identity	80
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]

Seq. No.	226190
Seq. ID	LIB3166-052-P1-K1-A4
Method	BLASTX
NCBI GI	g2245136
BLAST score	297
E value	5.0e-33
Match length	112
% identity	66
NCBI Description	(Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana]

Seq. No.	226191
Seq. ID	LIB3166-052-P1-K1-A7
Method	BLASTX
NCBI GI	g4164408
BLAST score	602
E value	9.0e-63
Match length	123
% identity	88
NCBI Description	(AJ132228) amino acid carrier [Ricinus communis]

Seq. No.	226192
Seq. ID	LIB3166-052-P1-K1-A8
Method	BLASTX
NCBI GI	g1346524
BLAST score	489
E value	1.0e-49
Match length	103
% identity	92
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi_497900 (M73430) S-adenosyl methionine synthetase [Populus deltoides]

Seq. No.	226193
Seq. ID	LIB3166-052-P1-K1-A9
Method	BLASTX
NCBI GI	g1354849
BLAST score	184
E value	8.0e-14
Match length	59
% identity	64
NCBI Description	(U57350) epoxide hydrolase [Nicotiana tabacum]

Seq. No.	226194
Seq. ID	LIB3166-052-P1-K1-B10

Method	BLASTX
NCBI GI	g445612
BLAST score	492
E value	7.0e-50
Match length	104
% identity	91
NCBI Description	ribosomal protein S19 [Solanum tuberosum]

Seq. No.	226195
Seq. ID	LIB3166-052-P1-K1-B11
Method	BLASTX
NCBI GI	g2072626
BLAST score	293
E value	2.0e-26
Match length	79
% identity	71
NCBI Description	(Y12904) hypothetical protein [Arabidopsis thaliana] >gi_3281856_emb_CAA19751_ (AL031004) Transcription factor II homolog [Arabidopsis thaliana]

Seq. No.	226196
Seq. ID	LIB3166-052-P1-K1-B12
Method	BLASTX
NCBI GI	g2129944
BLAST score	326
E value	2.0e-30
Match length	84
% identity	73
NCBI Description	RNA-binding protein RZ-1 - wood tobacco >gi_1395193_dbj_BAA12064_ (D83696) RNA-binding protein RZ-1 [Nicotiana sylvestris] >gi_1435062_dbj_BAA06012_ (D28861) RNA binding protein, RZ-1 [Nicotiana sylvestris]

Seq. No.	226197
Seq. ID	LIB3166-052-P1-K1-B2
Method	BLASTX
NCBI GI	g2708744
BLAST score	245
E value	6.0e-24
Match length	121
% identity	52
NCBI Description	(AC003952) putative Bop-like zinc finger protein [Arabidopsis thaliana]

Seq. No.	226198
Seq. ID	LIB3166-052-P1-K1-B5
Method	BLASTX
NCBI GI	g4457221
BLAST score	167
E value	9.0e-12
Match length	45
% identity	89
NCBI Description	(AF127797) putative bZIP DNA-binding protein [Capsicum chinense]

Seq. No.	226199
Seq. ID	LIB3166-052-P1-K1-B7

Method	BLASTX
NCBI GI	g4105696
BLAST score	449
E value	8.0e-45
Match length	116
% identity	78
NCBI Description	(AF049870) beta tubulin 1 [Arabidopsis thaliana]

Seq. No.	226200
Seq. ID	LIB3166-052-P1-K1-B8
Method	BLASTX
NCBI GI	g2511574
BLAST score	414
E value	9.0e-41
Match length	90
% identity	94
NCBI Description	(Y13176) multicatalytic endopeptidase [Arabidopsis thaliana] >gi_3421075 (AF043520) 20S proteasome subunit PAB1 [Arabidopsis thaliana]

Seq. No.	226201
Seq. ID	LIB3166-052-P1-K1-B9
Method	BLASTX
NCBI GI	g116923
BLAST score	421
E value	1.0e-41
Match length	123
% identity	66
NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi_111414_pir__S13520 beta-COP protein - rat >gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus norvegicus]

Seq. No.	226202
Seq. ID	LIB3166-052-P1-K1-C1
Method	BLASTX
NCBI GI	g2088662
BLAST score	145
E value	3.0e-09
Match length	48
% identity	56
NCBI Description	(AF002109) unknown protein [Arabidopsis thaliana]

Seq. No.	226203
Seq. ID	LIB3166-052-P1-K1-C11
Method	BLASTX
NCBI GI	g4164408
BLAST score	450
E value	6.0e-45
Match length	99
% identity	85
NCBI Description	(AJ132228) amino acid carrier [Ricinus communis]

Seq. No.	226204
Seq. ID	LIB3166-052-P1-K1-C12
Method	BLASTX
NCBI GI	g3850111

BLAST score	163
E value	3.0e-11
Match length	51
% identity	55
NCBI Description	(AL033388) hypothetical integral membrane protein, putative involvement in lipid metabolism [Schizosaccharomyces pombe]

Seq. No.	226205
Seq. ID	LIB3166-052-P1-K1-C3
Method	BLASTX
NCBI GI	g1843527
BLAST score	167
E value	9.0e-12
Match length	36
% identity	89
NCBI Description	(U73747) annexin [Gossypium hirsutum]

Seq. No.	226206
Seq. ID	LIB3166-052-P1-K1-C7
Method	BLASTX
NCBI GI	g2832677
BLAST score	278
E value	9.0e-25
Match length	103
% identity	50
NCBI Description	(AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No.	226207
Seq. ID	LIB3166-052-P1-K1-C8
Method	BLASTX
NCBI GI	g1843527
BLAST score	517
E value	5.0e-55
Match length	115
% identity	57
NCBI Description	(U73747) annexin [Gossypium hirsutum]

Seq. No.	226208
Seq. ID	LIB3166-052-P1-K1-C9
Method	BLASTX
NCBI GI	g4580460
BLAST score	215
E value	1.0e-30
Match length	81
% identity	91
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No.	226209
Seq. ID	LIB3166-052-P1-K1-D10
Method	BLASTX
NCBI GI	g3434973
BLAST score	253
E value	8.0e-22
Match length	76
% identity	71
NCBI Description	(AB008106) ethylene responsive element binding factor 4

[Arabidopsis thaliana]

Seq. No.	226210
Seq. ID	LIB3166-052-P1-K1-D12
Method	BLASTX
NCBI GI	g3885338
BLAST score	202
E value	5.0e-16
Match length	61
% identity	57
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	226211
Seq. ID	LIB3166-052-P1-K1-D2
Method	BLASTX
NCBI GI	g4510363
BLAST score	434
E value	5.0e-43
Match length	92
% identity	90
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	226212
Seq. ID	LIB3166-052-P1-K1-D3
Method	BLASTX
NCBI GI	g1403024
BLAST score	215
E value	2.0e-17
Match length	82
% identity	55
NCBI Description	(Z54163) hnRNP protein [Chironomus tentans]

Seq. No.	226213
Seq. ID	LIB3166-052-P1-K1-D4
Method	BLASTX
NCBI GI	g4165323
BLAST score	600
E value	2.0e-62
Match length	125
% identity	88
NCBI Description	(AB022442) p-type H+-ATPase [Vicia faba]

Seq. No.	226214
Seq. ID	LIB3166-052-P1-K1-D6
Method	BLASTX
NCBI GI	g2764574
BLAST score	347
E value	8.0e-33
Match length	102
% identity	68
NCBI Description	(AJ001009) pore protein of 24 kD (OEP24) [Pisum sativum]

Seq. No.	226215
Seq. ID	LIB3166-052-P1-K1-D8
Method	BLASTX
NCBI GI	g832876

BLAST score	483
E value	8.0e-49
Match length	100
% identity	94
NCBI Description	(L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi_1097368_prf__2113407A ascorbate free radical reductase [Lycopersicon esculentum]

Seq. No.	226216
Seq. ID	LIB3166-052-P1-K1-D9
Method	BLASTX
NCBI GI	g3695384
BLAST score	203
E value	5.0e-16
Match length	60
% identity	62
NCBI Description	(AF096370) contains similarity to the helix-loop-helix DNA-binding domain (Pfam: PF00010 HLH, E-value: 0.0046) [Arabidopsis thaliana]

Seq. No.	226217
Seq. ID	LIB3166-052-P1-K1-E10
Method	BLASTX
NCBI GI	g2493146
BLAST score	355
E value	8.0e-34
Match length	89
% identity	53
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_755148 (U13669) vacuolar H+-ATPase proteolipid (16 kDa) subunit [Gossypium hirsutum] >gi_4519415_dbj_BAA75542.1_ (AB024275) vacuolar H+-ATPase c subunit [Citrus unshiu]

Seq. No.	226218
Seq. ID	LIB3166-052-P1-K1-E12
Method	BLASTX
NCBI GI	g2129715
BLAST score	225
E value	2.0e-18
Match length	99
% identity	42
NCBI Description	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta25 (fragment)

Seq. No.	226219
Seq. ID	LIB3166-052-P1-K1-E3
Method	BLASTX
NCBI GI	g3661603
BLAST score	124
E value	1.0e-10
Match length	74
% identity	57
NCBI Description	(AF092841) ribonucleoside-diphosphate reductase large subunit [Arabidopsis thaliana]

Seq. No.	226220
Seq. ID	LIB3166-052-P1-K1-E5

Method	BLASTX
NCBI GI	g4102727
BLAST score	144
E value	5.0e-09
Match length	75
% identity	43
NCBI Description	(AF015782) blight-associated protein p12 precursor [Citrus jambhiri]

Seq. No.	226221
Seq. ID	LIB3166-052-P1-K1-E6
Method	BLASTX
NCBI GI	g349379
BLAST score	421
E value	2.0e-41
Match length	128
% identity	75
NCBI Description	(L22847) HAHB-1 [Helianthus annuus]

Seq. No.	226222
Seq. ID	LIB3166-052-P1-K1-E8
Method	BLASTX
NCBI GI	g3063396
BLAST score	444
E value	3.0e-44
Match length	103
% identity	81
NCBI Description	(AB012947) vcCyP [Vicia faba]

Seq. No.	226223
Seq. ID	LIB3166-052-P1-K1-E9
Method	BLASTX
NCBI GI	g3281846
BLAST score	144
E value	4.0e-09
Match length	112
% identity	32
NCBI Description	(AJ006404) late elongated hypocotyl [Arabidopsis thaliana]

Seq. No.	226224
Seq. ID	LIB3166-052-P1-K1-F10
Method	BLASTX
NCBI GI	g1363325
BLAST score	328
E value	7.0e-31
Match length	83
% identity	72
NCBI Description	RNA helicase HEL117 - rat >gi_897915 (U25746) RNA helicase [Rattus norvegicus]

Seq. No.	226225
Seq. ID	LIB3166-052-P1-K1-F11
Method	BLASTX
NCBI GI	g4538905
BLAST score	529
E value	3.0e-54
Match length	126

% identity	79
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

Seq. No.	226226
Seq. ID	LIB3166-052-P1-K1-F12
Method	BLASTX
NCBI GI	g2764941
BLAST score	369
E value	2.0e-35
Match length	93
% identity	69
NCBI Description	(X98255) transcriptionally stimulated by gibberellins; expressed in meristematic region, and style [Arabidopsis thaliana]

Seq. No.	226227
Seq. ID	LIB3166-052-P1-K1-F2
Method	BLASTX
NCBI GI	g3702332
BLAST score	270
E value	8.0e-24
Match length	90
% identity	62
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	226228
Seq. ID	LIB3166-052-P1-K1-F3
Method	BLASTX
NCBI GI	g3341685
BLAST score	270
E value	8.0e-24
Match length	86
% identity	67
NCBI Description	(AC003672) unknown protein [Arabidopsis thaliana]

Seq. No.	226229
Seq. ID	LIB3166-052-P1-K1-F5
Method	BLASTX
NCBI GI	g2213867
BLAST score	261
E value	1.0e-45
Match length	127
% identity	77
NCBI Description	(AF003124) fructose-biphosphate aldolase [Mesembryanthemum crystallinum]

Seq. No.	226230
Seq. ID	LIB3166-052-P1-K1-F7
Method	BLASTX
NCBI GI	g3334322
BLAST score	429
E value	2.0e-42
Match length	83
% identity	96
NCBI Description	GTP-BINDING PROTEIN SAR1B >gi_2108347 (U55036) small GTP-binding protein Bsar1b [Brassica rapa]

Seq. No.	226231
Seq. ID	LIB3166-052-P1-K1-F9
Method	BLASTX
NCBI GI	g399046
BLAST score	284
E value	1.0e-25
Match length	106
% identity	54
NCBI Description	ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_99657_pir__S20867 adenine phosphoribosyltransferase (EC 2.4.2.7) - Arabidopsis thaliana >gi_16164_emb_CAA41497_ (X58640) adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi_433050 (L19637) adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi_3935182 (AC004557) F17L21.25 [Arabidopsis thaliana]

Seq. No.	226232
Seq. ID	LIB3166-052-P1-K1-G1
Method	BLASTX
NCBI GI	g3281858
BLAST score	222
E value	3.0e-18
Match length	50
% identity	86
NCBI Description	(AL031004) ribosomal protein S6 - like [Arabidopsis thaliana]

Seq. No.	226233
Seq. ID	LIB3166-052-P1-K1-G11
Method	BLASTX
NCBI GI	g1763063
BLAST score	221
E value	5.0e-18
Match length	101
% identity	49
NCBI Description	(U68763) SCOF-1 [Glycine max]

Seq. No.	226234
Seq. ID	LIB3166-052-P1-K1-G12
Method	BLASTX
NCBI GI	g951427
BLAST score	559
E value	1.0e-57
Match length	120
% identity	88
NCBI Description	(M59857) stearoyl-acyl-carrier protein desaturase [Ricinus communis]

Seq. No.	226235
Seq. ID	LIB3166-052-P1-K1-G2
Method	BLASTX
NCBI GI	g4574320
BLAST score	239
E value	3.0e-20
Match length	74
% identity	69
NCBI Description	(AF117224) wound-induced protein WI12 [Mesembryanthemum

crystallinum]

Seq. No.	226236
Seq. ID	LIB3166-052-P1-K1-G3
Method	BLASTX
NCBI GI	g3643603
BLAST score	245
E value	4.0e-26
Match length	116
% identity	54
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	226237
Seq. ID	LIB3166-052-P1-K1-G4
Method	BLASTX
NCBI GI	g3831444
BLAST score	398
E value	8.0e-39
Match length	109
% identity	72
NCBI Description	(AC005819) putative protein kinase [Arabidopsis thaliana]

Seq. No.	226238
Seq. ID	LIB3166-052-P1-K1-G6
Method	BLASTX
NCBI GI	g3283072
BLAST score	374
E value	5.0e-36
Match length	124
% identity	62
NCBI Description	(AF056022) p60 katanin [Homo sapiens]

Seq. No.	226239
Seq. ID	LIB3166-052-P1-K1-G7
Method	BLASTX
NCBI GI	g2245005
BLAST score	298
E value	3.0e-27
Match length	77
% identity	81
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	226240
Seq. ID	LIB3166-052-P1-K1-G9
Method	BLASTX
NCBI GI	g3868758
BLAST score	465
E value	1.0e-46
Match length	122
% identity	70
NCBI Description	(D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No.	226241
Seq. ID	LIB3166-052-P1-K1-H1
Method	BLASTX
NCBI GI	g3882081
BLAST score	613

09604804.960304

E value	5.0e-64
Match length	124
% identity	33
NCBI Description	(AJ012552) polyubiquitin [Vicia faba]

Seq. No.	226242
Seq. ID	LIB3166-052-P1-K1-H10
Method	BLASTX
NCBI GI	g3183088
BLAST score	240
E value	2.0e-20
Match length	70
% identity	64
NCBI Description	PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer like protein [Vigna unguiculata]

Seq. No.	226243
Seq. ID	LIB3166-052-P1-K1-H12
Method	BLASTX
NCBI GI	g136636
BLAST score	568
E value	9.0e-59
Match length	107
% identity	97
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	226244
Seq. ID	LIB3166-052-P1-K1-H2
Method	BLASTX
NCBI GI	g3095075
BLAST score	179
E value	4.0e-13
Match length	113
% identity	37
NCBI Description	(AF031471) pollen allergen [Juniperus oxycedrus]

Seq. No.	226245
Seq. ID	LIB3166-052-P1-K1-H4
Method	BLASTX
NCBI GI	g1330399
BLAST score	169
E value	6.0e-12
Match length	77
% identity	44
NCBI Description	(U58762) coded for by C. elegans cDNA yk27e9.5; coded for by C. elegans cDNA yk27e9.3 [Caenorhabditis elegans]

Seq. No.	226246
Seq. ID	LIB3166-052-P1-K1-H6
Method	BLASTX
NCBI GI	g3426043
BLAST score	368
E value	3.0e-35
Match length	120
% identity	62
NCBI Description	(AC005168) putative choline kinase [Arabidopsis thaliana]

Seq. No.	226247
Seq. ID	LIB3166-052-P1-K1-H8
Method	BLASTX
NCBI GI	g3540181
BLAST score	187
E value	3.0e-14
Match length	59
% identity	56
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	226248
Seq. ID	LIB3166-053-P1-K1-A10
Method	BLASTX
NCBI GI	g3785989
BLAST score	462
E value	2.0e-46
Match length	104
% identity	86
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	226249
Seq. ID	LIB3166-053-P1-K1-A12
Method	BLASTX
NCBI GI	g4415931
BLAST score	222
E value	4.0e-18
Match length	99
% identity	51
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana] >gi_4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	226250
Seq. ID	LIB3166-053-P1-K1-A2
Method	BLASTX
NCBI GI	g3540181
BLAST score	148
E value	1.0e-09
Match length	91
% identity	44
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	226251
Seq. ID	LIB3166-053-P1-K1-A6
Method	BLASTX
NCBI GI	g144985
BLAST score	175

E value	1.0e-12
Match length	120
% identity	29
NCBI Description	(M25819) phosphoenolpyruvate carboxylase [Corynebacterium glutamicum]

Seq. No.	226252
Seq. ID	LIB3166-053-P1-K1-A7
Method	BLASTX
NCBI GI	g441457
BLAST score	277
E value	7.0e-25
Match length	66
% identity	79
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]

Seq. No.	226253
Seq. ID	LIB3166-053-P1-K1-A8
Method	BLASTX
NCBI GI	g2662341
BLAST score	565
E value	2.0e-58
Match length	120
% identity	92
NCBI Description	(D63580) EF-1 alpha [Oryza sativa] >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza sativa] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha [Oryza sativa]

Seq. No.	226254
Seq. ID	LIB3166-053-P1-K1-B7
Method	BLASTX
NCBI GI	g4490341
BLAST score	327
E value	2.0e-30
Match length	72
% identity	85
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	226255
Seq. ID	LIB3166-053-P1-K1-B8
Method	BLASTX
NCBI GI	g2894606
BLAST score	133
E value	1.0e-11
Match length	102
% identity	40
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	226256
Seq. ID	LIB3166-053-P1-K1-C10
Method	BLASTX
NCBI GI	g3549666
BLAST score	348
E value	6.0e-33
Match length	83

% identity	81
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	226257
Seq. ID	LIB3166-053-P1-K1-C7
Method	BLASTX
NCBI GI	g3288883
BLAST score	372
E value	8.0e-36
Match length	102
% identity	74
NCBI Description	(AB015431) SAR DNA binding protein [Oryza sativa]

Seq. No.	226258
Seq. ID	LIB3166-053-P1-K1-C8
Method	BLASTX
NCBI GI	g1168191
BLAST score	377
E value	9.0e-42
Match length	108
% identity	87
NCBI Description	14-3-3-LIKE PROTEIN 4 (PBLT4) >gi_1362089_pir__S57272 14-3-3 brain protein homolog (clone pBLT4) - tomato >gi_466336 (L29150) 14-3-3 protein homologue [Solanum lycopersicum] >gi_1090847_prf__2019487B 14-3-3 protein [Lycopersicon esculentum]

Seq. No.	226259
Seq. ID	LIB3166-053-P1-K1-D1
Method	BLASTX
NCBI GI	g2465434
BLAST score	323
E value	4.0e-30
Match length	71
% identity	86
NCBI Description	(AF022142) flavanone 3beta-hydroxylase [Petunia x hybrida]

Seq. No.	226260
Seq. ID	LIB3166-053-P1-K1-D12
Method	BLASTX
NCBI GI	g2464855
BLAST score	139
E value	1.0e-08
Match length	37
% identity	68
NCBI Description	(Z99707) myb-related protein [Arabidopsis thaliana]

Seq. No.	226261
Seq. ID	LIB3166-053-P1-K1-D2
Method	BLASTX
NCBI GI	g2465925
BLAST score	334
E value	3.0e-31
Match length	128
% identity	54
NCBI Description	(AF024649) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	226262
Seq. ID	LIB3166-053-P1-K1-D3
Method	BLASTX
NCBI GI	g4454484
BLAST score	508
E value	1.0e-51
Match length	127
% identity	80
NCBI Description	(AC006234) putative diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	226263
Seq. ID	LIB3166-053-P1-K1-D4
Method	BLASTX
NCBI GI	g3650028
BLAST score	196
E value	4.0e-15
Match length	63
% identity	59
NCBI Description	(AC005396) putative 22 kDa peroxisomal membrane protein [Arabidopsis thaliana]

Seq. No.	226264
Seq. ID	LIB3166-053-P1-K1-D8
Method	BLASTX
NCBI GI	g2829869
BLAST score	266
E value	2.0e-23
Match length	83
% identity	65
NCBI Description	(AC002396) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	226265
Seq. ID	LIB3166-053-P1-K1-E1
Method	BLASTX
NCBI GI	g1850968
BLAST score	439
E value	1.0e-43
Match length	125
% identity	65
NCBI Description	(U79733) Hs1pro-1 [Beta procumbens]

Seq. No.	226266
Seq. ID	LIB3166-053-P1-K1-E12
Method	BLASTX
NCBI GI	g3158474
BLAST score	413
E value	1.0e-40
Match length	105
% identity	68
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]

Seq. No.	226267
Seq. ID	LIB3166-053-P1-K1-E2
Method	BLASTX

NCBI GI	g131397
BLAST score	254
E value	6.0e-22
Match length	116
% identity	52
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_81480_pir__S00008 photosystem II oxygen-evolving complex protein 3 precursor - spinach >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi_225597_prf__1307179B luminal protein 16kD [Spinacia oleracea]

Seq. No.	226268
Seq. ID	LIB3166-053-P1-K1-E3
Method	BLASTX
NCBI GI	g1362152
BLAST score	550
E value	1.0e-56
Match length	120
% identity	88
NCBI Description	ribosomal protein S6 kinase homolog (clone Aspk11) - oat >gi_871986_emb_CAA56313_ (X79992) putative pp70 ribosomal protein S6 kinase [Avena sativa]

Seq. No.	226269
Seq. ID	LIB3166-053-P1-K1-E5
Method	BLASTX
NCBI GI	g3193316
BLAST score	150
E value	5.0e-10
Match length	87
% identity	45
NCBI Description	(AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No.	226270
Seq. ID	LIB3166-053-P1-K1-E7
Method	BLASTX
NCBI GI	g4490705
BLAST score	496
E value	3.0e-50
Match length	116
% identity	86
NCBI Description	(AL035680) ribosomal protein L14-like protein [Arabidopsis thaliana]

Seq. No.	226271
Seq. ID	LIB3166-053-P1-K1-F1
Method	BLASTX
NCBI GI	g541847
BLAST score	301
E value	2.0e-27
Match length	99
% identity	63
NCBI Description	alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana

Seq. No.	226272
Seq. ID	LIB3166-053-P1-K1-F10
Method	BLASTX
NCBI GI	g3786314
BLAST score	250
E value	1.0e-21
Match length	86
% identity	57
NCBI Description	(AB012141) translation elongation factor3 [Candida glabrata]

Seq. No.	226273
Seq. ID	LIB3166-053-P1-K1-F2
Method	BLASTX
NCBI GI	g4539301
BLAST score	423
E value	1.0e-41
Match length	110
% identity	73
NCBI Description	(AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	226274
Seq. ID	LIB3166-053-P1-K1-F4
Method	BLASTX
NCBI GI	g4321762
BLAST score	177
E value	3.0e-13
Match length	81
% identity	48
NCBI Description	(AF061107) transcription factor MYC7E [Zea mays]

Seq. No.	226275
Seq. ID	LIB3166-053-P1-K1-F7
Method	BLASTX
NCBI GI	g2500115
BLAST score	387
E value	1.0e-37
Match length	90
% identity	82
NCBI Description	GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE) >gi_529375_dbj_BAA07108_ (D37870) Glutathione Reductase precursor [Spinacia oleracea]

Seq. No.	226276
Seq. ID	LIB3166-053-P1-K1-F8
Method	BLASTX
NCBI GI	g1362067
BLAST score	598
E value	3.0e-62
Match length	124
% identity	94
NCBI Description	small GTP-binding protein - garden pea >gi_871508_emb_CAA90082_ (Z49902) small GTP-binding protein [Pisum sativum]

Seq. No.	226277
Seq. ID	LIB3166-053-P1-K1-F9
Method	BLASTX
NCBI GI	g1055130
BLAST score	163
E value	1.0e-11
Match length	76
% identity	46
NCBI Description	(U39998) coded for by C. elegans cDNA yk92b11.3; coded for by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA yk78c2.3

Seq. No.	226278
Seq. ID	LIB3166-053-P1-K1-G10
Method	BLASTX
NCBI GI	g1345919
BLAST score	603
E value	7.0e-63
Match length	124
% identity	94
NCBI Description	APOCYTOCHROME F PRECURSOR >gi_984315 (U26948) cytochrome f precursor [Glycine max]

Seq. No.	226279
Seq. ID	LIB3166-053-P1-K1-G11
Method	BLASTX
NCBI GI	g3550454
BLAST score	195
E value	1.0e-15
Match length	44
% identity	82
NCBI Description	(AF085820) alcohol dehydrogenase A [Gossypium barbadense] >gi_3550458 (AF085821) alcohol dehydrogenase A [Gossypium barbadense] >gi_3551965 (AF085064) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551967 (AF085065) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551971 (AF085067) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551975 (AF085069) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551977 (AF085070) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140594 (AF090146) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140604 (AF090151) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140606 (AF090152) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140608 (AF090153) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140610 (AF090154) alcohol dehydrogenase A [Gossypium hirsutum]

Seq. No.	226280
Seq. ID	LIB3166-053-P1-K1-G12
Method	BLASTX
NCBI GI	g70642
BLAST score	421
E value	1.0e-41
Match length	103
% identity	18

NCBI Description	ubiquitin precursor - Arabidopsis thaliana >gi_17678_emb_CAA31331_ (X12853) polyubiquitin (AA 1 - 382) [Arabidopsis thaliana] >gi_987519 (U33014) polyubiquitin [Arabidopsis thaliana] >gi_226499_prf__1515347A poly-ubiquitin [Arabidopsis thaliana]
Seq. No.	226281
Seq. ID	LIB3166-053-P1-K1-G2
Method	BLASTX
NCBI GI	g68200
BLAST score	487
E value	3.0e-49
Match length	124
% identity	81
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]
Seq. No.	226282
Seq. ID	LIB3166-053-P1-K1-G3
Method	BLASTX
NCBI GI	g3868758
BLAST score	405
E value	1.0e-39
Match length	101
% identity	74
NCBI Description	(D89802) elongation factor 1B gamma [Oryza sativa]
Seq. No.	226283
Seq. ID	LIB3166-053-P1-K1-G5
Method	BLASTX
NCBI GI	g2462762
BLAST score	185
E value	6.0e-14
Match length	64
% identity	55
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.	226284
Seq. ID	LIB3166-053-P1-K1-G6
Method	BLASTX
NCBI GI	g1944216
BLAST score	386
E value	1.0e-37
Match length	84
% identity	86
NCBI Description	(D84246) alcohol dehydrogenase [Arabidopsis thaliana]
Seq. No.	226285
Seq. ID	LIB3166-053-P1-K1-G7
Method	BLASTX
NCBI GI	g2842485
BLAST score	152
E value	4.0e-10
Match length	80
% identity	41

NCBI Description	(AL021749) hypothetical protein [Arabidopsis thaliana]
Seq. No.	226286
Seq. ID	LIB3166-053-P1-K1-G8
Method	BLASTX
NCBI GI	g1871192
BLAST score	203
E value	6.0e-16
Match length	73
% identity	55
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]
Seq. No.	226287
Seq. ID	LIB3166-053-P1-K1-H11
Method	BLASTX
NCBI GI	g3334259
BLAST score	461
E value	3.0e-46
Match length	116
% identity	79
NCBI Description	WD-40 REPEAT PROTEIN MSI4 >gi_2599092 (AF028711) WD-40 repeat protein MSI4 [Arabidopsis thaliana]
Seq. No.	226288
Seq. ID	LIB3166-053-P1-K1-H12
Method	BLASTX
NCBI GI	g2832625
BLAST score	362
E value	1.0e-34
Match length	127
% identity	50
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]
Seq. No.	226289
Seq. ID	LIB3166-053-P1-K1-H3
Method	BLASTX
NCBI GI	g3367515
BLAST score	381
E value	8.0e-37
Match length	97
% identity	72
NCBI Description	(AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb_AF020814 from Pisum sativum. [Arabidopsis thaliana]
Seq. No.	226290
Seq. ID	LIB3166-053-P1-K1-H6
Method	BLASTX
NCBI GI	g4249385
BLAST score	434
E value	3.0e-43
Match length	79
% identity	96
NCBI Description	(AC005966) T2K10.11 [Arabidopsis thaliana]
Seq. No.	226291

Seq. ID	LIB3166-054-P1-K1-A5
Method	BLASTX
NCBI GI	g2879811
BLAST score	339
E value	4.0e-32
Match length	71
% identity	94
NCBI Description	(AJ223316) ribosomal protein L30 [Lupinus luteus]

Seq. No.	226292
Seq. ID	LIB3166-054-P1-K1-A9
Method	BLASTX
NCBI GI	g3068717
BLAST score	432
E value	9.0e-43
Match length	116
% identity	72
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	226293
Seq. ID	LIB3166-054-P1-K1-B10
Method	BLASTX
NCBI GI	g3023190
BLAST score	288
E value	3.0e-26
Match length	69
% identity	84
NCBI Description	14-3-3-LIKE PROTEIN 16R >gi_1888459_emb_CAA72381_ (Y11685) 14-3-3 protein [Solanum tuberosum]

Seq. No.	226294
Seq. ID	LIB3166-054-P1-K1-B12
Method	BLASTX
NCBI GI	g417154
BLAST score	230
E value	3.0e-19
Match length	80
% identity	65
NCBI Description	HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

Seq. No.	226295
Seq. ID	LIB3166-054-P1-K1-B2
Method	BLASTX
NCBI GI	g3894385
BLAST score	169
E value	5.0e-12
Match length	112
% identity	4
NCBI Description	(AF053994) Hcr2-0A [Lycopersicon esculentum]

Seq. No.	226296
Seq. ID	LIB3166-054-P1-K1-B3
Method	BLASTX
NCBI GI	g1934730

BLAST score 207
E value 2.0e-16
Match length 73
% identity 52
NCBI Description (U95036) germin-like protein [Arabidopsis thaliana]

Seq. No. 226297
Seq. ID LIB3166-054-P1-K1-B6
Method BLASTX
NCBI GI g4455278
BLAST score 202
E value 5.0e-16
Match length 90
% identity 41
NCBI Description (AL035527) hypothetical protein [Arabidopsis thaliana]

Seq. No. 226298
Seq. ID LIB3166-054-P1-K1-B9
Method BLASTX
NCBI GI g3935148
BLAST score 282
E value 3.0e-25
Match length 72
% identity 71
NCBI Description (AC005106) T25N20.12 [Arabidopsis thaliana]

Seq. No. 226299
Seq. ID LIB3166-054-P1-K1-C10
Method BLASTX
NCBI GI g289920
BLAST score 523
E value 1.0e-53
Match length 103
% identity 64
NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No. 226300
Seq. ID LIB3166-054-P1-K1-C11
Method BLASTX
NCBI GI g3860323
BLAST score 210
E value 6.0e-17
Match length 63
% identity 65
NCBI Description (AJ012688) hypothetical protein [Cicer arietinum]

Seq. No. 226301
Seq. ID LIB3166-054-P1-K1-C6
Method BLASTX
NCBI GI g4580513
BLAST score 385
E value 2.0e-37
Match length 104
% identity 72
NCBI Description (AF036300) scarecrow-like 1 [Arabidopsis thaliana]

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Seq. No.	226302
Seq. ID	LIB3166-054-P1-K1-C9
Method	BLASTX
NCBI GI	g3212869
BLAST score	490
E value	1.0e-49
Match length	106
% identity	86
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	226303
Seq. ID	LIB3166-054-P1-K1-D10
Method	BLASTX
NCBI GI	g100616
BLAST score	367
E value	2.0e-35
Match length	82
% identity	82
NCBI Description	ribulose-bisphosphate carboxylase activase B precursor - barley >gi_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	226304
Seq. ID	LIB3166-054-P1-K1-D11
Method	BLASTX
NCBI GI	g4539301
BLAST score	226
E value	4.0e-19
Match length	60
% identity	68
NCBI Description	(AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	226305
Seq. ID	LIB3166-054-P1-K1-D2
Method	BLASTX
NCBI GI	g3552003
BLAST score	601
E value	1.0e-62
Match length	113
% identity	99
NCBI Description	(AF085083) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3552005 (AF085084) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3552007 (AF085085) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140632 (AF090165) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140634 (AF090166) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140636 (AF090167) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140638 (AF090168) alcohol dehydrogenase A [Gossypium hirsutum]

Seq. No.	226306
Seq. ID	LIB3166-054-P1-K1-D8
Method	BLASTX
NCBI GI	g439489

09084705.1000

BLAST score	183
E value	1.0e-13
Match length	84
% identity	54
NCBI Description	(D26084) zinc-finger DNA binding protein [Petunia x hybrida]

Seq. No.	226307
Seq. ID	LIB3166-054-P1-K1-D9
Method	BLASTX
NCBI GI	g2924792
BLAST score	446
E value	1.0e-44
Match length	101
% identity	79
NCBI Description	(AC002334) similar to synaptobrevin [Arabidopsis thaliana]

Seq. No.	226308
Seq. ID	LIB3166-054-P1-K1-E10
Method	BLASTX
NCBI GI	g1928981
BLAST score	325
E value	1.0e-30
Match length	72
% identity	90
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	226309
Seq. ID	LIB3166-054-P1-K1-E2
Method	BLASTX
NCBI GI	g3901012
BLAST score	369
E value	2.0e-35
Match length	93
% identity	72
NCBI Description	(AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]

Seq. No.	226310
Seq. ID	LIB3166-054-P1-K1-E3
Method	BLASTX
NCBI GI	g4102859
BLAST score	505
E value	3.0e-56
Match length	128
% identity	80
NCBI Description	(AF016892) cytoplasmic superoxide dismutase 1 [Populus tremuloides]

Seq. No.	226311
Seq. ID	LIB3166-054-P1-K1-E8
Method	BLASTX
NCBI GI	g4544460
BLAST score	139
E value	1.0e-08
Match length	48

% identity	52
NCBI Description	(AC006592) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	226312
Seq. ID	LIB3166-054-P1-K1-E9
Method	BLASTX
NCBI GI	g1076715
BLAST score	187
E value	3.0e-14
Match length	63
% identity	54
NCBI Description	abscisic acid-induced protein HVA22 - barley >gi_404589 (L19119) A22 [Hordeum vulgare]

Seq. No.	226313
Seq. ID	LIB3166-054-P1-K1-F11
Method	BLASTX
NCBI GI	g1706958
BLAST score	507
E value	9.0e-52
Match length	97
% identity	97
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	226314
Seq. ID	LIB3166-054-P1-K1-F3
Method	BLASTX
NCBI GI	g2961346
BLAST score	358
E value	2.0e-34
Match length	98
% identity	67
NCBI Description	(AL022140) pectinesterase like protein [Arabidopsis thaliana]

Seq. No.	226315
Seq. ID	LIB3166-054-P1-K1-F7
Method	BLASTX
NCBI GI	g4539344
BLAST score	267
E value	9.0e-24
Match length	80
% identity	68
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	226316
Seq. ID	LIB3166-054-P1-K1-F9
Method	BLASTX
NCBI GI	g1353352
BLAST score	335
E value	1.0e-31
Match length	98
% identity	61
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	226317
Seq. ID	LIB3166-054-P1-K1-G11
Method	BLASTX
NCBI GI	g1353352
BLAST score	247
E value	3.0e-21
Match length	77
% identity	58
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	226318
Seq. ID	LIB3166-054-P1-K1-G12
Method	BLASTX
NCBI GI	g4539452
BLAST score	336
E value	8.0e-32
Match length	84
% identity	76
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	226319
Seq. ID	LIB3166-054-P1-K1-G4
Method	BLASTX
NCBI GI	g4220482
BLAST score	182
E value	1.0e-13
Match length	70
% identity	53
NCBI Description	(AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	226320
Seq. ID	LIB3166-054-P1-K1-G8
Method	BLASTX
NCBI GI	g1527191
BLAST score	301
E value	1.0e-27
Match length	67
% identity	84
NCBI Description	(U67861) 1-aminocyclopropane-1-carboxylate oxidase [Pelargonium x hortorum]

Seq. No.	226321
Seq. ID	LIB3166-054-P1-K1-G9
Method	BLASTX
NCBI GI	g3550440
BLAST score	262
E value	3.0e-23
Match length	79
% identity	71
NCBI Description	(AF085816) alcohol dehydrogenase A [Gossypium barbadense]

Seq. No.	226322
Seq. ID	LIB3166-054-P1-K1-H1
Method	BLASTX
NCBI GI	g2129915

BLAST score	150
E value	6.0e-10
Match length	59
% identity	54
NCBI Description	ferredoxin precursor - sweet orange >gi_1360725_emb_CAA87068_ (Z46944) non-photosynthetic ferredoxin [Citrus sinensis]

Seq. No.	226323
Seq. ID	LIB3166-054-P1-K1-H10
Method	BLASTX
NCBI GI	g4538929
BLAST score	257
E value	2.0e-22
Match length	110
% identity	55
NCBI Description	(AL049483) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No.	226324
Seq. ID	LIB3166-054-P1-K1-H11
Method	BLASTX
NCBI GI	g4455364
BLAST score	356
E value	5.0e-34
Match length	89
% identity	74
NCBI Description	(AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No.	226325
Seq. ID	LIB3166-054-P1-K1-H2
Method	BLASTX
NCBI GI	g3183088
BLAST score	176
E value	5.0e-13
Match length	51
% identity	63
NCBI Description	PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer like protein [Vigna unguiculata]

Seq. No.	226326
Seq. ID	LIB3166-054-P1-K1-H4
Method	BLASTX
NCBI GI	g119150
BLAST score	295
E value	4.0e-31
Match length	82
% identity	88
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_82081_pir__S10507 translation elongation factor eEF-1 alpha chain - tomato >gi_19273_emb_CAA32618_ (X14449) EF 1-alpha (AA 1-448) [Lycopersicon esculentum] >gi_295810_emb_CAA37212_ (X53043) elongation factor 1-alpha [Lycopersicon esculentum]

Seq. No.	226327
Seq. ID	LIB3166-054-P1-K1-H5
Method	BLASTX
NCBI GI	g4455208
BLAST score	461
E value	2.0e-46
Match length	101
% identity	86
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	226328
Seq. ID	LIB3166-054-P1-K1-H8
Method	BLASTX
NCBI GI	g4220477
BLAST score	166
E value	7.0e-12
Match length	77
% identity	52
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	226329
Seq. ID	LIB3166-054-P1-K1-H9
Method	BLASTX
NCBI GI	g2444178
BLAST score	271
E value	3.0e-24
Match length	91
% identity	67
NCBI Description	(U94784) unconventional myosin [Helianthus annuus]

Seq. No.	226330
Seq. ID	LIB3166-055-P1-K1-A11
Method	BLASTX
NCBI GI	g3337350
BLAST score	428
E value	2.0e-42
Match length	102
% identity	80
NCBI Description	(AC004481) putative permease [Arabidopsis thaliana]

Seq. No.	226331
Seq. ID	LIB3166-055-P1-K1-A3
Method	BLASTX
NCBI GI	g2995384
BLAST score	186
E value	4.0e-14
Match length	65
% identity	62
NCBI Description	(AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No.	226332
Seq. ID	LIB3166-055-P1-K1-A6
Method	BLASTX
NCBI GI	g4204294
BLAST score	416
E value	7.0e-41

Match length	123
% identity	73
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	226333
Seq. ID	LIB3166-055-P1-K1-A7
Method	BLASTX
NCBI GI	g1220196
BLAST score	475
E value	8.0e-48
Match length	117
% identity	82
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	226334
Seq. ID	LIB3166-055-P1-K1-A8
Method	BLASTX
NCBI GI	g1732511
BLAST score	463
E value	2.0e-46
Match length	100
% identity	85
NCBI Description	(U62742) Ran binding protein 1 homolog [Arabidopsis thaliana]

Seq. No.	226335
Seq. ID	LIB3166-055-P1-K1-A9
Method	BLASTX
NCBI GI	g2129471
BLAST score	524
E value	1.0e-53
Match length	128
% identity	81
NCBI Description	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) precursor - Scotch pine >gi_1100223 (L32560) glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]

Seq. No.	226336
Seq. ID	LIB3166-055-P1-K1-B10
Method	BLASTX
NCBI GI	g1850546
BLAST score	329
E value	9.0e-31
Match length	86
% identity	79
NCBI Description	(U88045) syntaxin related protein AtVam3p [Arabidopsis thaliana]

Seq. No.	226337
Seq. ID	LIB3166-055-P1-K1-B11
Method	BLASTX
NCBI GI	g4544409
BLAST score	430
E value	1.0e-42
Match length	116
% identity	69

NCBI Description	(AC006955) putative transcription factor [Arabidopsis thaliana]
Seq. No.	226338
Seq. ID	LIB3166-055-P1-K1-B12
Method	BLASTX
NCBI GI	g3249066
BLAST score	436
E value	3.0e-43
Match length	120
% identity	72
NCBI Description	(AC004473) Similar to S. cerevisiae SIK1P protein gb_984964. ESTs gb_F15433 and gb_AA395158 come from this gene. [Arabidopsis thaliana]
Seq. No.	226339
Seq. ID	LIB3166-055-P1-K1-B2
Method	BLASTX
NCBI GI	g1220196
BLAST score	152
E value	3.0e-10
Match length	80
% identity	46
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.	226340
Seq. ID	LIB3166-055-P1-K1-B4
Method	BLASTX
NCBI GI	g3068717
BLAST score	427
E value	3.0e-42
Match length	131
% identity	60
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]
Seq. No.	226341
Seq. ID	LIB3166-055-P1-K1-C1
Method	BLASTX
NCBI GI	g228210
BLAST score	396
E value	1.0e-38
Match length	113
% identity	68
NCBI Description	granule-bound starch synthase [Solanum tuberosum]
Seq. No.	226342
Seq. ID	LIB3166-055-P1-K1-C10
Method	BLASTX
NCBI GI	g2791834
BLAST score	385
E value	3.0e-43
Match length	94
% identity	97
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]
Seq. No.	226343
Seq. ID	LIB3166-055-P1-K1-C11

Method	BLASTX
NCBI GI	g4432866
BLAST score	142
E value	9.0e-09
Match length	121
% identity	31
NCBI Description	(AC006300) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	226344
Seq. ID	LIB3166-055-P1-K1-C2
Method	BLASTX
NCBI GI	g2370232
BLAST score	225
E value	6.0e-36
Match length	112
% identity	71
NCBI Description	(AJ001341) putative acyl-CoA oxidase [Hordeum vulgare]

Seq. No.	226345
Seq. ID	LIB3166-055-P1-K1-C3
Method	BLASTX
NCBI GI	g1946369
BLAST score	197
E value	3.0e-15
Match length	78
% identity	50
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	226346
Seq. ID	LIB3166-055-P1-K1-C4
Method	BLASTX
NCBI GI	g1174149
BLAST score	143
E value	6.0e-09
Match length	51
% identity	82
NCBI Description	(U44104) small GTP binding protein Rab7 [Homo sapiens]

Seq. No.	226347
Seq. ID	LIB3166-055-P1-K1-C6
Method	BLASTX
NCBI GI	g3551983
BLAST score	704
E value	1.0e-74
Match length	129
% identity	98
NCBI Description	(AF085073) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551985 (AF085074) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551987 (AF085075) alcohol dehydrogenase A [Gossypium hirsutum] >gi_3551989 (AF085076) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140602 (AF090150) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140612 (AF090155) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140614 (AF090156) alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140616 (AF090157) alcohol dehydrogenase A [Gossypium hirsutum]

Seq. No.	226348
Seq. ID	LIB3166-055-P1-K1-C7
Method	BLASTX
NCBI GI	g464707
BLAST score	574
E value	2.0e-59
Match length	117
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	226349
Seq. ID	LIB3166-055-P1-K1-C9
Method	BLASTX
NCBI GI	g120669
BLAST score	245
E value	2.0e-21
Match length	69
% identity	70
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	226350
Seq. ID	LIB3166-055-P1-K1-D10
Method	BLASTX
NCBI GI	g3776559
BLAST score	303
E value	1.0e-27
Match length	114
% identity	55
NCBI Description	(AC005388) Strong similarity to gene F14J9.26 gi_3482933 cdc2 protein kinase homolog from A. thaliana BAC gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this gene. [Arabidopsis thaliana]

Seq. No.	226351
Seq. ID	LIB3166-055-P1-K1-D11
Method	BLASTX
NCBI GI	g3402684
BLAST score	572

E value 3.0e-59
Match length 130
% identity 79
NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No. 226352
Seq. ID LIB3166-055-P1-K1-D2
Method BLASTX
NCBI GI g2769642
BLAST score 405
E value 9.0e-40
Match length 101
% identity 76
NCBI Description (Z97215) nine-cis-epoxycarotenoid dioxygenase [Lycopersicon esculentum]

Seq. No. 226353
Seq. ID LIB3166-055-P1-K1-D3
Method BLASTX
NCBI GI g3355467
BLAST score 275
E value 2.0e-24
Match length 129
% identity 40
NCBI Description (AC004218) hypothetical protein [Arabidopsis thaliana]

Seq. No. 226354
Seq. ID LIB3166-055-P1-K1-E10
Method BLASTX
NCBI GI g2961357
BLAST score 574
E value 2.0e-59
Match length 128
% identity 82
NCBI Description (AL022140) putative protein [Arabidopsis thaliana]

Seq. No. 226355
Seq. ID LIB3166-055-P1-K1-E11
Method BLASTX
NCBI GI g3402750
BLAST score 212
E value 5.0e-17
Match length 102
% identity 46
NCBI Description (AL031187) putative protein [Arabidopsis thaliana]

Seq. No. 226356
Seq. ID LIB3166-055-P1-K1-E12
Method BLASTX
NCBI GI g586004
BLAST score 570
E value 6.0e-59
Match length 116
% identity 90
NCBI Description SUPEROXIDE DISMUTASE [CU-ZN] >gi_421962_pir__S34267 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato >gi_542090_pir__S40404 superoxide dismutase (EC 1.15.1.1)

	(Cu-Zn) - sweet potato >gi_311971_emb_CAA51654_ (X73139) superoxide dismutase [Ipomoea batatas]
Seq. No.	226357
Seq. ID	LIB3166-055-P1-K1-E2
Method	BLASTX
NCBI GI	g132168
BLAST score	463
E value	2.0e-46
Match length	115
% identity	74
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_81488_pir__A31082 ribulose-bisphosphate carboxylase activase precursor - spinach >gi_170129 (J03610) rubisco activase precursor [Spinacia oleracea]
Seq. No.	226358
Seq. ID	LIB3166-055-P1-K1-E4
Method	BLASTX
NCBI GI	g4376815
BLAST score	236
E value	8.0e-20
Match length	123
% identity	37
NCBI Description	(AE001637) GutQ/KpsF Family Sugar-P Isomerase [Chlamydia pneumoniae]
Seq. No.	226359
Seq. ID	LIB3166-055-P1-K1-E5
Method	BLASTX
NCBI GI	g1321661
BLAST score	351
E value	3.0e-33
Match length	111
% identity	64
NCBI Description	(D45423) ascorbate peroxidase [Oryza sativa]
Seq. No.	226360
Seq. ID	LIB3166-055-P1-K1-E6
Method	BLASTX
NCBI GI	g860932
BLAST score	175
E value	3.0e-13
Match length	67
% identity	52
NCBI Description	(Z49856) alpha-tubulin [Epidinium sp.]
Seq. No.	226361
Seq. ID	LIB3166-055-P1-K1-F1
Method	BLASTX
NCBI GI	g4539330
BLAST score	377
E value	1.0e-37
Match length	123
% identity	67
NCBI Description	(AL035679) putative receptor-like protein kinase (fragment)

[Arabidopsis thaliana]

Seq. No.	226362
Seq. ID	LIB3166-055-P1-K1-F10
Method	BLASTX
NCBI GI	g2149955
BLAST score	178
E value	8.0e-27
Match length	97
% identity	68
NCBI Description	(U97023) putative aquaporin-1 [Phaseolus vulgaris]

Seq. No.	226363
Seq. ID	LIB3166-055-P1-K1-F11
Method	BLASTX
NCBI GI	g4220455
BLAST score	315
E value	4.0e-29
Match length	124
% identity	59
NCBI Description	(AC006216) Identical to gene gb_D88746 AR791 from Arabidopsis thaliana. [Arabidopsis thaliana]

Seq. No.	226364
Seq. ID	LIB3166-055-P1-K1-F2
Method	BLASTX
NCBI GI	g1944216
BLAST score	394
E value	1.0e-38
Match length	82
% identity	89
NCBI Description	(D84246) alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	226365
Seq. ID	LIB3166-055-P1-K1-F3
Method	BLASTX
NCBI GI	g2827630
BLAST score	398
E value	8.0e-39
Match length	114
% identity	69
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	226366
Seq. ID	LIB3166-055-P1-K1-F5
Method	BLASTX
NCBI GI	g130600
BLAST score	417
E value	5.0e-41
Match length	129
% identity	63
NCBI Description	ENZYMATIC POLYPROTEIN [CONTAINS: ASPARTIC PROTEASE ; ENDONUCLEASE; REVERSE TRANSCRIPTASE] >gi_76782_pir__S01283 hypothetical protein 5 - figwort mosaic virus >gi_58813_emb_CAA29527_ (X06166) ORF V (AA 1-666) [Figwort mosaic virus]

Seq. No.	226367
Seq. ID	LIB3166-055-P1-K1-F9
Method	BLASTX
NCBI GI	g2623297
BLAST score	468
E value	2.0e-48
Match length	122
% identity	75
NCBI Description	(AC002409) unknown protein [Arabidopsis thaliana] >gi_3790583 (AF079180) RING-H2 finger protein RHC1a [Arabidopsis thaliana]

Seq. No.	226368
Seq. ID	LIB3166-055-P1-K1-G10
Method	BLASTX
NCBI GI	g2760830
BLAST score	629
E value	7.0e-66
Match length	128
% identity	86
NCBI Description	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	226369
Seq. ID	LIB3166-055-P1-K1-G11
Method	BLASTX
NCBI GI	g3318611
BLAST score	144
E value	1.0e-10
Match length	74
% identity	55
NCBI Description	(AB016063) mitochondrial phosphate transporter [Glycine max]

Seq. No.	226370
Seq. ID	LIB3166-055-P1-K1-G12
Method	BLASTX
NCBI GI	g2194142
BLAST score	552
E value	7.0e-57
Match length	131
% identity	73
NCBI Description	(AC002062) ESTs gb_N38288,gb_T43486,gb_AA395242 come from this gene. [Arabidopsis thaliana]

Seq. No.	226371
Seq. ID	LIB3166-055-P1-K1-G2
Method	BLASTX
NCBI GI	g4056506
BLAST score	347
E value	8.0e-33
Match length	107
% identity	59
NCBI Description	(AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	226372
Seq. ID	LIB3166-055-P1-K1-G4

Method	BLASTX
NCBI GI	g1709825
BLAST score	197
E value	3.0e-15
Match length	118
% identity	42
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No.	226373
Seq. ID	LIB3166-055-P1-K1-H1
Method	BLASTX
NCBI GI	g3860264
BLAST score	558
E value	1.0e-57
Match length	119
% identity	87
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	226374
Seq. ID	LIB3166-055-P1-K1-H12
Method	BLASTX
NCBI GI	g1263291
BLAST score	589
E value	3.0e-61
Match length	129
% identity	81
NCBI Description	(U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No.	226375
Seq. ID	LIB3166-055-P1-K1-H5
Method	BLASTX
NCBI GI	g2129832
BLAST score	561
E value	7.0e-58
Match length	110
% identity	93
NCBI Description	heat shock transcription factor 5 - soybean >gi_671868_emb_CAA87080_ (Z46956) heat shock transcription factor 5 [Glycine max]

Seq. No.	226376
Seq. ID	LIB3166-055-P1-K1-H9
Method	BLASTX
NCBI GI	g4539348
BLAST score	252
E value	1.0e-21
Match length	92
% identity	51
NCBI Description	(AL035539) putative pollen allergen [Arabidopsis thaliana]

Seq. No.	226377
Seq. ID	LIB3166-056-P1-K1-A11
Method	BLASTX
NCBI GI	g3608171
BLAST score	174
E value	6.0e-13

Match length	58
% identity	66
NCBI Description	(D86306) proton-translocating inorganic pyrophosphatase [Cucurbita moschata]

Seq. No.	226378
Seq. ID	LIB3166-056-P1-K1-A4
Method	BLASTX
NCBI GI	g4467128
BLAST score	163
E value	8.0e-12
Match length	58
% identity	60
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	226379
Seq. ID	LIB3166-056-P1-K1-A8
Method	BLASTX
NCBI GI	g1345674
BLAST score	285
E value	8.0e-26
Match length	95
% identity	62
NCBI Description	CATALASE ISOZYME 1 >gi_99598_pir__S10770 catalase (EC 1.11.1.6) - upland cotton >gi_18484_emb_CAA36380_ (X52135) catalase subunit 1 (AA 1-492) [Gossypium hirsutum]

Seq. No.	226380
Seq. ID	LIB3166-056-P1-K1-B10
Method	BLASTX
NCBI GI	g2493046
BLAST score	178
E value	5.0e-13
Match length	66
% identity	55
NCBI Description	ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR >gi_82297_pir__A41740 H+-transporting ATP synthase (EC 3.6.1.34), delta' chain precursor - sweet potato >gi_217938_dbj_BAA01511_ (D10660) mitochondrial F1-ATPase delta subunit [Ipomoea batatas]

Seq. No.	226381
Seq. ID	LIB3166-056-P1-K1-B8
Method	BLASTX
NCBI GI	g2827699
BLAST score	173
E value	1.0e-12
Match length	66
% identity	56
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	226382
Seq. ID	LIB3166-056-P1-K1-C11
Method	BLASTX
NCBI GI	g1888357
BLAST score	262
E value	4.0e-23

Match length	92
% identity	54
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No.	226383
Seq. ID	LIB3166-056-P1-K1-D3
Method	BLASTX
NCBI GI	g2996202
BLAST score	184
E value	3.0e-14
Match length	48
% identity	67
NCBI Description	(AF053725) myristoyl-CoA: protein N-myristoyl transferase [Drosophila melanogaster]

Seq. No.	226384
Seq. ID	LIB3166-056-P1-K1-D7
Method	BLASTX
NCBI GI	g3367593
BLAST score	178
E value	2.0e-13
Match length	60
% identity	68
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana] >gi_3805841_emb_CAA21461_ (AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	226385
Seq. ID	LIB3166-056-P1-K1-E1
Method	BLASTX
NCBI GI	g3688600
BLAST score	188
E value	1.0e-14
Match length	61
% identity	62
NCBI Description	(AB009030) beta-Amyrin Synthase [Panax ginseng]

Seq. No.	226386
Seq. ID	LIB3166-056-P1-K1-E10
Method	BLASTX
NCBI GI	g4406780
BLAST score	263
E value	3.0e-23
Match length	86
% identity	65
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	226387
Seq. ID	LIB3166-056-P1-K1-E11
Method	BLASTX
NCBI GI	g1076511
BLAST score	440
E value	7.0e-44
Match length	103

% identity	79
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - kidney bean >gi_758250_emb_CAA59799_ (X85804) H(+)-transporting ATPase [Phaseolus vulgaris]

Seq. No.	226388
Seq. ID	LIB3166-056-P1-K1-G9
Method	BLASTX
NCBI GI	g198884
BLAST score	142
E value	2.0e-09
Match length	47
% identity	51
NCBI Description	(M63848) leukotriene A-4 hydrolase [Mus musculus]

Seq. No.	226389
Seq. ID	LIB3166-057-P1-K1-A1
Method	BLASTX
NCBI GI	g1362051
BLAST score	514
E value	2.0e-52
Match length	118
% identity	69
NCBI Description	protein kinase 3 - soybean >gi_310582 (L19361) protein kinase 3 [Glycine max]

Seq. No.	226390
Seq. ID	LIB3166-057-P1-K1-A11
Method	BLASTX
NCBI GI	g3204108
BLAST score	301
E value	1.0e-27
Match length	72
% identity	76
NCBI Description	(AJ006764) putative deoxycytidylate deaminase [Cicer arietinum]

Seq. No.	226391
Seq. ID	LIB3166-057-P1-K1-A12
Method	BLASTX
NCBI GI	g1255951
BLAST score	128
E value	4.0e-17
Match length	51
% identity	73
NCBI Description	(X96932) PS60 [Nicotiana tabacum]

Seq. No.	226392
Seq. ID	LIB3166-057-P1-K1-A3
Method	BLASTX
NCBI GI	g1346180
BLAST score	193
E value	1.0e-19
Match length	95
% identity	58
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN GRP1A >gi_496233 (L31374) homology with RNA-binding proteins in meristematic tissue

[Sinapis alba]

Seq. No.	226393
Seq. ID	LIB3166-057-P1-K1-A5
Method	BLASTX
NCBI GI	g123650
BLAST score	416
E value	5.0e-41
Match length	79
% identity	100
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN >gi_82245_pir__S03250 heat shock protein 70 (clone pMON9743) - garden petunia >gi_20557_emb_CAA30018_ (X06932) heat shock protein 70 [Petunia x hybrida]

Seq. No.	226394
Seq. ID	LIB3166-057-P1-K1-A6
Method	BLASTX
NCBI GI	g541816
BLAST score	236
E value	7.0e-20
Match length	80
% identity	62
NCBI Description	protein kinase - common ice plant >gi_457689_emb_CAA82990_ (Z30329) protein kinase [Mesembryanthemum crystallinum]

Seq. No.	226395
Seq. ID	LIB3166-057-P1-K1-A8
Method	BLASTX
NCBI GI	g2864625
BLAST score	280
E value	6.0e-25
Match length	62
% identity	77
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	226396
Seq. ID	LIB3166-057-P1-K1-B11
Method	BLASTX
NCBI GI	g1170747
BLAST score	309
E value	2.0e-28
Match length	63
% identity	100
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345 (M88324) late embryogenesis-abundant protein [Gossypium hirsutum] >gi_167347 (M37697) Lea5-A late embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No.	226397
Seq. ID	LIB3166-057-P1-K1-B12
Method	BLASTX
NCBI GI	g2982303
BLAST score	305
E value	6.0e-28
Match length	69
% identity	83

NCBI Description (AF051236) hypothetical protein [Picea mariana]

Seq. No. 226398
Seq. ID LIB3166-057-P1-K1-B2
Method BLASTX
NCBI GI g2664200
BLAST score 182
E value 1.0e-13
Match length 103
% identity 32
NCBI Description (AJ003216) GTL2 [Arabidopsis thaliana]

Seq. No. 226399
Seq. ID LIB3166-057-P1-K1-B3
Method BLASTX
NCBI GI g4039155
BLAST score 432
E value 7.0e-43
Match length 116
% identity 66
NCBI Description (AF104258) putative copper-inducible 35.6 kDa protein [Festuca rubra]

Seq. No. 226400
Seq. ID LIB3166-057-P1-K1-C11
Method BLASTX
NCBI GI g3047114
BLAST score 435
E value 3.0e-43
Match length 118
% identity 63
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 226401
Seq. ID LIB3166-057-P1-K1-C2
Method BLASTX
NCBI GI g3024127
BLAST score 490
E value 8.0e-51
Match length 117
% identity 79
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1655578_emb_CAA95857_ (Z71272) S-adenosyl-L-methionine synthetase 2 [Catharanthus roseus]

Seq. No. 226402
Seq. ID LIB3166-057-P1-K1-C5
Method BLASTX
NCBI GI g4415931
BLAST score 425
E value 5.0e-42
Match length 114
% identity 71
NCBI Description (AC006418) unknown protein [Arabidopsis thaliana] >gi_4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	226403
Seq. ID	LIB3166-057-P1-K1-C7
Method	BLASTX
NCBI GI	g1173198
BLAST score	337
E value	6.0e-32
Match length	76
% identity	88
NCBI Description	40S RIBOSOMAL PROTEIN S13 >gi_480095_pir__S36423 ribosomal protein S13.e - garden pea >gi_396639_emb_CAA80974_ (Z25509) ribosomal protein S13 [Pisum sativum]

Seq. No.	226404
Seq. ID	LIB3166-057-P1-K1-D2
Method	BLASTX
NCBI GI	g2160756
BLAST score	188
E value	1.0e-23
Match length	112
% identity	54
NCBI Description	(U96879) CLV1 receptor kinase [Arabidopsis thaliana]

Seq. No.	226405
Seq. ID	LIB3166-057-P1-K1-D5
Method	BLASTX
NCBI GI	g4539543
BLAST score	561
E value	5.0e-58
Match length	116
% identity	95
NCBI Description	(AJ133422) glyceraldehyde-3-phosphate dehydrogenase [Nicotiana tabacum]

Seq. No.	226406
Seq. ID	LIB3166-057-P1-K1-D6
Method	BLASTX
NCBI GI	g1723125
BLAST score	197
E value	3.0e-15
Match length	71
% identity	55
NCBI Description	HYPOTHETICAL 27.8 KD PROTEIN SLL0194 >gi_1001604_dbj_BAA10232_ (D64000) hypothetical protein [Synechocystis sp.]

Seq. No.	226407
Seq. ID	LIB3166-057-P1-K1-D8
Method	BLASTX
NCBI GI	g2495365
BLAST score	344
E value	2.0e-32
Match length	86
% identity	78
NCBI Description	HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B heat shock protein HSP81-2 [Arabidopsis thaliana]

Seq. No.	226408
Seq. ID	LIB3166-057-P1-K1-E1
Method	BLASTX
NCBI GI	g2462758
BLAST score	341
E value	3.0e-32
Match length	90
% identity	73
NCBI Description	(AC002292) putative RNA-binding protein [Arabidopsis thaliana]

Seq. No.	226409
Seq. ID	LIB3166-057-P1-K1-E10
Method	BLASTX
NCBI GI	g3600040
BLAST score	241
E value	2.0e-20
Match length	118
% identity	47
NCBI Description	(AF080119) similar to Arabidopsis thaliana disease resistance protein RPS2 (GB:U14158) [Arabidopsis thaliana]

Seq. No.	226410
Seq. ID	LIB3166-057-P1-K1-E11
Method	BLASTX
NCBI GI	g3334320
BLAST score	434
E value	4.0e-43
Match length	94
% identity	95
NCBI Description	40S RIBOSOMAL PROTEIN SA (P40) >gi_2444420 (AF020553) ribosome-associated protein p40 [Glycine max]

Seq. No.	226411
Seq. ID	LIB3166-057-P1-K1-E12
Method	BLASTX
NCBI GI	g2583108
BLAST score	251
E value	1.0e-21
Match length	95
% identity	56
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.	226412
Seq. ID	LIB3166-057-P1-K1-E2
Method	BLASTX
NCBI GI	g2204077
BLAST score	190
E value	2.0e-14
Match length	86
% identity	50
NCBI Description	(D85623) extracellular insoluble cystatin [Daucus carota]

Seq. No.	226413
Seq. ID	LIB3166-057-P1-K1-E3
Method	BLASTX
NCBI GI	g231574

BLAST score	195
E value	4.0e-15
Match length	64
% identity	61
NCBI Description	L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE) >gi_81837_pir__S22523 asparaginase (EC 3.5.1.1) - tree lupine (fragment) >gi_19137_emb_CAA36824_ (X52588) asparaginase [Lupinus arboreus]

Seq. No.	226414
Seq. ID	LIB3166-057-P1-K1-E4
Method	BLASTX
NCBI GI	g3549626
BLAST score	476
E value	5.0e-48
Match length	120
% identity	76
NCBI Description	(AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]

Seq. No.	226415
Seq. ID	LIB3166-057-P1-K1-E6
Method	BLASTX
NCBI GI	g100490
BLAST score	556
E value	2.0e-57
Match length	112
% identity	25
NCBI Description	polyubiquitin - garden snapdragon (fragment) >gi_16071_emb_CAA48140_ (X67957) ubiquitin [Antirrhinum majus]

Seq. No.	226416
Seq. ID	LIB3166-057-P1-K1-E8
Method	BLASTX
NCBI GI	g3193326
BLAST score	150
E value	1.0e-12
Match length	88
% identity	57
NCBI Description	(AF069299) contains similarity to transcriptional activators such as Ra-like and myc-like regulatory R proteins [Arabidopsis thaliana]

Seq. No.	226417
Seq. ID	LIB3166-057-P1-K1-F1
Method	BLASTX
NCBI GI	g3560264
BLAST score	195
E value	4.0e-15
Match length	103
% identity	48
NCBI Description	(AL031535) soll family protein [Schizosaccharomyces pombe]

Seq. No.	226418
Seq. ID	LIB3166-057-P1-K1-F12
Method	BLASTX
NCBI GI	g2662415

BLAST score	141
E value	1.0e-08
Match length	48
% identity	56
NCBI Description	(U97494) metallothionein-like protein [Prunus armeniaca]

Seq. No.	226419
Seq. ID	LIB3166-057-P1-K1-F3
Method	BLASTX
NCBI GI	g3832528
BLAST score	355
E value	8.0e-34
Match length	100
% identity	71
NCBI Description	(AF100167) unknown [Glycine max]

Seq. No.	226420
Seq. ID	LIB3166-057-P1-K1-F5
Method	BLASTX
NCBI GI	g967125
BLAST score	543
E value	1.0e-56
Match length	120
% identity	93
NCBI Description	(U08140) calcium dependent protein kinase [Vigna radiata]

Seq. No.	226421
Seq. ID	LIB3166-057-P1-K1-F8
Method	BLASTX
NCBI GI	g3482967
BLAST score	129
E value	4.0e-17
Match length	56
% identity	82
NCBI Description	(AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	226422
Seq. ID	LIB3166-057-P1-K1-G4
Method	BLASTX
NCBI GI	g4490937
BLAST score	226
E value	1.0e-18
Match length	121
% identity	33
NCBI Description	(AJ132261) hypothetical helicase K12H4.8-like protein [Homo sapiens]

Seq. No.	226423
Seq. ID	LIB3166-057-P1-K1-G5
Method	BLASTX
NCBI GI	g3176681
BLAST score	160
E value	6.0e-11
Match length	91
% identity	42

NCBI Description	(AC003671) F17O7.11 [Arabidopsis thaliana]

Seq. No.	226424
Seq. ID	LIB3166-057-P1-K1-G6
Method	BLASTX
NCBI GI	g100226
BLAST score	490
E value	1.0e-49
Match length	115
% identity	83
NCBI Description	hypothetical protein - tomato >gi_19275_emb_CAA78112_ (Z12127) protein of unknown function [Lycopersicon esculentum] >gi_445619_prf__1909366A Leu zipper protein [Lycopersicon esculentum]

Seq. No.	226425
Seq. ID	LIB3166-057-P1-K1-G9
Method	BLASTX
NCBI GI	g2981169
BLAST score	226
E value	1.0e-18
Match length	96
% identity	60
NCBI Description	(AF053077) osmotic stress-induced zinc-finger protein [Nicotiana tabacum]

Seq. No.	226426
Seq. ID	LIB3166-057-P1-K1-H10
Method	BLASTX
NCBI GI	g2454182
BLAST score	306
E value	4.0e-28
Match length	79
% identity	72
NCBI Description	(U80185) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	226427
Seq. ID	LIB3166-057-P1-K1-H4
Method	BLASTX
NCBI GI	g2583130
BLAST score	155
E value	2.0e-10
Match length	114
% identity	32
NCBI Description	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	226428
Seq. ID	LIB3166-057-P1-K1-H5
Method	BLASTX
NCBI GI	g4309742
BLAST score	141
E value	1.0e-08
Match length	53
% identity	45
NCBI Description	(AC006439) putative Rer1 protein [Arabidopsis thaliana]

Seq. No.	226429
Seq. ID	LIB3166-057-P1-K1-H9
Method	BLASTX
NCBI GI	g1076764
BLAST score	274
E value	3.0e-24
Match length	105
% identity	18
NCBI Description	AWJL236 protein - wheat >gi_551214_emb_CAA57135_ (X81370) AWJL236 [Triticum aestivum]

Seq. No.	226430
Seq. ID	LIB3166-058-P1-K1-A1
Method	BLASTX
NCBI GI	g1345970
BLAST score	532
E value	1.0e-54
Match length	112
% identity	83
NCBI Description	OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi_870784 (U25817) omega-3 fatty acid desaturase [Sesamum indicum]

Seq. No.	226431
Seq. ID	LIB3166-058-P1-K1-A2
Method	BLASTX
NCBI GI	g2982459
BLAST score	373
E value	6.0e-36
Match length	99
% identity	73
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	226432
Seq. ID	LIB3166-058-P1-K1-A5
Method	BLASTX
NCBI GI	g2108252
BLAST score	283
E value	2.0e-25
Match length	117
% identity	23
NCBI Description	(Y10228) P-glycoprotein-2 [Arabidopsis thaliana] >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2 [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1_ (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]

Seq. No.	226433
Seq. ID	LIB3166-058-P1-K1-A6
Method	BLASTX
NCBI GI	g3766377
BLAST score	148
E value	2.0e-09
Match length	95
% identity	33
NCBI Description	(AL031907) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	226434
Seq. ID	LIB3166-058-P1-K1-A9
Method	BLASTX
NCBI GI	g2245066
BLAST score	182
E value	1.0e-13
Match length	111
% identity	42
NCBI Description	(Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No.	226435
Seq. ID	LIB3166-058-P1-K1-B12
Method	BLASTX
NCBI GI	g4432835
BLAST score	175
E value	7.0e-13
Match length	52
% identity	58
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	226436
Seq. ID	LIB3166-058-P1-K1-B2
Method	BLASTX
NCBI GI	g3885329
BLAST score	366
E value	4.0e-35
Match length	76
% identity	88
NCBI Description	(AC005623) alien-like protein [Arabidopsis thaliana]

Seq. No.	226437
Seq. ID	LIB3166-058-P1-K1-B3
Method	BLASTX
NCBI GI	g3047125
BLAST score	362
E value	1.0e-34
Match length	116
% identity	65
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	226438
Seq. ID	LIB3166-058-P1-K1-B4
Method	BLASTX
NCBI GI	g4559339
BLAST score	185
E value	6.0e-14
Match length	76
% identity	50
NCBI Description	(AC007087) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	226439
Seq. ID	LIB3166-058-P1-K1-B6
Method	BLASTX
NCBI GI	g602076
BLAST score	567
E value	1.0e-58

Match length	118
% identity	22
NCBI Description	(X77456) pentameric polyubiquitin [Nicotiana tabacum]

Seq. No.	226440
Seq. ID	LIB3166-058-P1-K1-C1
Method	BLASTX
NCBI GI	g3434971
BLAST score	201
E value	9.0e-16
Match length	40
% identity	88
NCBI Description	(AB008105) ethylene responsive element binding factor 3 [Arabidopsis thaliana]

Seq. No.	226441
Seq. ID	LIB3166-058-P1-K1-C10
Method	BLASTX
NCBI GI	g122007
BLAST score	256
E value	3.0e-22
Match length	74
% identity	70
NCBI Description	HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley >gi_20448_emb_CAA37828_ (X53831) H2A histone protein (AA 1 - 149) [Petroselinum crispum]

Seq. No.	226442
Seq. ID	LIB3166-058-P1-K1-C2
Method	BLASTX
NCBI GI	g3790554
BLAST score	140
E value	1.0e-08
Match length	98
% identity	33
NCBI Description	(AF078683) RING-H2 finger protein RHA1a [Arabidopsis thaliana]

Seq. No.	226443
Seq. ID	LIB3166-058-P1-K1-C5
Method	BLASTX
NCBI GI	g3023605
BLAST score	233
E value	3.0e-37
Match length	104
% identity	77
NCBI Description	CYTOCHROME B6 >gi_2224430_dbj_BAA57914_ (AB001684) cytochrome b6 [Chlorella vulgaris]

Seq. No.	226444
Seq. ID	LIB3166-058-P1-K1-C8
Method	BLASTX
NCBI GI	g3668089
BLAST score	308
E value	2.0e-28
Match length	116
% identity	51

NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.	226445
Seq. ID	LIB3166-058-P1-K1-C9
Method	BLASTX
NCBI GI	g1076755
BLAST score	194
E value	6.0e-15
Match length	112
% identity	36
NCBI Description	protein kinase - rice >gi_450300 (L27821) protein kinase [Oryza sativa]
Seq. No.	226446
Seq. ID	LIB3166-058-P1-K1-D1
Method	BLASTX
NCBI GI	g100226
BLAST score	309
E value	2.0e-28
Match length	117
% identity	45
NCBI Description	hypothetical protein - tomato >gi_19275_emb_CAA78112_ (Z12127) protein of unknown function [Lycopersicon esculentum] >gi_445619_prf__1909366A Leu zipper protein [Lycopersicon esculentum]
Seq. No.	226447
Seq. ID	LIB3166-058-P1-K1-D11
Method	BLASTX
NCBI GI	g3763916
BLAST score	249
E value	2.0e-21
Match length	116
% identity	46
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana] >gi_4531439_gb_AAD22124.1_AC006224_6 (AC006224) unknown protein [Arabidopsis thaliana]
Seq. No.	226448
Seq. ID	LIB3166-058-P1-K1-D5
Method	BLASTX
NCBI GI	g3924596
BLAST score	327
E value	1.0e-51
Match length	118
% identity	86
NCBI Description	(AF069442) putative phospho-ser/thr phosphatase [Arabidopsis thaliana]
Seq. No.	226449
Seq. ID	LIB3166-058-P1-K1-D9
Method	BLASTX
NCBI GI	g2827143
BLAST score	576
E value	9.0e-60
Match length	116
% identity	91

NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]
Seq. No.	226450
Seq. ID	LIB3166-058-P1-K1-E1
Method	BLASTX
NCBI GI	g2275217
BLAST score	194
E value	6.0e-15
Match length	75
% identity	45
NCBI Description	(AC002337) chloroplast protein CP12 isolog [Arabidopsis thaliana]
Seq. No.	226451
Seq. ID	LIB3166-058-P1-K1-E11
Method	BLASTX
NCBI GI	g1362093
BLAST score	241
E value	2.0e-20
Match length	85
% identity	62
NCBI Description	hypothetical protein (clone TPP15) - tomato (fragment) >gi_924632 (U20595) unknown [Solanum lycopersicum]
Seq. No.	226452
Seq. ID	LIB3166-058-P1-K1-E2
Method	BLASTX
NCBI GI	g4190952
BLAST score	429
E value	2.0e-42
Match length	110
% identity	71
NCBI Description	(AB022689) similar to hsr203J [Lycopersicon esculentum]
Seq. No.	226453
Seq. ID	LIB3166-058-P1-K1-E9
Method	BLASTX
NCBI GI	g4263712
BLAST score	294
E value	1.0e-26
Match length	77
% identity	70
NCBI Description	(AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]
Seq. No.	226454
Seq. ID	LIB3166-058-P1-K1-F10
Method	BLASTX
NCBI GI	g3033400
BLAST score	556
E value	2.0e-57
Match length	127
% identity	85
NCBI Description	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	226455
Seq. ID	LIB3166-058-P1-K1-F11
Method	BLASTX
NCBI GI	g3549667
BLAST score	219
E value	8.0e-18
Match length	69
% identity	62
NCBI Description	(AL031394) Arabidopsis dynamin-like protein ADL2 [Arabidopsis thaliana]

Seq. No.	226456
Seq. ID	LIB3166-058-P1-K1-F12
Method	BLASTX
NCBI GI	g2245005
BLAST score	170
E value	4.0e-12
Match length	58
% identity	59
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	226457
Seq. ID	LIB3166-058-P1-K1-F4
Method	BLASTX
NCBI GI	g2981169
BLAST score	271
E value	5.0e-24
Match length	104
% identity	52
NCBI Description	(AF053077) osmotic stress-induced zinc-finger protein [Nicotiana tabacum]

Seq. No.	226458
Seq. ID	LIB3166-058-P1-K1-F8
Method	BLASTX
NCBI GI	g1008904
BLAST score	524
E value	1.0e-57
Match length	116
% identity	88
NCBI Description	(L43094) xyloglucan endotransglycosylase [Tropaeolum majus]

Seq. No.	226459
Seq. ID	LIB3166-058-P1-K1-G1
Method	BLASTX
NCBI GI	g2462762
BLAST score	291
E value	2.0e-26
Match length	109
% identity	56
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	226460
Seq. ID	LIB3166-058-P1-K1-G12
Method	BLASTX
NCBI GI	g1076633

BLAST score	430
E value	1.0e-42
Match length	101
% identity	85
NCBI Description	protein kinase NPK5 (EC 2.7.1.-) - common tobacco >gi_496385_dbj_BAA05649_ (D26602) protein kinase [Nicotiana tabacum]

Seq. No.	226461
Seq. ID	LIB3166-058-P1-K1-G2
Method	BLASTX
NCBI GI	g4544443
BLAST score	343
E value	2.0e-32
Match length	119
% identity	62
NCBI Description	(AC006592) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	226462
Seq. ID	LIB3166-058-P1-K1-G3
Method	BLASTX
NCBI GI	g3850816
BLAST score	327
E value	2.0e-30
Match length	61
% identity	93
NCBI Description	(Y18348) U2 snRNP auxiliary factor, small subunit [Oryza sativa]

Seq. No.	226463
Seq. ID	LIB3166-058-P1-K1-G4
Method	BLASTX
NCBI GI	g1730566
BLAST score	440
E value	8.0e-44
Match length	119
% identity	45
NCBI Description	PHYTOCHROME E >gi_1145714 (U39787) phytochrome E [Ipomoea nil]

Seq. No.	226464
Seq. ID	LIB3166-058-P1-K1-G8
Method	BLASTX
NCBI GI	g1871192
BLAST score	145
E value	3.0e-09
Match length	64
% identity	45
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	226465
Seq. ID	LIB3166-058-P1-K1-H10
Method	BLASTX
NCBI GI	g1871192
BLAST score	180

E value	3.0e-13
Match length	115
% identity	39
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No.	226466
Seq. ID	LIB3166-058-P1-K1-H12
Method	BLASTX
NCBI GI	g3281848
BLAST score	334
E value	3.0e-31
Match length	107
% identity	72
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	226467
Seq. ID	LIB3166-058-P1-K1-H2
Method	BLASTX
NCBI GI	g4455364
BLAST score	326
E value	2.0e-30
Match length	94
% identity	66
NCBI Description	(AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No.	226468
Seq. ID	LIB3166-058-P1-K1-H8
Method	BLASTX
NCBI GI	g3759184
BLAST score	462
E value	2.0e-46
Match length	104
% identity	82
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	226469
Seq. ID	LIB3166-059-P1-K1-B12
Method	BLASTX
NCBI GI	g4337025
BLAST score	370
E value	1.0e-35
Match length	88
% identity	77
NCBI Description	(AF123253) AIM1 protein [Arabidopsis thaliana]

Seq. No.	226470
Seq. ID	LIB3166-059-P1-K1-B4
Method	BLASTX
NCBI GI	g2495179
BLAST score	437
E value	1.0e-43
Match length	99
% identity	84
NCBI Description	PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG) (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN

SYNTHASE) >gi_1084340_pir__S50762 hydroxymethylbilane synthase (EC 4.3.1.8) precursor - Arabidopsis thaliana >gi_313150_emb_CAA51941_ (X73535) hydroxymethylbilane synthase [Arabidopsis thaliana] >gi_313838_emb_CAA52061_ (X73839) hydroxymethylbilane synthase [Arabidopsis thaliana]

Seq. No.	226471
Seq. ID	LIB3166-059-P1-K1-C1
Method	BLASTX
NCBI GI	g434759
BLAST score	378
E value	1.0e-36
Match length	96
% identity	72
NCBI Description	(D21163) similar to human elongation factor 2 mRNA (HSEF2). [Homo sapiens]

Seq. No.	226472
Seq. ID	LIB3166-059-P1-K1-C2
Method	BLASTX
NCBI GI	g4008441
BLAST score	204
E value	3.0e-16
Match length	72
% identity	56
NCBI Description	(AL034488) predicted using Genefinder; cDNA EST yk433c6.3 comes from this gene; cDNA EST EMBL:D72601 comes from this gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST yk433c6.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	226473
Seq. ID	LIB3166-059-P1-K1-C3
Method	BLASTX
NCBI GI	g1914685
BLAST score	279
E value	5.0e-25
Match length	60
% identity	87
NCBI Description	(Y12014) RAD23 protein, isoform II [Daucus carota]

Seq. No.	226474
Seq. ID	LIB3166-059-P1-K1-D1
Method	BLASTX
NCBI GI	g2347199
BLAST score	360
E value	2.0e-34
Match length	107
% identity	64
NCBI Description	(AC002338) protein kinase isolog [Arabidopsis thaliana]

Seq. No.	226475
Seq. ID	LIB3166-059-P1-K1-D3
Method	BLASTX
NCBI GI	g2980760
BLAST score	221
E value	4.0e-18

Match length	75
% identity	59
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	226476
Seq. ID	LIB3166-059-P1-K1-E1
Method	BLASTX
NCBI GI	g1170507
BLAST score	337
E value	1.0e-31
Match length	66
% identity	100
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3) >gi_100276_pir__S22579 translation initiation factor eIF-4A - curled-leaved tobacco >gi_19699_emb_CAA43514_ (X61206) nicotiana eukaryotic translation initiation factor 4A [Nicotiana plumbaginifolia]

Seq. No.	226477
Seq. ID	LIB3166-059-P1-K1-F10
Method	BLASTX
NCBI GI	g4539359
BLAST score	161
E value	5.0e-11
Match length	67
% identity	39
NCBI Description	(AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	226478
Seq. ID	LIB3166-059-P1-K1-G10
Method	BLASTX
NCBI GI	g1946220
BLAST score	241
E value	2.0e-20
Match length	120
% identity	62
NCBI Description	(Z71979) kn1-like protein [Malus domestica]

Seq. No.	226479
Seq. ID	LIB3166-059-P1-K1-H5
Method	BLASTX
NCBI GI	g3914002
BLAST score	198
E value	3.0e-19
Match length	73
% identity	77
NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_2935279 (AF033862) Lon protease [Arabidopsis thaliana]

Seq. No.	226480
Seq. ID	LIB3189-001-P1-K1-A1
Method	BLASTX
NCBI GI	g3513727
BLAST score	397
E value	8.0e-39
Match length	99
% identity	81

NCBI Description	(AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	226481
Seq. ID	LIB3189-001-P1-K1-A2
Method	BLASTX
NCBI GI	g3319353
BLAST score	148
E value	1.0e-09
Match length	48
% identity	58
NCBI Description	(AF077407) contains similarity to copper-binding proteins [Arabidopsis thaliana]

Seq. No.	226482
Seq. ID	LIB3189-001-P1-K1-A3
Method	BLASTX
NCBI GI	g3063467
BLAST score	331
E value	4.0e-31
Match length	85
% identity	74
NCBI Description	(AC003981) F22O13.29 [Arabidopsis thaliana]

Seq. No.	226483
Seq. ID	LIB3189-001-P1-K1-A7
Method	BLASTX
NCBI GI	g3176725
BLAST score	189
E value	3.0e-14
Match length	64
% identity	48
NCBI Description	(AC002392) unknown protein [Arabidopsis thaliana]

Seq. No.	226484
Seq. ID	LIB3189-001-P1-K1-A8
Method	BLASTX
NCBI GI	g2370595
BLAST score	196
E value	4.0e-15
Match length	79
% identity	48
NCBI Description	(AJ001414) GTPase activating protein [Yarrowia lipolytica]

Seq. No.	226485
Seq. ID	LIB3189-001-P1-K1-B1
Method	BLASTX
NCBI GI	g1173055
BLAST score	577
E value	8.0e-60
Match length	116
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir__S42497 ribosomal protein L11.e - alfalfa >gi_1076504_pir__S51819

RL5 ribosomal protein - alfalfa >gi_463252_emb_CAA55090_
(X78284) RL5 ribosomal protein [Medicago sativa]

Seq. No.	226486
Seq. ID	LIB3189-001-P1-K1-B10
Method	BLASTX
NCBI GI	g4539292
BLAST score	502
E value	5.0e-51
Match length	108
% identity	86
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	226487
Seq. ID	LIB3189-001-P1-K1-B3
Method	BLASTX
NCBI GI	g1619297
BLAST score	546
E value	4.0e-56
Match length	103
% identity	98
NCBI Description	(Y08490) alpha-tubulin 2 [Hordeum vulgare]

Seq. No.	226488
Seq. ID	LIB3189-001-P1-K1-B5
Method	BLASTX
NCBI GI	g4544399
BLAST score	439
E value	1.0e-43
Match length	128
% identity	65
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	226489
Seq. ID	LIB3189-001-P1-K1-B6
Method	BLASTX
NCBI GI	g3643609
BLAST score	100
E value	1.0e-10
Match length	89
% identity	45
NCBI Description	(AC005395) putative Cys3His zinc finger protein [Arabidopsis thaliana]

Seq. No.	226490
Seq. ID	LIB3189-001-P1-K1-C10
Method	BLASTX
NCBI GI	g3335355
BLAST score	575
E value	1.0e-59
Match length	118
% identity	27
NCBI Description	(AC004512) Match to polyubiquitin DNA gb_L05401 from A. thaliana. Contains insertion of mitochondrial NADH dehydrogenase gb_X82618 and gb_X98301. May be a pseudogene

with an expressed insert. EST gb_AA586248 comes from this region. [Arabi

Seq. No.	226491
Seq. ID	LIB3189-001-P1-K1-C11
Method	BLASTX
NCBI GI	g4126401
BLAST score	392
E value	4.0e-38
Match length	88
% identity	85
NCBI Description	(AB011795) flavanone 3-hydroxylase [Citrus sinensis]

Seq. No.	226492
Seq. ID	LIB3189-001-P1-K1-C12
Method	BLASTX
NCBI GI	g2677830
BLAST score	544
E value	6.0e-56
Match length	115
% identity	93
NCBI Description	(U93168) ribosomal protein L12 [Prunus armeniaca]

Seq. No.	226493
Seq. ID	LIB3189-001-P1-K1-C5
Method	BLASTX
NCBI GI	g1169534
BLAST score	362
E value	1.0e-34
Match length	104
% identity	70
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_542019_pir__S39203 phosphopyruvate hydratase (EC 4.2.1.11) - castor bean >gi_433609_emb_CAA82232_ (Z28386) enolase [Ricinus communis]

Seq. No.	226494
Seq. ID	LIB3189-001-P1-K1-C6
Method	BLASTX
NCBI GI	g629641
BLAST score	299
E value	9.0e-34
Match length	106
% identity	68
NCBI Description	PsHSC71.0 protein - garden pea >gi_1076530_pir__S53500 HSC71.0 protein - garden pea >gi_473217_emb_CAA83548_ (Z32537) PsHSC71.0 [Pisum sativum]

Seq. No.	226495
Seq. ID	LIB3189-001-P1-K1-D10
Method	BLASTX
NCBI GI	g586004
BLAST score	547
E value	3.0e-56
Match length	111
% identity	89

NCBI Description	SUPEROXIDE DISMUTASE [CU-ZN] >gi_421962_pir__S34267 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato >gi_542090_pir__S40404 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato >gi_311971_emb_CAA51654_ (X73139) superoxide dismutase [Ipomoea batatas]

Seq. No.	226496
Seq. ID	LIB3189-001-P1-K1-D11
Method	BLASTX
NCBI GI	g320552
BLAST score	213
E value	4.0e-17
Match length	93
% identity	51
NCBI Description	anthranilate synthase (EC 4.1.3.27) alpha-1 chain - Arabidopsis thaliana

Seq. No.	226497
Seq. ID	LIB3189-001-P1-K1-D2
Method	BLASTX
NCBI GI	g3334115
BLAST score	513
E value	3.0e-52
Match length	103
% identity	97
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

Seq. No.	226498
Seq. ID	LIB3189-001-P1-K1-D3
Method	BLASTX
NCBI GI	g2827548
BLAST score	397
E value	1.0e-38
Match length	127
% identity	55
NCBI Description	(AL021635) cytochrome P450 - like protein [Arabidopsis thaliana]

Seq. No.	226499
Seq. ID	LIB3189-001-P1-K1-D5
Method	BLASTX
NCBI GI	g2811278
BLAST score	238
E value	1.0e-20
Match length	46
% identity	93
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	226500
Seq. ID	LIB3189-001-P1-K1-D7
Method	BLASTX
NCBI GI	g4469015
BLAST score	608
E value	2.0e-63

Match length	131
% identity	92
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	226501
Seq. ID	LIB3189-001-P1-K1-D8
Method	BLASTX
NCBI GI	g2088651
BLAST score	179
E value	4.0e-13
Match length	82
% identity	38
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	226502
Seq. ID	LIB3189-001-P1-K1-E1
Method	BLASTX
NCBI GI	g1076660
BLAST score	231
E value	3.0e-19
Match length	47
% identity	89
NCBI Description	D13F(MYBST1) protein - potato >gi_786426_bbs_159122 (S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes, leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No.	226503
Seq. ID	LIB3189-001-P1-K1-E10
Method	BLASTX
NCBI GI	g1314711
BLAST score	586
E value	7.0e-61
Match length	131
% identity	87
NCBI Description	(U54615) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_3068712 (AF049236) calcium dependent protein kinase [Arabidopsis thaliana]

Seq. No.	226504
Seq. ID	LIB3189-001-P1-K1-E11
Method	BLASTX
NCBI GI	g3882185
BLAST score	194
E value	7.0e-15
Match length	98
% identity	41
NCBI Description	(AB018275) KIAA0732 protein [Homo sapiens]

Seq. No.	226505
Seq. ID	LIB3189-001-P1-K1-E12
Method	BLASTX
NCBI GI	g2058282
BLAST score	288
E value	7.0e-26
Match length	82

% identity	65
NCBI Description	(X97377) atranbp1a [Arabidopsis thaliana]
Seq. No.	226506
Seq. ID	LIB3189-001-P1-K1-E3
Method	BLASTX
NCBI GI	g1076746
BLAST score	463
E value	2.0e-46
Match length	122
% identity	76
NCBI Description	heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]
Seq. No.	226507
Seq. ID	LIB3189-001-P1-K1-E4
Method	BLASTX
NCBI GI	g4455170
BLAST score	145
E value	1.0e-09
Match length	57
% identity	47
NCBI Description	(AL035521) fatty acid elongase-like protein [Arabidopsis thaliana]
Seq. No.	226508
Seq. ID	LIB3189-001-P1-K1-E7
Method	BLASTX
NCBI GI	g3128175
BLAST score	174
E value	2.0e-12
Match length	126
% identity	33
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.	226509
Seq. ID	LIB3189-001-P1-K1-E8
Method	BLASTX
NCBI GI	g1001622
BLAST score	298
E value	4.0e-27
Match length	94
% identity	65
NCBI Description	(D64002) hypothetical protein [Synechocystis sp.]
Seq. No.	226510
Seq. ID	LIB3189-001-P1-K1-E9
Method	BLASTX
NCBI GI	g1350795
BLAST score	186
E value	6.0e-14
Match length	99
% identity	44
NCBI Description	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L24 PRECURSOR (YML24) >gi_1078342_pir__S50921 ribosomal protein YmL24, mitochondrial - yeast (Saccharomyces cerevisiae)

>gi_642285_emb_CAA87814_ (Z47815) ribosomal protein [Saccharomyces cerevisiae]

Seq. No.	226511
Seq. ID	LIB3189-001-P1-K1-F12
Method	BLASTX
NCBI GI	g285741
BLAST score	199
E value	2.0e-15
Match length	123
% identity	40
NCBI Description	(D14550) EDGP precursor [Daucus carota]

Seq. No.	226512
Seq. ID	LIB3189-001-P1-K1-F2
Method	BLASTX
NCBI GI	g3122785
BLAST score	384
E value	8.0e-46
Match length	109
% identity	91
NCBI Description	40S RIBOSOMAL PROTEIN S14 >gi_2565340 (AF026079) ribosomal protein S14 [Lupinus luteus]

Seq. No.	226513
Seq. ID	LIB3189-001-P1-K1-F7
Method	BLASTX
NCBI GI	g4490316
BLAST score	298
E value	4.0e-27
Match length	58
% identity	81
NCBI Description	(AL035678) nucellin-like protein [Arabidopsis thaliana]

Seq. No.	226514
Seq. ID	LIB3189-001-P1-K1-F8
Method	BLASTX
NCBI GI	g1706325
BLAST score	237
E value	5.0e-20
Match length	46
% identity	96
NCBI Description	PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC) >gi_476286 (U07339) pyruvate decarboxylase 1 [Oryza sativa] >gi_1098559 (U26660) pyruvate decarboxylase [Oryza sativa]

Seq. No.	226515
Seq. ID	LIB3189-001-P1-K1-G11
Method	BLASTX
NCBI GI	g3243234
BLAST score	271
E value	7.0e-24
Match length	123
% identity	44
NCBI Description	(AF071477) isoflavone reductase related protein [Pyrus communis]

Seq. No.	226516
Seq. ID	LIB3189-001-P1-K1-H11
Method	BLASTX
NCBI GI	g2832625
BLAST score	401
E value	4.0e-39
Match length	94
% identity	73
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	226517
Seq. ID	LIB3189-001-P1-K1-H4
Method	BLASTX
NCBI GI	g3023190
BLAST score	449
E value	8.0e-45
Match length	110
% identity	81
NCBI Description	14-3-3-LIKE PROTEIN 16R >gi_1888459_emb_CAA72381_ (Y11685) 14-3-3 protein [Solanum tuberosum]

Seq. No.	226518
Seq. ID	LIB3189-001-P1-K1-H6
Method	BLASTX
NCBI GI	g2811278
BLAST score	457
E value	1.0e-45
Match length	126
% identity	70
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	226519
Seq. ID	LIB3189-002-P1-K1-A10
Method	BLASTX
NCBI GI	g3319882
BLAST score	611
E value	8.0e-64
Match length	121
% identity	96
NCBI Description	(AJ004960) elongation factor-1-alpha (EF1-a) [Cicer arietinum]

Seq. No.	226520
Seq. ID	LIB3189-002-P1-K1-A11
Method	BLASTX
NCBI GI	g2431769
BLAST score	234
E value	1.0e-19
Match length	57
% identity	81
NCBI Description	(U62752) acidic ribosomal protein P1a [Zea mays]

Seq. No.	226521
Seq. ID	LIB3189-002-P1-K1-A12
Method	BLASTX
NCBI GI	g3176098
BLAST score	314

E value	5.0e-29
Match length	117
% identity	58
NCBI Description	(Y15036) annexin [Medicago truncatula]

Seq. No.	226522
Seq. ID	LIB3189-002-P1-K1-A2
Method	BLASTX
NCBI GI	g2244732
BLAST score	531
E value	2.0e-54
Match length	105
% identity	99
NCBI Description	(D88413) endo-xyloglucan transferase [Gossypium hirsutum]

Seq. No.	226523
Seq. ID	LIB3189-002-P1-K1-A3
Method	BLASTX
NCBI GI	g127112
BLAST score	311
E value	1.0e-28
Match length	93
% identity	61
NCBI Description	MAK16 PROTEIN >gi_73269_pir__BVBYK6 MAK16 protein - yeast (Saccharomyces cerevisiae) >gi_171880 (J03852) MAK16 protein [Saccharomyces cerevisiae] >gi_595561 (U12980) Mak16p: putative nuclear protein [Saccharomyces cerevisiae]

Seq. No.	226524
Seq. ID	LIB3189-002-P1-K1-A4
Method	BLASTX
NCBI GI	g2829204
BLAST score	330
E value	6.0e-31
Match length	83
% identity	80
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	226525
Seq. ID	LIB3189-002-P1-K1-A5
Method	BLASTX
NCBI GI	g3876865
BLAST score	161
E value	5.0e-11
Match length	73
% identity	40
NCBI Description	(Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No.	226526
Seq. ID	LIB3189-002-P1-K1-A6
Method	BLASTX
NCBI GI	g4469015
BLAST score	484

E value	1.0e-54
Match length	124
% identity	85
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	226527
Seq. ID	LIB3189-002-P1-K1-A9
Method	BLASTX
NCBI GI	g1657855
BLAST score	370
E value	2.0e-35
Match length	104
% identity	65
NCBI Description	(U73216) cold acclimation protein WCOR413 [Triticum aestivum]

Seq. No.	226528
Seq. ID	LIB3189-002-P1-K1-B1
Method	BLASTX
NCBI GI	g115765
BLAST score	395
E value	2.0e-38
Match length	90
% identity	77
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	226529
Seq. ID	LIB3189-002-P1-K1-B11
Method	BLASTX
NCBI GI	g4490316
BLAST score	245
E value	6.0e-21
Match length	48
% identity	81
NCBI Description	(AL035678) nucellin-like protein [Arabidopsis thaliana]

Seq. No.	226530
Seq. ID	LIB3189-002-P1-K1-B3
Method	BLASTX
NCBI GI	g4371290
BLAST score	232
E value	2.0e-19
Match length	98
% identity	48
NCBI Description	(AC006260) unknown protein [Arabidopsis thaliana]

Seq. No.	226531
Seq. ID	LIB3189-002-P1-K1-B6
Method	BLASTX
NCBI GI	g4490310

BLAST score	377
E value	2.0e-36
Match length	123
% identity	63
NCBI Description	(AL035678) somatic embryogenesis receptor-like kinase-like protein [Arabidopsis thaliana]

Seq. No.	226532
Seq. ID	LIB3189-002-P1-K1-B7
Method	BLASTX
NCBI GI	g2129879
BLAST score	245
E value	6.0e-21
Match length	59
% identity	71
NCBI Description	chlorophyll a/b-binding protein type II precursor, photosystem I - garden pea >gi_602359_emb_CAA57492_ (X81962) Type II chlorophyll a/b binding protein from photosystem I [Pisum sativum]

Seq. No.	226533
Seq. ID	LIB3189-002-P1-K1-C12
Method	BLASTX
NCBI GI	g4539308
BLAST score	158
E value	1.0e-10
Match length	39
% identity	74
NCBI Description	(AL049480) possible apospory-associated like protein [Arabidopsis thaliana]

Seq. No.	226534
Seq. ID	LIB3189-002-P1-K1-C2
Method	BLASTX
NCBI GI	g4457219
BLAST score	281
E value	4.0e-25
Match length	99
% identity	65
NCBI Description	(AF127796) acyl carrier protein [Capsicum chinense]

Seq. No.	226535
Seq. ID	LIB3189-002-P1-K1-C4
Method	BLASTX
NCBI GI	g1703375
BLAST score	432
E value	8.0e-43
Match length	89
% identity	97
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]

Seq. No.	226536
Seq. ID	LIB3189-002-P1-K1-C6
Method	BLASTX
NCBI GI	g2827755
BLAST score	406

E value	9.0e-40
Match length	103
% identity	74
NCBI Description	INORGANIC PYROPHOSPHATASE, VACUOLAR (PYROPHOSPHATE PHOSPHOHYDROLASE) (PPASE) >gi_951323 (U31467) pyrophosphatase [Vigna radiata]

Seq. No.	226537
Seq. ID	LIB3189-002-P1-K1-C7
Method	BLASTX
NCBI GI	g1055368
BLAST score	678
E value	1.0e-71
Match length	124
% identity	99
NCBI Description	(U39567) ribulose-1,5-bisphosphate carboxylase small subunit [Glycine max]

Seq. No.	226538
Seq. ID	LIB3189-002-P1-K1-D11
Method	BLASTX
NCBI GI	g4406814
BLAST score	254
E value	5.0e-22
Match length	65
% identity	74
NCBI Description	(AC006201) putative peptidyl-prolyl isomerase [Arabidopsis thaliana]

Seq. No.	226539
Seq. ID	LIB3189-002-P1-K1-D12
Method	BLASTX
NCBI GI	g2832783
BLAST score	481
E value	1.0e-48
Match length	95
% identity	92
NCBI Description	(AJ225806) potassium channel beta subunit [Egeria densa]

Seq. No.	226540
Seq. ID	LIB3189-002-P1-K1-D4
Method	BLASTX
NCBI GI	g1049293
BLAST score	341
E value	4.0e-44
Match length	122
% identity	80
NCBI Description	(U37247) SecY homolog; targetted to the thylakoid membrane; the protein has a chloroplast targetting signal, but the processing site is not known [Arabidopsis thaliana]

Seq. No.	226541
Seq. ID	LIB3189-002-P1-K1-D5
Method	BLASTX
NCBI GI	g4539292
BLAST score	483
E value	8.0e-49

Match length	103
% identity	85
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	226542
Seq. ID	LIB3189-002-P1-K1-E10
Method	BLASTX
NCBI GI	g133940
BLAST score	378
E value	2.0e-36
Match length	87
% identity	90
NCBI Description	40S RIBOSOMAL PROTEIN S3A (S1A) >gi_70851_pir__R3XL3A ribosomal protein S3a - African clawed frog >gi_65091_emb_CAA40592_ (X57322) ribosomal protein S1a [Xenopus laevis]

Seq. No.	226543
Seq. ID	LIB3189-002-P1-K1-E11
Method	BLASTX
NCBI GI	g3831440
BLAST score	212
E value	5.0e-17
Match length	86
% identity	47
NCBI Description	(AC005819) putative cytochrome P450 [Arabidopsis thaliana] >gi_4415946_gb_AAD20176_ (AC006418) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	226544
Seq. ID	LIB3189-002-P1-K1-E3
Method	BLASTX
NCBI GI	g3249113
BLAST score	270
E value	8.0e-24
Match length	102
% identity	50
NCBI Description	(AC003114) Strong similarity to kinesin homolog IG002P16.12 gb_2191180 from A. thaliana BAC gb_AF007270. [Arabidopsis thaliana]

Seq. No.	226545
Seq. ID	LIB3189-002-P1-K1-E4
Method	BLASTX
NCBI GI	g3249113
BLAST score	239
E value	3.0e-20
Match length	105
% identity	47
NCBI Description	(AC003114) Strong similarity to kinesin homolog IG002P16.12 gb_2191180 from A. thaliana BAC gb_AF007270. [Arabidopsis thaliana]

Seq. No.	226546
Seq. ID	LIB3189-002-P1-K1-E5
Method	BLASTX